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Catalogue of Gene Symbols for Wheat

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PREFACE

This 2013 edition of the Catalogue of Gene Symbols for Wheat represents 45 years of curation of wheat genetic information which began with my appointment as Curator at the Third International Wheat Genetics Symposium held in Canberra, Australia, in 1968. Prior to that time there was a reference catalogue of 17 pages {047} published in Agronomy Journal. The current Catalogue exceeds 400 pages of information and references.

The objective of this Catalogue is to have a document that is helpful to a wide range of people, from ‘coal-face’ researchers to extension workers, and even farmers. Different sections of the Catalogue were prepared in different ways and a major challenge for our Japanese colleagues has been to continue to evolve the database as new information became available and as older material became less relevant. Consensus maps are not yet adequately integrated with the Catalogue. As we adapt to the increasing universality of genetics across species, we must not lose track of our agricultural background and the fact that our main target organism is polyploid wheat. Farmers grow wheat!

Annual supplements continue to be published in Annual Wheat Newsletter as well as displayed on the GrainGenes and Komugi websites. In the future it may be possible to update the entire database on an annual basis. I acknowledge the contributions of past members of the curation team, especially Drs Yukiko Yamazaki, Gary Hart, Mike Gale and Katrien Devos, as well as others, who from time to time helped with sectional revisions. Curators tend to do their best work on sections with which they are most familiar. In order to encompass the full breadth of wheat genetics and to present data in the best way, the suggestions and advice of all wheat workers are appreciated and suggested revision to any section are always welcome. I thank the University of Sydney and the Director of the Plant Breeding Institute, Professor Peter Sharp, for allowing me to continue to work in an honorary capacity.

My usual request for advice on the Catalogue (your catalogue!) is as imperative as in the past. Please advise omissions, errors, typos so we can fix them and your suggestions on better ways to provide and display wheat genetics information will always be welcome.

I would especially like to acknowledge and thank Dr Yukiko Yamazaki the tremendous effort in developing and maintaining the MacGene database and for provided the online updates over the past 14 years. Dr Yamazaki will be stepping down from that responsibility following this meeting.

R.A. McIntosh
September, 2013

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I Gene Nomenclature

1. Recommended Rules for Gene Symbolization in Wheat

Adapted from the International Rules of Genetic Nomenclature and compiled by R.A. McIntosh;approved at the 4th IWGS

1.1. In naming hereditary factors, the use of languages of higher internationality should be given preference.

1.2. Symbols of hereditary factors, derived from their original names, should be written in italics, or in Roman letters of distinctive type.

1.3. Whenever unambiguous, the name and symbol of a dominant should begin with a capital letter and those of a recessive with a small letter (see also special rules for symbolizing biochemical and DNA loci and host:pathogen/pest systems).

1.4. All letters and numbers used in symbolization should be written on one line; as far as possible no superscripts or subscripts should be used.

1.5. The plus sign (+) will not be used in symbolization of hereditary factors in wheat.

1.6. Two or more genes having phenotypically similar effects should be designated by a common basic symbol. Non-allelic loci (mimics, polymeric genes, etc.) will be designated in accordance with two procedures:
(i) in sequential polymeric series where an Arabic numeral immediately follows the gene symbol; e.g., *Sr9*.
(ii) in orthologous sets where the basic symbol is followed by a hyphen ("-") followed by the locus designation taking the form of the accepted genome symbol and a homoeologous set number represented by an Arabic numeral; e.g., *Adh-A1* designates the A-genome member of the first *Adh* set. Different alleles, or alleles of independent mutational origin, are designated by a lower-case Roman letter following the locus number designation; e.g., *Sr9a, Adh-Ala.* (See also guidelines for nomenclature of biochemical and DNA loci).

1.7. Temporary symbol designations: Where linkage data are not available, provision has been made for temporary symbols. These shall consist of the basic symbol followed by an abbreviation for the line or stock and an Arabic number referring to the gene; e.g., *SrFr1*, *SrFr2*, etc., refer to two genes for reaction to *Puccinia graminis* in cultivar Federation. It is recommended that official records of temporary designations be kept, but it is not essential that subsequent numbers from other laboratories (e.g., *SrFr3*) be checked against earlier numbers either phenotypically or genetically.

1.8. Inhibitors, suppressors, and enhancers are designated by the symbols *I, Su,* and *En,* or by *i, su,* and *en* if they are recessive, followed by a space and the symbol of the allele affected.

1.9. In wheat and related species, linkage groups and corresponding chromosomes are designated by an Arabic numeral (1-7) followed by genome designated by a capital Roman letter; i.e., for hexaploid wheat of group *aestivum* (Morris and Sears {1038}), 1A-7D. This system supersedes the original designations using Roman numerals; i.e., I-XXI. The designations for homoeologous group 4 chromosomes of wheat are as agreed at Workshop I, 7th International Wheat Genetics Symposium, Cambridge, UK (see Proceedings, Miller TE & Koebner RMD eds. pp. 1205-1211); that is, the previously designated chromosome 4A was redesignated 4B and the previous 4B was redesignated 4A. Consequently, the former 4AS became 4BS and the former 4AL is 4BL. Likewise, the former 4BS and 4BL were redesignated 4AS and 4AL, respectively. Chinese Spring is accepted as having the standard chromosome arrangement. Chromosome arms (or telocentric chromosome derivatives) are designated S (short), L (long), on the basis of relative arm length within the chromosome. In the case of equal arms they are arbitrarily designated S or L on the basis of homoeology with the short or long arms of the other chromosomes of their homoeologous group (see Workshop I Proceedings of the 7th International Wheat Genetics Symposium).

1.10. Genetic formulae may be written as fractions, with the maternal alleles given first or above. Each fraction corresponds to a single linkage group.

1.11. Chromosomal aberrations should be indicated by the abbreviations Df for deficiency, Dp for duplication, In for inversion, T for translocation, and Tp for transposition. In wheat there are a number of genes derived from related species by introgression. Such genes in different instances reside at different locations. One location may be taken as standard. Other locations will be considered as transpositions relative to a designated standard. When a gene does not reside in its standard chromosome position, the new chromosome designation may be given in brackets following the gene designation; e.g., Hp (Tp 6D) refers to a line carrying the introgressed "hairy neck" gene on chromosome 6D instead of 4B which is taken as standard. Alternatively, the chromosome involved may be described as a translocation. Guidelines for the description of translocated chromosomes both within wheat, and between wheat and alien chromosomes are provided in {705}.

1.12. The zygotic number of chromosomes is indicated by 2n, the gametic number by n and the basic number by x.

1.13. Symbols for extra-chromosomal factors should be enclosed within brackets and precede the genetic formula.

2. Guidelines for Nomenclature of Biochemical Molecular Loci in Wheat and Related Species

Developed by G.E. Hart and M.D. Gale {515} and approved at the 7th IWGS

2.1 **Biochemical nomenclature**: Biochemical nomenclature should be in accordance with the rules of the Joint Commission of Biochemical Nomenclature (JCBN) of the International Union of Pure and Applied Chemistry. The nomenclature recommended by the JCBN is published periodically in major international biochemical journals, such as the Journal of Biological Chemistry and the European Journal of Biochemistry. Also, for enzymes, the publication Enzy me Nomenclature {035,036} may be consulted. Enzymes and other macromolecules have both formal and trivial names. The formal name should be given the first time a macromolecule is mentioned in a publication; the trivial name or an abbreviated name may be used subsequently. For example, ADH is the commonly used abbreviation for aliphatic alcohol dehydrogenase (E.C.1.1.1.1; Alcohol: NAD+oxidoreductase).

2.2 Symbols for gene loci and alleles

2.2.1 *Basic symbol*: The basic symbol for a gene locus should consist of a two-, three-, or fourletter abbreviation of the trivial name of the enzyme, protein, or other macromolecule affected. The initial letter should be a capital and all characters in the symbol should be italicised.

2.2.2 *Loci specifying the structure of similar macromolecules*: Non-allelic gene loci that specify the structure of similar non-enzymatic proteins, of enzymes that catalyse the same or similar reactions, or of similar RNA molecules should be assigned the same basic symbol. The remainder of the symbol for each such locus should be formulated in accordance with one or the other of two procedures, depending upon whether or not evidence is available to assign the locus to an homologous set.

2.2.2.1 Loci that are members of an orthologous set. The basic symbol should be followed by a hyphen (-), the accepted symbol for the genome to which the locus belongs and an homologous set number in the form of an Arabic numeral. For example, *Adh-A1*, *Adh-B1*, *Adh-D1* and *Adh-E1* designate the A-, B-, D-, and E- genome members, respectively, of the first-designated homologous set of aliphatic alcohol dehydrogenase structural gene loci. Identification of a minimum of two members of a set is required to use this nomenclature.

2.2.2.2 Other loci. In the absence of evidence to assign loci to an homologous set, they should be designated in sequential series by a common basic symbol followed immediately by an Arabic numeral. If evidence to assign the loci to an homologous set is obtained subsequently, the loci should be re-designated in accordance with the procedures in section 2.2.2.1.

Rye loci should be designated in accordance with these procedures (see {1448}). For barley loci, the procedures described in section 2.2.2.1 should be used when designation of a locus as a member of an homologous set of Triticeae loci is desired; otherwise, barley genetic nomenclature should be employed. Thus, for example, *Adh-H1* and *Adh-R1* designate the H- and R- genome members, respectively, of the *Adh-1* set of loci.

Evidence regarding phylogenetic relationships among structural genes may be obtained by comparative studies of (1) nucleotide sequences and other molecular properties of genes, (2) physical and/or biochemical properties of gene products, and (3) intra-chromosomal map positions and/or physical locations of genes in homoeologous chromosomes or segments. Criteria for determining whether or not gene loci that encode isozymes are homologous and, for homologous gene loci, whether they belong to the same or different homologous sets, are described in {512}. Most of the criteria are also applicable to nonenzymatic proteins. The evidence that is the basis for designating gene loci as members of an homologous set should be stated in the publication in which symbols for the loci are proposed.

2.2.3 *Alleles*: Different alleles are designated by a lower case italic letter following the locus designation. For example, *a-Amy-A1a* and *a-Amy-A1b* are two alleles of the A genome *a-Amy-1* locus. One strain should be designated the prototype strain for each allele discovered, since variation that has not been detected by the methods used may be present within each allelic class. Currently, Chinese Spring should be the prototype for allele 'a'. If an apparently identical allele in other strains is found by new methods to be different from that in the prototype strain, it should be assigned a new lower case italic letter and a prototype strain designated. This system allows the orderly assignment of symbols to newly-identified alleles and allows ready comparisons of new variants with previously reported variants.

2.2.4 Haplotypes Alleles are based on phenotype. Haplotypes refer to DNA sequences of unspecified length within alleles, or anonymous DNA; for example, incomplete gene sequences, open treading frames, and may include variable upstream and downstream regions. Haplotypes designated sequentially within alleles should be specific to particular projects or publications.

2.3. Gene complexes

Gene complexes, also called compound loci, consist of a number of functionally related genes that are genetically closely linked. Whether composed of a few or many genes, a gene complex should be assigned one symbol, in accordance with the procedures described in section 2.2. The individual genes that compose gene complexes may be designated by adding a hyphen (-) and an Arabic numeral to the locus designation. For example, *Glu-A1-1* and *Glu-B1-1* designate, respectively, the A- and B- genome genes that encode the x-type glutenin-1 proteins while *Glu-A1-2* and *Glu-B1-2* designate, respectively, the A- and B-genome genes that encode the y-type glutenin-1 proteins. Different alleles of genes that are components of gene complexes may be designated following the system described in section 2.2.2, but with the lower-case italic letter following the gene designation rather than the locus designation. For example, *Glu-A1-1a* designates the Chinese Spring A genome allele that encodes the x- type glutenin-1 protein. Triticeae enzyme and protein gene loci are commonly initially identified and assigned designations based on studies of aneuploid strains that lack and/or contain extra copies of whole chromosomes or telosomes. Consequently, evidence may be obtained for the production of two or more similar enzyme or protein promoters by one chromosome arm without genetic evidence as to whether or not the promoters are the products of one gene, of different genes that are members of a gene complex, or of two or more genes that are not members of one gene complex. In these situations, only one locus designation for similar proteins or enzymes should be assigned to a chromosome arm until recombination evidence indicates otherwise.

2.4. Phenotype symbols

The basic symbol for a macromolecule should be identical to the basic symbol for the locus or loci that encode the macromolecule (see Section 2.2.1) except that each letter in the symbol should be a capital Roman letter. For a macromolecule encoded by the members of a homologous set of loci, the phenotype symbol should consist of the basic symbol followed by a hyphen (-) and the same Arabic numeral as is contained in the genotype symbol. For example, the products of the *Adh-1* set of gene loci are designated ADH-1.

2.5. Symbols for DNA markers and alleles

This section describes nomenclature for genetic markers that are detected at the DNA level, including those detected by hybridization with DNA probes [e.g., RFLPs (restriction-fragment-length polymorphisms)) and by amplification with primers [e.g. RAPDs (random-amplified-polymorphic DNAs) and STSs (sequence-tagged sites, including loci detected with sequenced RFLP clones, sequenced RAPDs and clones containing micro- and mini-satellites).

2.5.1 *Basic symbol*: The basic symbol for DNA markers of unknown function should be 'X'

2.5.1.1 Locus symbols : The ‘X’ should be followed by a laboratory designator (see section 8), a number that identifies the probe or primer(s) used to detect the locus, a hyphen (-), and the symbol for the chromosome in which the locus is located. The laboratory designator and number should be assigned by the laboratory that produced the clone or sequenced the primer(s) or, if that laboratory chooses not to do so, then by the laboratory that mapped the locus. The number should consist of one or more Arabic numerals and should begin with a numeral other than zero, i.e. numbers such as ‘01', ‘001', and ‘002' should not be used. The number assigned to a probe need bear no relationship to the name of the clone used to produce the probe and, likewise, the number assigned to a primer(s) need bear no relationship to any name that may have been assigned to the prime r(s). The letters in the laboratory designator should be lower-case and all characters in the locus symbol should be italicized. For example, *Xpsr119-7A* designates an RFLP locus located in chromosome 7A detected with *P*lant *S*cience *R*esearch probe 119 of the John Innes Centre. DNA markers detected in different chromosomes with the same probe or primer(s) should be assigned the same symbol except for the chromosome designation. For example, *Xpsr119-7D* and *Xpsr119-4A* designate other loci detected with probe 119.

2.5.1.2 Locus symbols for DNA markers detected with ‘known-function’ probes or with primers that amplify genes: The locus symbols for RFLP markers of unknown function that are detected with ‘known-function’ probes may include, in parentheses following the probe number, a symbol for the gene from which the probe was obtained. For example, *Xpsr804(Sbp)-3A* designates a chromosome 3A locus detected with a sedoheptulose-1,7-bisphosphatase gene probe. Likewise, when the primers used to amplify a DNA marker of unknown-function are of sufficient length and similarity to a known gene to amplify the gene, the DNA-marker symbol may include the gene symbol in parentheses following the number assigned to the primers. For genes for which the Commission on Plant Gene Nomenclature has assigned mnemonic designations, the set number and other numbers assigned by the Commission may also be included inside the parentheses immediately after the gene symbol.

2.5.2 *'Known-function' DNA Markers*: Loci that are detected with a DNA probe or DNA primers and whose function has been demonstrated should be designated with a symbol that indicates the function of the locus, as described in either Section 2 or in the Recommended Rules for Gene Symbolization in Wheat. It must be emphasized, however, that some clones and primers are likely to detect both loci whose function is known (proven, for example, by a segregational test against allelic forms of a gene encoding a protein) and additional loci of unknown (i.e. unproven) function (either pseudogenes or unrelated loci whose sequence homology to the probe or primers is sufficient to allow detection by it). In this case, the two types of loci require different nomenclature, namely, that described in Section 2, or in the Recommended Rules for Gene Symbolization in Wheat and in Section 2.5.1, respectively.

2.5.3 *Duplicate DNA-marker loci*: DNA markers located in the same chromosome that hybridize with the same probe or that are amplified with the same primer(s) should be assigned the same symbol except for the addition of a period and an Arabic numeral immediately after the chromosome designation. For example, *Xpsr933-2A.1* and *Xpsr933-2A.2* designate duplicate loci located in 2A that are detected with probe PSR933. As when two or more enzyme or protein promoters are produced by one chromosome arm, multiple DNA fragments from one chromosome arm that hybridize to one probe or that are amplified by one pair of primers (or by one primer) should be assigned to only one locus until recombination evidence indicates otherwise. As noted in Section 2.5.1, DNA markers located in different chromosomes that hybridize with the same probe or that are amplified with the same primer(s) should be assigned the same symbol except for the chromosome designation.

2.5.4 *Allele symbols*: Alleles should be designated as outlined in Section 2.2.3 with the exception that restriction-enzyme-specific alleles, e.g. RFLP- and indirect-STS alleles, should be designated with the name of the restriction enzyme followed by a lower-case letter. For example, *Xtam-5A-HindIIIa* denotes an allele detected with *Hind*III. Where possible, Chinese Spring should be the prototype for allele ‘a’. When a double-digest is used to detect an allele, both restriction enzymes should be listed, separated by a slash.

The name and source of the probe or primer(s) and the length(s) of the DNA fragment(s) detected normally should be stated in the first publication describing an allele.

2.5.5 *Abbreviation of locus and allele symbols*: The chromosome designation is an integral part of the locus symbol for DNA markers. Nevertheless, on chromosome maps and in a limited number of other contexts, the chromosome designation and the hyphen preceding it may be omitted. For example, *Xpsr35-3A* may be abbreviated as *Xpsr35* on a map of chromosome 3A, *Xpsr933-2A.1* and *Xpsr933-2A.2* may be abbreviated as *Xpsr933.1* and *Xpsr933.2*, respectively, on a map of 2A, and *Xpsr804(Sbp)-3A* may be abbreviated as *Xpsr804(Sbp)* on a map of 3A. Also the chromosome designation and the hyphen preceding it may be omitted on chromosome maps from the symbols for intrachromosomally duplicated loci that are detected with a ‘known-function’ probe (or with primers that amplify a gene) but that do not include a gene symbol. For example, if *Xtam200-1A.1* and *Xtam200-1A.2* were the symbols for duplicated loci detected with a ‘known-function’ clone designated TAM200, the symbols could be abbreviated as *Xtam200.1* and *Xtam200.2* respectively, on a map of 1A.

Finally, *Xbgl485(Ger)-4D.2* may be abbreviated on a map of 4D by omission of the hyphen, the chromosome designation and the period, i.e. as *Xbgl485(Ger)2*. In some contexts it will also be possible to abbreviate the symbols for alleles as, for example, *BamH1b*, or even simply *b*.

2.5.6 *Laboratory designators*: Laboratory designators should consist of from two to four and preferably three letters. When used in locus symbols, all of the letters should be lowercase and italicized (see Section 6.1.2).

Laboratory designators should be chosen carefully to insure that they differ both from those used by other laboratories and from those that compose gene symbols. As an aid in this regard, a list of laboratory designators that have appeared in the literature is available electronically via the Internet Gopher from host greengenes.cit.cornell.edu, port 70, menu "Grains files to browse" / "Reserved Laboratory Designators for DNA Probes, Primers and Markers".

Laboratories that are investigating DNA markers in different species and/or of different types, e.g., RFLPs, STS, and RAPDs, may choose to use more than one designator. For example, oat and barley cDNA clones isolated at Cornell University have been designated with the prefixes CDO and BCD, respectively, and *cdo* and *bcd*, respectively, are appropriately used as laboratory designators in symbols for loci detected with these clones.

Likewise, *tam* and *txs*, respectively, are being used as laboratory designators in symbols for loci detected with wheat and sorghum DNA clones isolated at Texas A&M University, and the John Innes Centre is using *psr* and *psm* as laboratory designators in the symbols for DNA markers detected with wheat and millet probes, respectively, and *psp* for wheat PCR markers.

2.5.7 *Clone designations*: Clone designations should minimally identify the type of vector, the species from which the cloned DNA was obtained, and the source laboratory and cloned DNA, in that order. p = plasmid, l = lambda, c = cosmid, and m = M13 should be used to identify vectors. Initials of the species name, e.g., TA = *Triticum aestivum* and SC = *Secale cereale*, should be used to designate the source of the cloned DNA and a unique letter-number combination chosen by the source laboratory should be used to designate the source laboratory and the cloned DNA.

3. Symbols for Loci and Alleles Controlling Quantitative Characters

Developed largely by G.E. Hart and approved at the 8th IWGS

3.1 Genes identified by segregational analysis: Symbols for loci and alleles controlling quantitative characters that are identified by segregational analysis should be in accord with the Recommended Rules for Gene Symbolization in Wheat.

3.2 Quantitative trait loci (QTLs): QTLs are loci controlling quantitative characters whose allelic classes do not exhibit discontinuous variation or clear segregational patterns. They are identified by association with one or more linked markers.

3.2.1 *Basic symbol*: The basic symbol for QTLs should be '*Q*'.

3.2.2. *Locus symbols*: The '*Q*' should be followed by a trait designator, a period, a laboratory designator (see Section 8), a hyphen (-) and the symbol for the chromosome in which the QTL is located. The trait designator should consist of no more than four and preferably three letters, the first of which is capitalized. Different QTLs for the same trait that are identified in one chromosome should be assigned the same symbol except for the addition of a period and an Arabic numeral after the chromosome designation. All characters in the locus symbol should be italicized. For example, *QYld.psr-7B.*1 and *QYld.psr-7B.2* would designate two yield QTLs identified in chromosome 7B by the John Innes Centre. On a map of 7B, these could be abbreviated as *QYld.psr.1* and *QYld.psr.2*. R_2 values,where given, indicate the proportion of variation explained by the QTL.

3.2.3 *Allele symbols*: Alleles at QTL loci should be designated by a lower-case italic letter following the locus designation.

4. AFLP: Amplified Fragment Length Polymorphism

Developed largely by M.D. Gale and approved at the 8th IWGS

A nomenclature proposal for AFLP loci has been received from Marc Zabeau at Keygene with the format '*XxyzAN1N2N3*, where '*X*' is the usual symbol for a DNA marker of unknown function; 'xyz' is the usual laboratory designator (e.g., *kg* for Keygene); A is a single upper-case letter denoting the rare-cutter enzyme used, e.g., P for *PstI*, etc.; N1 and N2 are two-digit numbers identifying standard one, two or three base-pair extensions (standard lists will be provided by Keygene); and N3 is a three-digit number corresponding to the molecular weight of the fragment.

The foregoing should be considered only as a proposal at this time as no AFLPs are listed in the catalogue. Comments regarding the proposal are welcomed and should be sent to the authors.

5. Single Nucleotide Polymorphism

Submitted for approval at the 11IWGS

Single nucleotide polymorphisms (SNP) will be designated using the Genebank accession number followed by a dash (-) and the nucleotide position. For example, *BF482680-541-4B* will represent an SNP at position 541in the alpha tubulin gene on chromosome 4B. Where appropriate, *SNP* and *-4B* can be deleted.

6. Guidelines for Nomenclature of Genes for Reaction to Pathogenic Diseases and Pests

Approved at the 4th IWGS

6.1. Symbol: All genes for resistance (low reaction) will be designated with a capital letter, even though they behave as recessive alleles. Moreover, the dominance of individual alleles may vary with the environment, the genetic background and the particular culture of the pathogen. Symbols for disease/pest-reaction genes are used by people of many disciplines, and since they are frequently communicated verbally, dominance relationships are not clear. Those alleles initially designated with a lower-case letter have tended to be miswritten with a capital. For example, the usually recessive resistance allele *Sr17* was initially designated *sr17* but its presentation in some reports was confusing.

6.2. Pleiotrophic genes: Where no recombination occurs between genes conferring resistance to more than one pathogen, the gene(s) segment shall be designated separately for each disease; e.g. *Pm1, Sr15* and *Lr20.*

6.3. Alleles: Where recombination occurs between two closely linked factors for reaction to a pathogen, the recombined 'allele' may be designated as a combination of the separate alleles; e.g. the recombined 'allele' obtained by combining *Lr14a* and *Lr14b* was designated as *Lr14ab*. The decision as to whether a designation should be as a combination or as separate genes shall be at the discretion of particular workers. A maximum value of 1 crossover unit for designation as an 'allele' is suggested.

Although the need to consider uniform symbolization of corresponding genes in pathogens is recognized, no recommendations are proposed.

7. Organisation of the Catalogue

7.1. Data listing

Information is given in the following order, where possible:

1. Gene symbol, with principal reference to the particular gene or gene symbol in parenthesis.
2. Synonyms (with reference(s) in parenthesis).
3. Chromo some and chromosome-arm location, if known, with references in parenthesis.
4. Stocks carrying the particular gene in order of presentation.

i: = Near-isogenic stocks, with number of backcrosses indicated.
s: = Homologous chromosome-substitution stocks, with number of backcrosses indicated.
tr: = Translocation line of common wheat.
v: = Cultivaral hexaploid stocks in increasing order of genetic complexity.
v2 : = Cultivaral hexaploid stocks with two or more genes affecting the trait.
ad: = Alien chromosome addition line.
su: = Alien chromosome substitution line.
itv: = Near-isogenic tetraploid stocks.
tv: = Tetraploid stocks.
tv2: = Tetraploid stocks with two or more genes affecting the trait.
idv: = Near-isogenic line of diploid wheat.
dv: = Diploid stocks.
al: = Alien species.
ma: = Reference to mapping information involving agronomic and morphological traits and molecular markers under gene entries will generally be restricted to values of less than 10 cM. Values higher than this would be of less use in genetics and plant breeding and, in any case, should be available from the genetic linkage section of the Catalogue or from genetic maps. Higher values will be used in the case of flanking markers.
c: = Cloning details and gene structure

Where more than a single gene affecting a character is listed, e.g., Gabo *D3* {645} under *D1*, the reference refers to the literature source reporting *D1* in Gabo, and not necessarily to *D3*. Abbreviations: CS =Chinese Spring; Tc = Thatcher.

7.2 DNA Markers

See 'Genetic nomenclature proposal' in Introduction for a proposal for the naming of AFLP loci.

The following list catalogues DNA-marker loci that (1) were detected either by Southern hybridization of DNA restriction fragments or as sequence-tagged-sites by amplification of DNA fragments with primers and (2) have been localized to specific wheat chromosomes. The formal listings of the 5S-RNA or 18S-5.8S-26S rRNA (Nor) loci are included elsewhere in the catalogue. No attempt has been made to list orthologous loci in related species, although many have been identified {e.g., 1329,1330}. In addition we list genes that appear on consensus maps prepared by Dr R. Appels and various colleagues.

The nomenclature used is that originally published in the 1994 Supplement, except for some loci detected with 'known-function' clones for which other nomenclature has been used in the publications cited. The reference(s) that follow the locus symbols designate the publication(s) in which the chromosomal locations or map positions of the loci were first reported. References that are in parentheses { } contain the listed locus symbol. Temporary symbols for a few DNA markers detected with known-function DNA probes are marked with an asterisk, *, ; these are temporary, pending assignment of the laboratory designator.' Synonyms are listed in parentheses [ ] in the second column. Where symbols were assigned by the curators to comply with nomenclature guidelines the same reference numbers follow the gene symbol and the synonym. Other chromosomes bearing markers detected with the same probe or the same primers are indicated in parentheses after the probe or the primers. To permit flexibility in using the database, each homoeologous group is bracketed separately.

Three revisions were made in the organization of the DNA Markers section, as follows:

1. Markers in homoeologous chromosome groups 4, 5 and 7 (with the exception of those in T. monococcum chromosome 4Am; see #2 below) are listed in groups composed of loci located in homoeologous segments. The groups include the six classical homoeologous arm groups, namely, 4S (4AL:4BS:4DS), 4L (4AS:4BL:4DL), 5S (5AS:5BS:5DS), 5L (5AL:5BL:5DL), 7S (7AS:7BS:7DS) and 7L (7AL:7BL:7DL), and five new groups, 4AL:4BL:4DL, 5AL:4BL:4DL,

4AL:5BL:5DL, 7BS:5BL:7DS, and 7AS:4AL:7DS. Evidence is not available regarding the correct group location for a few of the markers listed in groups 4S, 4L, and 7S; a double asterisk (**) after the locus reference identifies these markers.

2. Markers in T. monococcum $4A^m$ are listed separately (under $4A^mS$, $4A^mL$, or $4A^m$), due to the several rearrangements that distinguish 4A and $4A^m$.
3. Superscripts appended to locus references designate the species in which loci were analyzed, as follows,

'1'	*T. aestivum,*
'2'	*T. turgidum,*
'3'	*T. monococcum,*
'4'	*Ae. tauschii*, and
'5'	Species hybrid,

with the exception that the superscript is omitted for markers studied only in *T. aestivum*.

'a' Designates primer pairs that identify loci that cap the genetic maps. The forward primer is a degenerate telomeric sequence and the reverse primer is a specific sequence. Each primer combination identified multiple loci; however, only telomeric *(Tel)* loci are included {888}.
'b' Designates loci detected by hybridization with DNA clones whose sequences are largely homologous with known gene in the EMBL database (1392).

STS's from RFLP clones: Certain STS markers are listed using sequences from previously listed RFLP clones. The convention adopted is to add a 'p' to the laboratory designator. The 'References' to PCR markers refer, however, to the paper(s) which reported the first chromosomal location detected by this PCR marker.

Order of presentation: Gene, synonym, map location (approximate distance in cM from the terminal end of the short arm), probe, all known locations in homoeologous groups. In the output files genes appear in alphabetical order with locus numbers in ascending order.

Note: Due to limitations with the database, Greek symbols were converted to words or Roman letters (alpha or a, beta or b, etc). For author names with accents or special letters, the most similar Roman letter
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9. Summary Table

Summary Table 1. Symbols with 'known function'

The term set(s) indicates that the loci have been grouped into one or (more than one) orthologous (='homoeologous') sets.

Symbol		Trait
Aadh-1,2	sets	Aromatic alcohol dehydrogenase
a-Amy1,2	sets	Alpha-amylase
Aco-1,2	sets	Aconitase
Acph-1	sets	Acid phosphatase
Adh-1	sets	Alcohol dehydrogenase (Aliphatic)
Adk-1	sets	Adenylate kinase
AhasL-1	sets	Acetohydroxyacid synthase (EC 4.1.3.18)
Alt1,2		Aluminium Tolerance
Amp-1,2,3	sets	Aminopeptidase
An5		Anthocyanin Pigmentation
Apd1,2		Hybrid Weakness
Ar1		Alkylresocinols Content in Grain
B1,2		Awnedness
Ba1,2		Blue Aleurone
b-Amy-1	sets	Beta-amylase
Bdv1,2,3		Reaction to Barley Yellow Dwarf Virus
b-Gls		Beta-glucosidase
bh-1	sets	Gross Morphology: Spike characteristics
Bla1		Glume Colour and Awn Colour
Bls1,2,3,4,5		Reaction to *Xanthomonas campestris* pv. *undulosa*
Bo1,2,3		Boron Tolerance
Br1,4		Brittle Rachis
Bt1 to 10		Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*
C		Club/Compact spike
Cat-B1		Catalase
cc		Glume Colour and Awn Colour
Cdu1		Cadmium Uptake
Ce		Copper Efficiency
Ch1,2		Hybrid Weakness
Cmc1,2,3,4		Resistance to Colonization by *Eriophyes tulipae* (*Aceria tulipae*)
Cn-1	sets	Chlorophyll Abnormalities
co1,2		Corroded
Cre1 to 8		Reaction to *Heterodera avenae* Woll.
Crr		Reaction to *Cochliobolus sativus* Ito & Kurib.
Cs1,2		Hybrid Weakness
D1,2,3,4		Grass-Clump Dwarfness/Grass Dwarfness
Dfq1		Herbicide Response
Dip-1	sets	Dipeptidase
Dn1 to 9		Reaction to *Diuraphis noxia* (Mordvilko)
Dreb-1	sets	Abiotic Stress Responses:Dehydrin-response Element Binding Factors
Ep-1	sets	Endopeptidase
Ep-1		Endopeptidase
Est1 to 9	sets	Esterase
F3h-1	sets	Flavone 3-hydroxylase (EC 1.14.11.9)
Fe1,2		Iron Deficiency
Fhb1,2,3,4,5		Reaction to *Fusarium* spp.
Fhs1,2		Reaction to *Fusarium* spp.
Fr1,2		Frost Resistance
Gai1,2,3		Gibberellic Acid Response (insensitivity)
Gb1 to 7		Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)
Gc1,2,3		Gametocidal Genes
Gli-1,2,3,5,6,7	sets	Gliadins
Gllu-A3y		Glutenins

Summary Table 1 (Cont.). Symbols with ‘known function’

Symbol		Trait
Glo-1	sets	Salt soluble globulins
Glu-1,3	sets	Glutenins
Glu-1-1	sets	Glutenins
Glu-1-2	sets	Glutenins
Got-1,2,3	sets	Glutamic oxaloacetic transaminase
Gpc-1		Grain protein content
Gpi-1	sets	Glucosephosphate isomerase
Gpt-1	sets	Glutamate-pyruvate transaminase
Gsp-1	sets	Grain softness protein
H_{WGRC4}		Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)
Ha		Grain Hardness/Endosperm Texture
Hd		Awnedness
Hg		Hairy Glume
Hk-1,2	sets	Hexokinase
Hl1,2		Hairy Leaf
Hn		Hairy Node/Pubescent Node
Hp		Hairy Neck/Pubescent Peduncle
Hs		Hairy Leaf Sheath
HstH1-1,2	sets	Histone H1 Proteins
Hyd-1,2	sets	Carotenoid beta-hydroxylase (non-heme di-iron type)
Ibf-1	sets	Iodine binding factor
Igc1		Gametocidal Genes
Iha-1		Inhibitors (dimeric) of heterologous alpha-amylases
Imi1,2,3		Herbicide Response
Isa-1	sets	Inhibitors of alpha-amylase and subtilisin
Iso-1		Isoamylase 1
Iw1,2,3		Glaucousness (Waxiness/Glossiness)
Kb1,2,3,4,5,6		Reaction to *Tilletia indica* Mitra
Ki		Pollen Killer
Kna1		Response to Salinity
Kr1,2,3,4		Crossability with Rye and *Hordeum* and *Aegilops* spp.
Lec-1	sets	Lectins
lg1,2,3		Lack of Ligules
lm		Lesion Mimicry
Lpx-1,2,3	sets	Lipoxygenase
Lr1 to 71		Reaction to *Puccinia triticina*
Ltn1,2		Leaf Tip Necrosis
ltp		Meiotic Characters
Lvl1		Grain Quality Parameters
Mal-1	sets	Malic enzyme
Mdh-1,2,3,4	sets	Malate dehydrogenase
Mg5		Reaction to *Magnaporthe grisea* (Herbert) Barr
Ml		Reaction to *Blumeria graminis* DC.
ms1,2,3,4,5		Male Sterility
Nax1,2		Response to Salinity
Ndh-1,2,3,4	sets	NADH dehydrogenase
Ne1,2		Hybrid Weakness
Ner1,2		Hybrid Weakness
Nor1 to 10	sets	Nucleolus Organizer Regions
Nra		Nitrate Reductase Activity
Or		Osmoregulation
P1,2		Gross Morphology: Spike characteristics
Pa		Hairy/Pubescent Auricles
Pan1,2		Anthocyanin Pigmentation
Pbc		Glume Colour and Awn Colour
Pc1,2		Anthocyanin Pigmentation
Pch1,2,3		Reaction to *Tapesia yallundae*. (Anomorph: *Pseudocerosporella herpotrichoides* (Fron) Deighton)

Summary Table 1 (Cont.). Symbols with ‘known function’

Symbol		Trait
Pde-1	sets	Phosphodiesterase
Pdi-1	sets	Protein disulfide isomerase (EC 5.3.4.1)
Per-1,2,3,4,5	sets	Peroxidase
Pg		Anthocyanin Pigmentation
Pgd1		Phosphogluconate dehydrogenase
PgdR1,2		Phosphogluconate dehydrogenase
Pgip1,2		Polygalacturonase-inhibiting proteins
Pgm-1	sets	Phosphoglucomutase
Ph1,2		Meiotic Characters
Phs1		Dormancy (Seed)
Pina1	sets	Puroindolines and grain softness protein
Pinb1	sets	Puroindolines and grain softness protein
Pis1		Gross Morphology: Spike characteristics
Plb		Anthocyanin Pigmentation
Pln		Sterol Esterification in Kernels - Synthesis of b-Sitosterol Esters
Pm1 to 47		Reaction to *Blumeria graminis* DC.
Pp1,2,3		Anthocyanin Pigmentation
Ppd-1,2	sets	Response to Photoperiod
Ppo-1	sets	Polyphenol oxidase
Pro1,2		Grain protein content
Psy2-1	sets	Phytoene synthase
Pur-1	sets	Lipopurothionins
Q		Squarehead/spelt
R-1	sets	Red Grain Colour
Ra1,2,3		Anthocyanin Pigmentation
Rc1	sets	Anthocyanin Pigmentation
Rf1 to 6		Restorers for Cytoplasmic Male Sterility
Rg-1,3	sets	Glume Colour and Awn Colour
Rht1 to 22	sets	Height
Rkn1,2,3		Reaction to *Meloidogyne* spp.
Rlnn1		Reaction to *Pratylenchus* spp.
Rmg1,2,3,4		Reaction to *Magnaporthe grisea* (Herbert) Barr
5S-Rna-1,2	sets	5S Ribosomal RNA-1,2
Rot1		Reaction to *Rhizoctonia* spp.
S1,2	sets	Sphaerococcum
Sa1		Reaction to *Sitobion avenae*
Sb1		Reaction to *Bipolaris sorokiniana*
SbeI1,2		Starch branching enzyme I
SbeII		Starch branching enzyme II
Sbm1		Reaction to Soil-Borne Cereal Mosaic Virus
sc		Seedling Leaf Chlorosis
scs		Nuclear-Cytoplasmic Compatability Enhancers
Sd1,2		Gametocidal Genes
Sgp-1,2,3	sets	Starch granule proteins
Shw		Male Sterility
Si-1,2	sets	Subtilisin inhibition
Skdh-1	sets	Shikimate dehydrogenase
Sm1		Reaction to *Sitodiplosis mosellana* (Gehin)
Snb1,2,3		Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano)
Snn1,2,3,4		Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano)
Sod-1	sets	Superoxide dismutase
Sog		Soft Glumes
Spa-1	sets	Endosperm-specific wheat basic region leucine zipper (bZIP) factor storage activator
Sr1 to 57		Reaction to *Puccinia graminis* Pers.
Srp-1	sets	Serine protease inhibitors

Summary Table 1 (Cont.). Symbols with ‘known function’

Symbol		**Trait**
SsI-1	sets	Starch synthase
SsII-1	sets	Starch synthase
Stb1 to 18		Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter
Su1		Herbicide Response
SuLr23		Reaction to *Puccinia triticina*
SuPm8		Reaction to *Blumeria graminis* DC.
TaCwi-A1		Yield and Yield Components
TaGW2-6A		Yield and Yield Components
Tc1,2,3		Phenol Colour Reaction of Kernels
Tg1,2		Tenacious Glumes
Ti-1,2	sets	Trypsin inhibition
tin1,2,3		Tiller Inhibition
Tpi-1,2	sets	Triosephosphate isomerase
Tri-1	sets	Other endosperm storage proteins
Tsc1,2		Reaction to *Pyrenophora tritici-repentis* (anomorph: *Drechlera tritici*-repentis)
Tsn1,2		Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano)
Tsr1 to 6		Reaction to *Pyrenophora tritici-repentis* (anomorph: *Drechlera tritici*-repentis)
Ut1,2,3,4		Reaction to *Ustilago tritici* (Pers.) Rostrup
V1,2		Chlorophyll Abnormalities
vg		Variegated Red Grain Colour
Vgw		Temperature-Sensitive Winter Variegation
Vi		Restorers for Cytoplasmic Male Sterility
Vil-1,2,3		Response to Vernalization
Vp-1	sets	Dormancy (Seed)
Vrn1,2,3,5	sets	Response to Vernalization
W1,2		Glaucousness (Waxiness/Glossiness)
wptms1,2		Male Sterility
Ws		Glaucousness (Waxiness/Glossiness)
Wsm1,2,3		Reaction to Wheat Streak Mosaic Virus
Wsp-1	sets	Water soluble proteins
Wss1		Reaction to Wheat Spindle Streak Mosaic Bymovirus (WSSMV)
wtms1		Male Sterility
Wx-1	sets	Waxy proteins
X		Basic symbol for DNA markers
Ym		Reaction to Wheat Yellow Mosaic Virus
Yr1 to 53		Reaction to *Puccinia striiformis* Westend.
Zds-1	sets	Zeta-carotene desaturase

Summary Table 2. Chromosomal locations of wheat genes that are known to be members of orthologous sets of Triticeae genes.

GENOME A		**GENOME B**		**GENOME D**	
Chromosome		**Chromosome**		**Chromosome**	
Arm	***Gene***	**Arm**	***Gene***	**Arm**	***Gene***
1AS	*Gli-A1*	1BS	*Gli-B1*	1DS	*Gli-D1*
	Gli-A3		*Gli-B3*		
	Gli-A5		*Gli-B5*		
	Gli-A6				
					Gli-A7
	Glo-A1		*Glo-B1*		*Glo-D1*
			Glu-B2		
	Glu-A3		*Glu-B3*		*Glu-D3*
	Gpi-A1		*Gpi-B1*		*Gpi-D1*
	Gpt-A1		*Gpt-B1*		*Gpt-D1*
			Hk-B1		*Hk-D1*
	Nor-A1		*Nor-B1*		
	Nor-A9				
			Per-B1		*Per-D1*
	Rg-A1		*Rg-B1*		
			Si-B2		*Si-D2*
	5S-Rrna-A1		*5S-Rrna-B1*		*5S-Rrna-D1*
	Tri-A1				*Tri-D1*
1AL	*Eps-1A*^{m}	1BL		1DL	
	Glu-A1		*Glu-B1*		*Glu-D1*
	Lec-A1				*Lec-D1*
	Mdh-A1		*Mdh-B1*		*Mdh-D1*
			Nor-B6		
	Pur-A1		*Pur-B1*		*Pur-D1*
	Spa-A1		*Spa-B1*		*Spa-D1*
1A		1B		1D	*Glu-D4*
			Lec-B1		
	Rg-A1c			1DL,1DS	*Rg-D1*
2AS	*bh-A1*	2BS		2DS	*bh-D1*
	Est-A6		*Est-B6*		*Est-D6*
	Per-A2		*Per-B2*		*Per-D2*
					Per-D5
			Ppd-B1a		*Ppd-D1a*
2AL		2BL		2DL	*Acph-D2*
	Est-A7		*Est-B7*		*Est-D7*
	F3h-A1		*F3h-B1*		*F3h-D1*
			F3h-B2		
	Hyd-A1		*Hyd-B1*		*Hyd-D1*
	Isa-A1		*Isa-B1*		*Isa-D1*
	Ppd-A1				
	Ppo-A1				
	Sod-A1		*Sod-B1*		*Sod-D1*
					Zds-D1
2A		2B	*Gc1-B1a*	2D	

Summary Table 2. (Cont.) : Chromosomal locations of wheat genes that are known to be members of orthologous sets of Triticeae genes.

GENOME A		**GENOME B**		**GENOME D**	
Chromosome		**Chromosome**		**Chromosome**	
Arm	***Gene***	**Arm**	***Gene***	**Arm**	***Gene***
			Gc1-B1b		
	Zds-A1		*Zds-B1*		
3AS	*Br-A1*	3BS	*Br-B1*	3DS	*Br-D1*
	Est-A1		*Est-B1*		*Est-D1*
	Est-A9		*Est-B9*		*Est-D9*
			Hk-B2		*Hk-D2*
			Iha-B1.1		*Iha-D1*
			Iha-B1.2		
	Ndh-A4		*Ndh-B4*		
					Nor-D8
	Pde-A1		*Pde-B1*		*Pde-D1*
	Tpi-A1		*Tpi-B1*		*Tpi-D1*
			Yrns-B1		
3AL		3BL	*Dreb-B1*	3DL	
	Eps-A1a				
			Est-B2		*Est-D2*
	Est-A5		*Est-B5*		*Est-D5*
	Est-A8		*Est-B8*		*Est-D8*
	Got-A3		*Got-B3*		*Got-D3*
	Mal-A1		*Mal-B1*		*Mal-D1*
	Ndh-A3		*Ndh-B3*		*Ndh-D3*
	Per-A3		*Per-B3*		*Per-D3*
	R-A1		*R-B1*		*R-D1*
	Vp-A1				*Vp-D1*
					Vp-D1a
3A	*Dreb-A1*	3B		3D	*Dreb-D1*
	Est-A2				
	Hk-A2				
	S-A1		*S-B1*		*S-D1*
4AS	*Acph-A1*	4BS		4DS	
			Adh-B1		*Adh-D1*
			Amp-B2		*Amp-D2*
			Lpx-B1		*Lpx-D1*
			Lpx-B1.1		
			Ndh-B1		*Ndh-D1*
			Pdi-D1		*Pdi-B1*
					Pgm-D1
			Rht-B1		*Rht-D1*
					Rht-D1b
4AL		4BL	*Aco-B2*	4DL	*Aco-D2*
			Acph-B1		*Acph-D1*
	Adh-A1				
			b-Amy-B1		*b-Amy-D1*
	Amp-A2				

Summary Table 2. **(Cont.) :** Chromosomal locations of wheat genes that are known to be members of orthologous sets of Triticeae genes.

GENOME A		GENOME B		GENOME D	
Chromosome		**Chromosome**		**Chromosome**	
Arm	***Gene***	**Arm**	***Gene***	**Arm**	***Gene***
			Cat-B1		
			Hyd-B2		*Hyd-D2*
	Lpx-A1				
	Lpx-A3				
	Ndh-A1				
	Pdi-A1				
	Per-B4				
	Pgm-A1				
	Wx-B1				
4A		4B	*Lpx-B1.2*	4D	
		4B	*Lpx-B3*		
5AS		5BS		5DS	*Gsp-D1*
	Mdh-A3		*Mdh-B3*		*Mdh-D3*
	Nor-A3				*Nor-D3*
	Nor-A10				*Pina-D1*
	Pina-A^{m}1				*Pinb-D1*
	Pinb-A^{m}1				*Pinb-D1b*
	5S-Rrna-A2		*5S-Rrna-B2*		*5S-Rrna-D2*
	Skdh-A1		*Skdh-B1*		*Skdh-D1*
5AL	*Aadh-A1*	5BL	*Aadh-B1*	5DL	*Aadh-D1*
	Aco-A2				
	b-Amy-A1				
			Eps-5BL.1		
			Eps-5BL.2		
	HstH1-A1		*HstH1-B1*		*HstH1-D1*
	HstH1-A2		*HstH1-B2*		*HstH1-D2*
	Hyd-A2				
	Ibf-A1		*Ibf-B1*		*Ibf-D1*
	Lpx-A2		*Lpx-B2*		*Lpx-D2*
	Nor-A7				
	Srp-A1		*Srp-B1*		*Srp-D1*
	Ti-A2		*Ti-B2*		*Ti-D2*
	Tpi-A2		*Tpi-B2*		*Tpi-D2*
	Vrn-A1a		*Vrn-B1a*		*Vrn-D1*
					Vrn-D5a
5A	*Gsp-A1*	5B	*Gsp-B1*	5D	
	Psy2-A1		*Psy2-B1*		
6AS	*Amp-A1*	6BS	*Amp-B1*	6DS	*Amp-D1*
			Ep-B2		

Summary Table 2. **(Cont.) :** Chromosomal locations of wheat genes that are known to be members of orthologous sets of Triticeae genes.

GENOME A		**GENOME B**		**GENOME D**	
Chromosome		**Chromosome**		**Chromosome**	
Arm	***Gene***	**Arm**	***Gene***	**Arm**	***Gene***
	Gli-A2		*Gli-B2*		*Gli-D2*
	Got-A1		*Got-B1*		*Got-D1*
			Gpc-B1b		
			Nor-B2		
6AL	*Aadh-A2*	6BL	*Aadh-B2*	6DL	*Aadh-D2*
	a-Amy-A1		*a-Amy-B1*		*a-Amy-D1*
	Aco-A1		*Aco-B1*		*Aco-D1*
	AhasL-A1		*AhasL-B1*		*AhasL-D1*
	Dip-A1		*Dip-B1*		*Dip-D1*
	Est-A4		*Est-B4*		*Est-D4*
	Got-A2		*Got-B2*		*Got-D2*
6A		6B	*Nor-B2a*	6D	
7AS	*Amp-A3*	7BS		7DS	
			Est-B3		*Est-D3*
					Ndh-D2
	Per-A4				*Per-D4*
			Pgip-B1		*Pgip-D1*
			Ppd-B2		
	Rc-A1a		*Rc-B1a*		*Rc-D1a*
	Sgp-A1		*Sgp-B1*		*Sgp-D1*
	Sgp-A3		*Sgp-B3*		*Sgp-D3*
			Vrn-B3		
	Wx-A1				*Wx-D1*
7AL	*a-Amy-A2*	7BL	*a-Amy-B2*	7DL	*a-Amy-D2*
	Adk-A1		*Adk-B1*		*Adk-D1*
	Cn-A1		*Cn-B1*		*Cn-D1*
	Ep-A1		*Ep-B1*		*Ep-D1*
					Nor-D4
	Psy1-A1		*Psy1-B1*		*Psy1-D1*
	Wsp-A1		*Wsp-B1*		*Wsp-D1*
7A		7B		7D	*Glu-D5*
	Ndh-A2				
	SsI-A1		*SsI-B1*		*SsI-D1*
	SsII-A1		*SsII-B1*		*SsII-D1*

Morphological and Physiological Traits

Note: Levy and Feldman {797} studied the inheritance of more than 20 morphological and biochemical traits in crosses of four *T. dicoccoides* lines and *T. durum*. Similarly, Kuspira *et al.* {744} studied 12 qualitative characters in *T. monococcum*. The symbols applied to the characters examined in these studies are not being reserved and listed in the Catalogue. However, both studies should serve as bases for future work.

In a large study of 6 agronomic traits in a AC Karma/87E03-S2B1 DH population, 24 QTLs were detected in 12 chromosomes {10434}.

1. Gross Morphology: Spike characteristics

Major hexaploid wheat types are categorized into groups with respect to three major gene pairs; viz. *Q, C* and *S1* {1038}.

1. Common wheat *Q c S1* v: vulgare group.
2. Club wheat *Q C S1* v: compactum group.
3. Shot wheat *Q c s1* v: sphaerococcum group.
4. Spelt wheat *q c S1 and q C S1* v: spelta group (including vavilovi).

The majority of hexaploid wheat stocks are already, or can be readily, classified into these groups.

Diploid wheat is assumed to be *q*. Durum and carthlicum groups have the genotype *Q* {1049}.

1.1. Squarehead/spelt

Q{881}. [*k*{1550}]. 5AL{1293}. **bin:** 5AL-17{10541}. **v:** Common wheats. CS; Iranian spelts{0140}. **tv:** *T. turgidum* ssp. *carthlicum, durum* and *polonicum*{10457}. **ma:** Complete linkage with cDNA clone PtAq22{0127}; *Q* was cloned and shown to have similarity to *AtAP2* (APETALA 2) ,the *Q* allele was more abundantly transcribed than the *q* allele transcription factors{10457}.

q{881}. [*K*{1550}]. **v:** Macha wheats; European spelt wheats{10457}; *vavilovi* wheats. **s:** CS*8/White Spring Spelt 5A{1048}. **tv:** *T. turgidum* ssp. *dicoccum, dicoccoides*{10457}. **ma:** Cent - *Xrsq805(Empb)-5A* - 4.6 cM - *Q* - 4.3 cM - *Xpsr370-5A*{419}; *Q* was physically mapped in 5AL, fraction length 0.87, bracketed by deletions 5AL-7 and 5AL-23{446}; *Q* - 9.3 cM - *Xpsr370-5A*{9903}.

The speltoid phenotype of at least some spelts may be caused by genes at other loci {0140}. Fine mapping of the 20 cM region possessing Q and delimited by deletions 5AL -7 and -23 is reported in {0324}.

1.2. Club/Compact spike

C{1517}. [*Cd*{047}]. 2D{1192}.2DL{1192,1517}.probably 2DL{10578}. **bin:** C-2DS1 - C-2DL3, markers flanking *C* were located on either side of the centromere{10578}. **i:** S-615*11/Elgin{1500}. **s:** CS*6/Poso 2D{1304}; CS*5/Red Egyptian 2D{1304}. **v:** Club wheats; Coda{10578}; Corrigin{10578}. **ma:** Coda / Brundage: *Xwmc144-2D* - 1 cM - *C* - 8 cM - *Xwmc18-2D*; Corrigin / CS (tauschii 2D): *Xwmc245-2D* - 1 cM - *Xcfd16-2D / Xgwm358-2D / C / Xcfd-2D* - 1 cM - *Xbarc145-2D*{10578}.

QTL: Six QTLs for spike compactness were detected in Courtot/Chinese Spring but only 4 on chromosome arms 1AL, 2BS, 2DS and 4AS were consistent for at least two years{0114} .

Two additional QTLs for spike compactness were detected in Courtot/Chinese Spring {10080} on chromosome arms 5DL (*QCp.icf-5D*) and 6DL (*QCp.icf-6D*). Markers *Xcfd26-5D* and *Xcfd38-6D* explained 13.6% and 12.2% of the variance in spike compactness, respectively {10080}.

Although gene C may be present in some forms of group *macha* {1447} and *spelta* {0623}, it is not universally present. Tsunewaki {1500} found that compact spike in one form was controlled by polygenes.

C may be orthologous to gene *Sog* for soft glumes on chromosome 2A^{m} {10578}

Tetraploid wheat: A compact spike gene *C*^{17648} in mutant line MA 17648 wad located in chromosome 5AL {10541}. *Xbarc319-5A* - 9.7 cM - *C*^{17648} - 24.8 cM - *Xgwm179-5A* {10541}. *C*^{17648} was distal to the *Q* locus {10541}.

1.3. Sphaerococcum

The naturally-occurring sphaerococcum gene in chromosome 3D and various mutant alleles conferring a similar phenotype form a homoeologous series. The sphaerococcoid alleles are either recessive or incompletely dominant. All three mapped loci are closely linked to the respective centromeres {0030}. The "a" alleles are allocated to Chinese Spring or "normal" wheats.

s2. Partially dominant{1286}. [*sp2*{1286}]. **v:** Sphaerococcoid wheats. "*Sphaerococcum simulator*"{1286}.

Sphaerococcum-like tetraploid wheats were reported{122,475,1282,1286}, but comparisons between them, or with *s2*, were not made. Whereas Schmidt & Johnson{1281} reported a single recessive controlling the sphaerococcum character in tetraploid wheat, Joppa{621} using the same stock found that two recessive genes were necessary to produce this phenotype.

S-A1{0029}. 3A{0056}. **v:** CS{0029}.

S-A1a{0029}. **v:** CS{0029}; common wheats{0029}.

S-A1b{0029}. [*S3*{0056}]. **v:** MS 1453{0056}. **ma:** *Xgwm2-3A*(S) - 5.1 cM - *S-A1* - 6.6 cM - *Xgwm720-3A*(L){0030}.

S-B1{0029}. 3B{0030}. **v:** CS{0029}.

S-B1a{0029}. **v:** CS{0029}; common wheats{0029}.

S-B1b{0029}. [*S2*{0030},*s*^{16219}{10541}]. **v:** MSK 2452{0056}; MSK 2454{0056}. **tv:** MA 16219{10541}. **ma:** *Xgwm685-3B*(S) - 4.2 cM - *S-B1* - 0.5 cM - *Xgwm566/Xgwm845/*cent{0030}.

S-D1{0029}. 3D{1292,0030}.3DS{1193,1194}.3DL{692}. **v:** CS{0029}.

S-D1a{0029}. **v:** CS{0029}; common wheats{0029}.

S-D1b{0029}. [*s1, sp1*{1286}]. **i:** S-615*11/*T. sphaerococcum* var. *rotundatum*{1500}. **s:** CS*7/*T. sphaerococcum rubiginosum* 3D{1304}. **v:** Sphaerococcum wheats{0029}; *T. antiquorum* K056397 & K56398{10234}.

S-D1c{0029}. [*S1*{0056}]. **v:** MS 3287{0056}. **ma:** *Xgdm72-3D*(S) - 8.0 cM - *S-D1* - 2.9 cM - *Xgwm456-3D/*cent{0030}.

1.4. Branched spike

Synonyms: branched spike, four-rowed spike, multi-rowed spike, supernumerary spikelet, tetrastichon spikelet.

Branched spike and multi-rowed spike are phenotypes involving the presence of supernumerary spikelets, or the presence of additional spikelets at rachis nodes. A similar condition in rye is known as 'monstrosum ear' (reviewed in {10637}). Genetic studies of branched spike in tetraploid and hexaploid wheats indicate that the phenotype is recessive, involves one or more genes, and is strongly influenced by environmental effects.

Comparative genetic studies suggest an orthologous gene series in homoeologous group 2 {10637}.

bh-A1{10637}. [*bh*{665}]. 2AS{665}. **tv:** PI 349056{665}.

bh-D1{10637}. [*mrs*{10637}]. 2DS{10637}. **bin:** 2DS-5 0.47-1.0{10637}. **v:** Ra1{10637}; Ruc163-1-02 = Ra1 / ZGK242-81{10637}; RUC163167-1-02 = Alana /3/Ra1/ZGK242-82 // Ra1{10637}. **ma:** *Xwmc453-2D / bh-D1* - 7.8 cM - *Xgwm988-2D*{10637}; *Xwwm484-2D* - 3.3 cM - *Xwmc453-2D/bh-D1* - 3 cM - *Xwgm988-2D*{10637}.

Ra1 is a mutant stock maintained at the NI Vavilov Research Institute of Plant Industry, St Petersburg, Russia.

A chromosome 2B gene of minor effect was identified {9907} . In a monosomic analysis of the hexaploid line LYB with supernumerary spikelets, Peng et al. {9908} located recessive genes in chromosomes 2A and 4A that promote the development of supernumerary spikelets and a gene in chromosome 2D that prevents their expression.

bh-R1{10637}. [*mo*{10637}]. 2R{10637}. **al:** *S. cereale* D40{10637}. **ma:** *Xrms056-2R* - 15.7 cM - *bh-R1* - 10.7 cM - *Xcfe209-2R*{10637}.

1.5. Elongated glume

Elongated glume is the phenotype associated with the polonicum group of tetraploid wheats. Expression in hexaploid wheat is much reduced compared with tetraploids. Matsumura {911} reported linkage of gene *P* and a gene for red coleoptiles implicating chromosomes 7A or 7B. A different gene was subsequently located in chromosome 7B {9990}.

P1. [*P*{911},*Eg*{922},*P-A*^{pol}*1*{0254},*P-A*^{pet}*1*{0254}]. 7AL{922,1547}.7A or 7B (based on linkage of 0.2 with a gene for red coleoptile){922}. **i:** Saratovskaya29*8//Novsibirskaya 67*2/*T. polonicum*{922,0066}. **itv:** P-LD222 = LD222*11/*T. turgidum* var *polonicum*{1546,1547}. **tv:** *T. polonicum*{0254}; *T. petropavlovskyi*{0254}. **ma:** *Xgwm260* - 7A(S) - 2.3 cM - *P1* - 5.6 cM - *Xgwm1083-7A*(L){0254}; *Xgwm890* -7A - 2.1 cM - *P1*{0254}; *Xgwm260-7AS* - 2.3 cM - *P1*^{pol} - 5.6 cM - *Xgwm1083-7AL* {0254}; *Xgwm890-7AS* - 2.1 cM - *P1*^{pet} {0254}.

Note: The loci determining elongated glumes in *T. turanicum* and *T. durum* conv. *falcatum* are not homoeologous to the *P* loci in the centromeric region of the group 7 chromosomes{0254}.

P2{9990}. 7BL{9990}. **itv:** LD222*7/*T. ispahanicum*{9990}. **tv:** *T. ispahanicum*{9990}.

According to {0254} the loci of *T. polonicum*, *T. petropavlovsky* and *T. isphanicum* are allelic ('homoeoallelic') whereas other workers had claimed genes in the first two forms were not allelic. Wang et al. {0254} however concluded that loci bearing alleles for elongated glumes in *T. turanicum* and *T. durum* conv. *falcatum* were not part of the above series.

1.6. Ear length

QEl.ocs-5A.1{0068}. 5AL{0068}. **v:** CS(*T. spelta* 5A)/CS(Cappelle-Desprez 5A) RI mapping population{9903}. **ma:** Associated with *Xbcd9*-5A{0068}.

1.7. Multi-gynoecium

Synonym: three pistils (TP).

This trait describes a dominant phenotype consisting of 3 kernels within each wheat floret; that is, the flower consists of 3 separate ovaries, 3 anthers and 2 lodicules.

Pis1{10636}. 2DL{10636}. **bin:** C-2DL3-0.49{10636}. **v:** TP Mutant{10636}. **ma:** *Xgwm539-2D* - 17.6 cM - *Pis1* - 19.5 cM *Xgwm349-2D*{10636}.

2. Accumulation of Abscisic Acid

A QTL was mapped on 5AL between *Xpsr575-5A* {proximal} and *Xpsr426-5A* {distal} {1180}.

3. Alkylresocinols Content in Grain

Ar1{0281}. High alkylresocinols content is dominant {0281}. 5AL{0281}. **tv:** Langdon{0281}.

ar1{0281}. **tv:** Ardente{0281}; this cultivar has a low content compared to all tested durum and common wheats{0281}.

4. Aluminium Tolerance

Alt1{234}. **v:** ET3 = Carazinho/4*Egret{234}.

alt1{234}. **v:** ES3 = Carazinho/4*Egret{234}.

Alt2{848}. [*Alt*$_{BH}${1213}]. 4DL{848}. **su:** *T. turgidum* cv. Langdon 4D(4B){848}. **v:** BH1146{1213,0115}; IAC-24{0115}; IAC-60{0115}; 13 induced mutants of Anahuac{0115}. **ma:** *Alt2* was mapped to a 4 cM interval flanked by *Xpsr914-4D* and *Xpsr1051-4D*{848}; on a consensus 4B-4D map of *T. aestivum; Alt2* - 1.1 cM - *Xbcd1230-4D*{1213}; *Alt2* cosegregated with *Xbcd1230-4D* and fell within the interval *Xgdm125-4D* - 4.8 cM - *Alt2 -1.1 cM* - *Xpsr914-4D*{0248}.

Malate transporter *Almt-D1* gene (GenBank AB081803) is completely linked to aluminium tolerance in chromosome arm 4DL between SSR markers *Xwmc48b* and *Xwmc331* in a similar region to *Alt2* {10285}. *Almt1* transgenic expression in barley conferred and Al-activated efflux of malate with properties similar to those of *Al*-tolerant wheat {10286}.

Allelic variation at the promoter of *Almt-D1* is associated with differences in Al tolerance. Molecular and pedigree analysis suggest that Al resistance in modern wheat germplasm is derived from several independent sources {10532}.

QTL: Atlas 66/Century: A QTL in the region *Xdgm125-4DL* - *Xwmc331-4DL* accounted for nearly 50% of the phenotypic variation in root growth rate in hydroponic solution {10265}. An Al-activated malate transporter (*LMT1*) was earlier mapped to the same location {10266}. Atlas 66 (insensitive)/Chisholm (sensitive) RILs: One QTL, located in chromosome 4DL, corresponded to ALMT1 and accounted for 50% of the phenotypic variation {10483}. A second QTL was located on 3BL(R^2 = 0.11); nearest marker *Xbarc164-3B* {10483}. Both QTLs were verified in Atlas/Century {10483}.

FSW (A1 tolerant) / ND35 (A1 sensitive): 3 QTLs for tolerance, *Qalt.pser-4DL* co-segregating with *Xups4*, a marker for the promoter of the *ALMT1* gene, *Qalt.pser-3BL* (*Xbarc164-3B* - *Xbarc344-3B*) and *Qalt.pser-2A* (*Xgwm515-2A* - *Xgwm296-2A*) {10605}.

In D genome introgression lines of Chinese Spring a major QTL was located in the interval *Xgwm125-4D* - *Xgwm976-4D*, R^2=0.31 {10598}, probably coinciding with *Alt2*. A second QTL from CS, *Qalt*$_{cs}$*ipk-3B*, R^2=0.49, occurred in interval *Xgwm1029-3BL* - *Xgwm1005-3BL* in a CS / CS (Synthetic 3B) population {10598}.

5. Anthocyanin Pigmentation

The genetic determinants of anthocyanin pigmentation of various tissues are largely located in homoeologous regions in group 7, viz. 7BS (*Rc-B1, Pc-B1, Plb-B1, Pls-B1*) and 7DS (*Rc-D1, Pc-d1, Plb-D1*), and appear to be linked clusters rather than multiple alleles on each chromosome {10700}. Their relationship with genes for purple auricle and purple pericarp are still not clear.

5.1. Purple anthers.

A single, dominant factor was reported {1326}.

Pan1{921}. 7DS{921}. **v:** Ilyitchevka{921}; Mironovskaya 808{921}; Novosibirskaya 67{921}; Pyrothrix 28{921}; Saratovskaya 210{921}; Strela{921}; Ukrainka{921}. **tv:** *T. polonicum*{921}.

Pan2. 7AS{9959}. **tv:** *T. turgidum* ssp. *dicoccoides* acc. MG4343{9959}. **ma:** *Pan2* - 9.2 cM - *Rc1* - 12.2 cM - *Xutv1267-7A* (proximal){9959}.

5.2. Purple/Red auricles. Purple leaf base/sheath

For review see {1641}.

Melz and Thiele {983} described a "purple leaf base" phenotype where anthocyanin pigmentation extended to the leaf base as well as auricles. Purple leaf base was expressed only when pigmentation occurred in the coleoptiles.

An5{983}. 5R{983}.

Pc/Pls/Plb{10692}. 7B{10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben){10692}. **ma:** *Xgwm951-7B* - 6.7 cM - *Pc/Pls/Plb* - 8.2 cM - *Pp1* - 8.9 cM - *Xgwm753-7B*{10692}.

Ra1. [*Ra*{1645}]. 1D Gulyeeva{474,983}.2D{1645}. **v:** Kenya 58{1645}.

Ra2{983}. 4B{983}.

Ra3{983}. 6B{983}.

5.3. Red/purple coleoptiles.

There is an orthologous gene series on the short arms of homoeologous group 7. The 'a' alleles confer red coleoptiles.

Rc-A1{10451}. [*Rc*{10451}[3]]. 7AS[3]{10451}. **dv:** PAU14087{10451}. **ma:** *Xcfa2174-7AS* - 11.1 cM - *Rc-A1* - 4.3 cM - *Xgwm573-7A/Xwmc17-7AL*{10451}[3].

Rc-A1a{0250}. [*Rc1, R*{401}]. 7A{769,1293}.7AS{0250}. **s:** CS*6/Hope 7A{1293}. **v:** Hope *Rc-B1a*{1293}. **tv:** *T. turgidum* ssp. *dicoccoides* acc. MG4343{9959}. **ma:** *Pan2* - 9.2 cM - *Rc-A1* - 12.2 cM - *Xutv1267-7A*(proximal){9959}; *Rc-A1*(distal) - 11.9 cM - *Xgwm913-7A*{0250}.

Rc-B1a. [*Rc2, R2*{401}]. 7B{742}.7BS{401,769,0250}. **s:** CS*6/Hope 7B{769}. **v:** Hope *Rc-A1*. **ma:** *Xgwm263-7B* - 26.1 cM - *Rc-B1* - 11.0 cM - *Xgwm1184-7B*{0250}.

Rc-D1a{0250}. [*Rc3*]. 7D{596}.7DS{1241,1444,0250}. **v:** Mironovskaya 808{1444}; Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271, RL 5404{1240}; Tetra Canthatch/*Ae. squarrosa* var. *meyeri* RL 5289, RL 5406{1240}; Sears' *T. dicoccoides /Ae. squarrosa* = Sears' Synthetic{596}. **ma:** *Rc-D1* (distal) - 3 cM - *Xpsr108-7D*{180}; *Xgwm44-7D* - 6.4 cM - *Rc-D1* - 13.7 cM - *Xgwm111-7D*{0250}.

Tahir & Tsunewaki{1453} reported that *T. spelta var. duhamelianum* carries genes promoting pigmentation on chromosomes 7A and 7D and genes suppressing pigmentation on 2A, 2B, 2D, 3B and 6A. Sutka{1444} reported a fourth factor in chromosome 6B and suppressors in 2A, 2B, 2D, 4B and 6A.

The *Rc* gene appears to encode a transcription activator of late biosynthesis genes involved in the light-regulation of anthocyanin systhesis (studies carried out on CS(Hope 7A) substitution line) {10317}.

5.4. Purple/red culm/straw/stem

Purple or red colour is dominant.

Pc1{743}. [*Pc*{743}]. 7B{743}.7BS{768}. **s:** CS*6/Hope 7B{743,768}. **itv:** LD222*11/CS (Hope 7B){1546}. **ma:** *Pc* (proximal) - 5.7 cM - *Xpsr490(Ss1)-7B*{110}[2].

Pc2{921}. 7DS{921}. **v:** Ilyitchevka{921}; Mironovskaya 808{921}; Novosibirskaya 67{921}; Pyrothrix 28{921}; Saratovskaya 210{921}; Strela{921}; Ukrainka{921}.

Pc/Pls/Plb{10692}. 7B{10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben){10692}. **ma:** *Xgwm951-7B* - 6.7 cM - *Pc/Pls/Plb* - 8.2 cM - *Pp1* - 8.9 cM - *Xgwm753-7B*{10692}.

5.5. Purple grain/pericarp

Genes for purple pericarp were transferred from tetraploid wheats to the hexaploid level {112,214,941,1138}. At the hexaploid level duplicate genes {112,941} and complementary genes {112,939,1138,438} were reported. At the tetraploid level, duplicate-gene {941} and single-gene {1327} inheritances were observed. Purple colour is dominant and may be affected by environment and genetic background. Complementary genes were located in chromosomes 3A and 7B {1138}. Possible pleiotropic relationships of genes affecting pigmentation of various tissues have not been studied in detail. *Pc2* and *Rc-B1a* may be the same gene {769}. Also, complementary genes involved in determination of purple pericarp could be related to culm colour {112}.

For review, see {1643}.

Complementary dominant genes.

Pp1{041}. 6A{041}.7BL{10392}. **i:** Saratovskaya 29*8/Purple {Australia} *Pp2*{040}. **v:** Novosibirsk 67 (this cultivar has white pericarp){10392}. **v2:** Purple K49426 *Pp3a*{10392}; Purple Feed *Pp3b*{10392}. **ma:** *Xgwm983-7B* - 15.2 cM - *Pp1* - 11.3 cM - *Xgwm767-7B*{10392}.

Pp2{041}. 7A{041}. **tv:** *T. durum* Desf. subsp. *abyssinicum* Vav{040}.

Piech and Evans{1138} located complementary genes on chromosomes 3A and 7B. *Pp2* was renamed *Pp3b*.

Pp3{10392}. 2A, not 6A{0066,10392}.

- ***Pp3a***{10392}. **v2:** Purple K49426 *Pp1*{10392}. **ma:** *Xgwm328-2AS* - 2.7 cM - *Pp3a* - 3.2 cM - *Xgwm817-2AL*{10392}.
- ***Pp3b***{10392}. [*Pp2*]. **v2:** Purple Feed{10392,0066}. **ma:** *Xgwm328-2AS* - 5.2 cM - *Pp3b/Xgwm817/Xgwm912-2A* - 3.6 cM - *Xgwm445-2A*{10392}.

pp1pp3. **v:** Saratovskaya 29 (this cultivar has red pericarp){10329}.

5.6. Purple glume

Pg{10692}. 2A{10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben){10692}. **ma:** *Xgwm328-2A* - 19.2 cM - *Pg* - 1.4 cM - *Pp3* - 5.1 cM - *Xgwm817-2A*{10692}.

5.7. Purple leaf blade

Plb{10692}. 7B{10692}. **tv:** TRI 15744 (IPK GeneBank, Gatersleben){10692}. **ma:** *Xgwm951-7B* - 6.7 cM - *Pc/Pls/Plb* - 8.2 cM - *Pp1* - 8.9 cM - *Xgwm753-7B*{10692}.

6. Awnedness

hd b1 b2. Bearded or fully awned genotype

6.1. Dominant inhibitors

6.1.1. Hooded

Hd{1551}. 4AS{1195,1293}. **i:** S-615*11/CS{1500}. **v:** Chinese Spring *B2*{1293}. **ma:** *Xcdo1387-4A* - 8.2 cM - *Hd* - 7.2 cM - *Xpsr163-4A* {0047} was mapped as a QTL with a peak on *Xfba78-4A*{0309}.

hd. **s:** CS*6/Hope 4A; CS*5/Thatcher 4A; CS*6/Timstein 4A.

6.1.2. Tipped 1

B1{1551}. 5AL{1293,0242}. **i:** S-615*11/Jones Fife{1500}. **v:** Timstein{741}; Redman{160}; WAWHT2046{10040}. **tv:** LD222{10541}. **ma:** *Xgwm410.2-5A* - 8.2 cM - *B1* - 12.2 cM - *Yr34*{10040}; Terminally located{10189}; *Xgwm291-5A.3* - 5.3 cM - *B1*{10330}. **matv:** *Xgwm291-5A* - 8.0 cM - *B1*{10541}.
B1 was mapped as a QTL with a peak on *Xwmc182-6B* {0309}.
B1a{041}. **s:** Saratovskaya 29*8/Festiguay 5A{041}.
B1b{041}. **s:** Saratovskaya 29*8/Aurora 5A{041}.
B1c{041}. **s:** Saratovskaya 29*8/Mironskaya 808 5A{041}.

In a common genetic background, carriers of *B1a* have the shortest tip-awned phenotype; carriers of *B1b* and *B1c* have awns 2 to 3 times longer depending on environment. In F1 hybrids, differences between the substitution line combinations are significant. The postulation of *B1* in both CS and Courtot {0309} based on the phenotype of a CS deletion stock is not supported by genetic observations

6.1.3. Tipped 2

B2{1551}. 6BL{1293,1297}. **i:** S-615*11/CS{1500}. **v:** Chinese Spring *Hd*{1293}.
b2. **s:** CS*6/Hope 6B; CS*5/Thatcher 6B; CS*9/Timstein 6B.

6.1.4. Awnless

Genotypes *Hd B2* (e.g., Chinese Spring) and *B1 B2* (e.g., Federation) are awnless. Presumably *Hd B1* is awnless. Watkins & Ellerton {1551} noted the probability of a third allele "*b1a*" leading to a half-awned condition, and in discussion they consider the possibility of a similar third allele at the *B2* locus. In view of more recent cytogenetic analyses, it seems that the half-awned condition could result from epistatic interactions between the alleles *B1* and/or *B2* and various promotor genes.
Although hooded, half-awned, tip-awned and awnless variants occur among tetraploid wheats, these are relatively infrequent. It has not been established with certainty that the above inhibitors are involved.
The inhibitor alleles have a pleiotropic effect on glume-beak shape {1348}. Acuminate beak is associated with full beardedness and occurs only in *b1 b2* types. *B2* reduces beak length producing an acute beak shape. *B1* reduces beak length producing an obtuse beak shape. In this effect *B1* is epistatic to *B2*.

6.2. Promotors

The effects of (recessive) awn-promoting genes were documented in a number of studies, mainly through monosomic and disomic F1 comparisons, and in tetraploids, whereas Heyne & Livers {549} provided genetic evidence of their effects. A series of "a" genes was documented, but the evidence for the existence of at least some of these was not well supported. Hence symbols for this gene series are not recognized.

6.3. Smooth awns

Smooth-awned tetraploid wheats were reported {016,045,690,1259} and genetic analyses {016,045,690} suggested a single recessive factor, with modifiers in most instances, relative to rough awns. The phenotype has not been reported in hexaploid wheats. No gene symbol is applied.

7. Basal Sterility in Speltoids

The presence of gene *Q* ensures the fertility of the first and subsequent florets in wheat spikelets {378}. In speltoids lacking *Q*, fertility of the second and subsequent florets is ensured by the dominant allele *Bs* (designated *A* in {378}) located on chromosome 5D {377}. In the presence of *Bs* the fertility of the first floret is under polygenic control.

In *bs bs* speltoids floret development is under polygenic control, and stocks with varying levels of basal fertility were isolated.

All group *vulgare* genotypes so far studied carry *Bs*.

The following stocks were described {378}:

	Genotype		**Approx. sterile-base score**
Group *vulgare*	**----**	***QQ Bs Bs***	**0.00**
Speltoids	**StFF**	***qq Bs Bs***	**0.00**
	StF	***qq Bs Bs***	**0.08**
	St1A	***qq Bs Bs***	**0.39**
	St1	***qq Bs Bs***	**0.96**
	St2	***qq bs bs***	**1.41**

8. Blue Aleurone

The *Ba* allele in *T. monococcum* spp. *aegilopoides* acc. G3116 determines a half-blue seed phenotype and is different from the allele present in *Elytrigia pontica* that determines a solid blue phenotype {282}. They are treated as different genes.

For review see {1643}.

Ba1{643}. Derived from *Elytrigia pontica* (2n=70). [*Ba*{643}]. 4B[4BS-4el$_2$]{643}. **tr:** UC66049B{594}.

Ba2. [*Ba*{10451}]. 4A^{m}L{282}^{3}. **dv:** G3116{282}; PAU5088 = G2610 = PI 427389{10451}. **ma:** *Ba2* cosegregated with *Xcdo1387-4A*, *Xmwg677-4A* and *Xbcd1092-4A* {282}; *Xcfd71-4A* - 10.3 cM - *Ba* - 16.5 cM - *Xcfa2173-4A*{10451}^{3}.

9. Brittle Rachis

Brittle rachis in *T. durum* was defined as a spike that disarticulated when the tip was bent by 45 degrees relative to the peduncle {10242}.

Br-A1{10061}. [*Br2*{9970},*Br-A2*{10280}]. 3A{0130}.3AS{10061}. **sutv:** LDN(DIC 3A){0130}. **itv:** ANW10A=LD222*7/LDN-DIC DS 3A{10242}. **ma:** *Xgwm2-3A* - 3 cM - *Br-A1* - 8 cM - *Xgwm666-3A.1/Xbarc356-3A/Xbarc19-3A/Xgwm674-3A/Xcfa2164-3A*{10280}.

Br-B1{10061}. [*Br3*{0130},*Br-A3*{10280}]. 3B{0130}.3BS{10061}. **sutv:** LTN(DIC 3B){0130}. **itv:** ANW10B=LD222*7/LDN-DIC DS 3B{10242}. **ma:** *Xbarc218-3B* - 22 cM - *Br-B1* - 2 cM - *Xwmc777-3B*{10280}. **tv:** Senatore Cappelle PI 242646{10242}; Sammartinara{10242}; others{10242}.

The presence of *Br-B1* in some durums apparently does not lead to significant shattering under conditions of Mediterranean agriculture {10242}.

Br-D1{10061}. [*Br1*{9970},*Br*^{61}{10362}]. 3DS{9970}. **v:** KU510, KU511, KU515{10061}; R-61{10362}; *T. aestivum* var. *tibetanum*{9970}. **dv:** *Ae. tauschii* KU2126{10227}. **ma:**

In *Ae. tauschii: Br^t* - 19.7 cM - *Xgdm72-3D*{10227}.
Evidence for an orthologous series extending to many related species is discussed in {0130} and {10061}.

Br4{10082}. 2A{10082}. **tv:** *T. dicoccoides*{10082}. **ma:** 33 cM distal to *Xgwm294-2A* (LOD=6.3, R^2=14.4%){10082}.

10. Boron Tolerance

Genes controlling tolerance to high concentrations of soil boron act additively.

Bo1{1111,1113}. 7B{177}.7BL{10460}. **v:** Carnamah{10460}; Frame{10460}; Krichauff{10460}; Yitpi{10460}; Additional genotypes{10833,10834}. **v2:** Halberd *Bo2Bo3*. **tv:** Kalka{10834}; Linzhi{10834}; Niloticum{10834}; Additional genotypes{10834}. **ma:** *Bo1* co-segregated with several STS-PCR markers, including *Xaww11-7BL*, falling within a 1.8 cM interval{10460}; The AWW7L7 (*Xaww11*) PCR marker allele was a good predictor of boron tolerance{10460}; Co-dominant PCR marker AWW5L7 co-segregated with *Bo1* and was predictive of the response of 94 Australian wheat genotypes{10833}; *Xbarc32-7B* - 2.4 cM - *Xaww5L7* - 1.2 cM - *Xbarc182-7B/Bo1* - 1.2 cM - *Xpsr680/Xmwg2062-7B*{10833}; *Xbarc32-7B* - 2.6 cM - *Xaww7L7/Bo1*{10834}.
QTL: Cranbrook (moderately tolerant) / Halberd (tolerant): DH population; QTLs for tolerance were identified on chromosomes 7B and 7D {10832}. For a review of boron tolerance in wheat, see {10835}.

Bo2{1111,1113}. **v2:** (W1*MMC)/Warigal *Bo3*. Halberd *Bo1 Bo3*.

Bo3{1111,1113}. 4A{0012}. **v2:** Warigal *Bo2*. Halberd *Bo1 Bo2*.
Very sensitive genotype: Kenya Farmer *bo1 bo2 bo3*.

Boron efficiency

In contrast to tolerance, boron efficiency was studied in {10135}. Monogenic segregation occured in Bonza (B inefficient)/SW41 (moderately B inefficient) and SW41/Fang60 (B efficient). Two genes, designated *Bod1* and *Bod2* segregated in Bonza/Fang60.

11. Cadmium Uptake

Low uptake is dominant.

11.1. Low cadmium uptake

Cdu1{963}. [*Cdu1*{1128}]. 5BL{10104}.corrected to 5BL{10894}. **itv:** Kyle*2/Biodur{10104}. **tv:** Biodur{1128}; Fanfarran{10894}; Hercules{1128}; Nile{1128}. **bin:** 5BL9 0.76-0.79. **ma:** *Xfcp2-5B* - 12 cM - *Cdu1* - 3 cM - *ScOPC20*{10894}; *ScOPC20/Xrz575-5B/XBG608197* - 0.5 cM - *Cdu1/XbF293297/XBF474090/Os03g53590(Xusw15-5B)* - 0.2 cM - *XBF474164*{10895}; *Cdu1* is close to *Vrn-B1*{10895}.

cdu1{963}. [*cdu 1*{1128}]. **itv:** Kofa{10104}. **tv:** Kyle{1128}; DT369{10894}. **ma:** *Cdu1* - 4.6 cM - *OPC-20*{1128}; *Cdu1* - 21.2 cM - *UBC-180*{1128}.

12. Chlorophyll Abnormalities

12.1. Virescent

V1. 3B{122,1311,1294}.3BS{1423}. **v:** CS.

v1a. [*v*{1294}]. **i:** S-615*11/Neatby's Virescent{1500}. **s:** CS*9/Neatby's Virescent{1304}. **v:** Neatby's Virescent{1055}.

v1b. **i:** CS*/Hermsen's Virescent *v2b*{1304}. **v:** Hermsen's Virescent *v2b*{1311}.

V2. 3A{1311,1545}. **v:** CS.

v2a. **v:** Viridis 508{1545}.

v2b. Expressed only when combined with *v2b* **i:** CS*/Hermsen's Virescent *v1a*{1304}. **v:** Hermsen's Virescent *v1a*{1311}.

v1b and *v2b* are expressed only when both are present. Corresponding normal alleles are designated *V1* {3B} and *V2* {3A} following Sears' {1295} demonstration of their effects on the expression of *v1a*.

12.2. Chlorina

Cn-A1. 7A{1132}.7AL{1131,1304,1311}. **v:** CS.

cn-A1a. [*cn1a*]. **i:** ANK-32{10820}; Chlorina-1{1311}.

cn-A1b. [*cn1b*]. **i:** Cornell Wheat Selection 507aB-2B-21/6*CS{1133}.

cn-A1c. [*cn2*]. **i:** Chlorina-448. (CS background){1545}.

cn-A1d{665}. **tv:** CDd6{665,666}. **itv:** ANW5A-7A{10820}. **ma:** Hexaploid wheat:*Xhbg234-7A* - 8.0 cM - *cn-A1* - 4.3 cM - *Xgwm282/Xgwm332-7A*{10820}; Tetraploid wheat:*Xbarc192-7A* - 19.5 cM - *cn-A1* - 11.4 cM - *Xgwm63-7A*{10820}; Diploid wheat:*Xgwm748-7A* - 29.2 cM - *cn-A1* - 33.3 cM - *Xhbg412-7A*{10820}.
Two mutants in diploid wheat are reported in {10820}.

Cn-B1. 7BL{1131}. **v:** Chinese Spring{1131}.

cn-B1a{665}. **tv:** CDd1{665,666}; CBC-CDd1{665}.

cn-B1b{665}. **tv:** CDd2{665,666}.

Cn-D1. [*Cn3*]. 7D{1545}.7DL{1131}. **v:** Chinese Spring{1131}.

cn-D1a. [*cn-D1,cn3*]. **i:** Chlorina-214{1545}. **v:** CD3{1583}.

12.3. Striato-virescens

A mutant of this type was described {376} but has been lost.

13. Cleistogamous Flowering in Durums

Cleistogamy, a rare flowering habit in durum wheats, is controlled by a single recessive gene relative to chasmogamy {191}.

Cleistogamous genotypes ***clcl.*** **tv**: HI8332 {191}; WH880 {191}.

Chasmogamous genotypes ***ClCl .*** **tv**: IWP5308 {191}; PWB34 {191}; WH872 {191}.

14. Copper Efficiency

Copper efficiency is a genetic attribute that enhances plant growth in copper deficient soil.

Ce{1276}. 4BL = T4BL.5RL{1276}. **v:** Cornell Selection 82a1-2-4-7{462}; Backcross derivatives of Cornell Selection to Oxley, Timgalen, Warigal{464}; Hairy necked Viking{1276}.

5BS = T5BS.5RL. **ad:** CS+5R{463}. **su:** CS 5R{5D}{463}. **v:** Sears' stock HN-2{464}; Backcross derivatives to Warigal and Timgalen{464}.

15. Corroded

co1. [*co*{1297}]. 6BS{1293}. **v:** Sears' corroded mutant.

co2. 6D{1570}. **v:** Kurrachee{1570}.

A gene(s) in chromosome 6A acts as an inhibitor of corroded {1039,1570}.

16. Crossability with Rye and *Hordeum* and *Aegilops* spp.

16.1. Common wheat

High crossability of some wheats, particularly those of Chinese origin, viz. Chinese 446 {790}, Chinese Spring {1216}, and TH 3929 {939}, with cereal rye, weed rye (*S. segetale L.*) {1646}, and other species, e.g., *Aegilops squarrosa* {691}, *Hordeum bulbosum* {1387,1397,1469} and *H. vulgare* {349,693], is determined by additive recessive genes. The *kr* genes influence crossability with *H. vulgare*. Allele *kr1* is more potent in suppressing crossability than *Kr2* which is stronger in effect than *Kr3* {1387}. According to Zheng et al. {1649}, the effect of *Kr4* falls between *Kr1* and *Kr2*.

Kr1. 5B{1216}.5BL{762}.
kr2. 5A{1216}.5AL{1387}.
kr3. 5D.
kr4. 1A{1649}.
kr1 kr2. **v:** Chinese 446{790}; Chinese Spring{762,1216,1025}; Martonvarsari 9*4/CS{1016}.
Kr1 kr2. **s:** CS*6/Hope 5B{762,1216}. **v:** Blausamtiger Kolben{790}.
kr1 Kr2. **s:** CS*6/Hope 5A{1216}.
Kr1 Kr2. **v:** Marquis{790}; Peragis{790}.
kr1 kr2 kr3 kr4. **v:** J-11{1649}.
Kr1 Kr2/Kr1 kr2. (heterogeneous). **v:** Martonvarsari 9{1016}.

Using the Chinese Spring/Cheyenne chromosome substitution series, Sasaki & Wada {1265} found significant differences in crossability for chromosome 5B, 7D, 1D and 4B. Differences between rye lines also occur {1265,1458}. Allelic variation in the potency of the dominant suppressor genes was reported {1385,343}. Evidence for allelic variation in dominant supressors is reported in {1386}. Lists of wheat/rye crossabilities:{1383,1642,850,858}.
QTL: 65% of the variability in a Courtot/CS population was associated with *Xfba-367-5A*(5AS), *Xwg583-5B*(5BL) and *Xtam51-7A*{0134}. Only the second QTL appears to coincide with known locations of *Kr* genes.

16.2. Tetraploid wheat

The Chinese tetraploid, Ailanmai, possesses recessive crossability genes on chromosomes 1A, 6A and 7A with the 6A gene being the least effective {0017}.

17. Dormancy (Seed)

Seed dormancy in wheat has several components, including factors associated with vivipary and red grain colour. Dormancy is an important component of resistance/tolerance to pre-harvest sprouting (PHS).

17.1. Vivipary

Orthologues of maize viviparous 1 (*Vp-1*) are located in chromosomes 3AL, 3BL and 3DL {9961} approximately 30 cM distal to the *R* loci. Variability at one or more of these loci may be related to germination index and hence to PHS {10468}.
Alleles of *Vp-A1* were recognized using STS marker A17-19 {10919}.
Three sequence variants of ***Vp-B1*** identified in {10468} were used to develop STS marker VpiB3 whose amplified products showed a significant, but not complete, association with germination index used as one measure of PHS.

Alleles of *Vp-B1* were recognised using STS marker Vp1B3 {10615, 10621}.

Vp-A1{10919}. 3AL{10919}.

Vp-A1a{10919}. **v:** Nongda 311{10919}. **c:** 599 bp{10919}.
Higher germination index.

Vp-A1b{10919}. **v:** Wanxianbaimaizi{10919}; Yannong 15{10919}. **c:** 596 bp{10919}.
Lower germination index.

Vp-A1c{10919}. **v:** Jing 411{10919}. **c:** 593 bp{10919}.
Higher germination index.

Vp-A1d{10919}. **v:** Xiaoyan 6{10919}. **c:** 590 bp{10919}.
Lower germination index.

Vp-A1e{10919}. **v:** Zhengzhou 6{10919}; Bainong 64{10919}. **c:** 581 bp{10919}.
Higher germination index.

Vp-A1f{10919}. **v:** Yumai 34{10919}. **c:** 545 bp{10919}.
Higher germination index.

Vp-B1.

Vp-B1a{10615}. **v:** Charger{10616}; Zhongyou 9507{10615}; 271 accessions{10616}. **c:** AJ400713{10615}.

Vp-B1b{10615}. **v:** Altria{10616}; Recital{10616}; Yongchuanbaimai{10615}; 2 accessions{10616}. **c:** 193 bp insertion in third intron relative to *Vp-A1a*.

Vp-B1c{10615}. **v:** Scipion{10616}; Xinong 979{10615}; 101 others{10616}. **c:** 83 bp deletion relative to *Vp-B1a*.

Vp-B1d{10616}. **c:** 25 bp deletion relative to *Vp-A1a*.

Vp-B1e{10621}. **v:** Hongheshangtou{10621}. **c:** 83 bp deletion, 4 bp insertion and 2 SNPs relative to *Vp-B1a*{10621}.

Vp-D1{10919}. AJ400714 {10919}. 3DL{10919}.

Vp-D1a{10919}. AJ400714 {10919} 3DL{10919}. **v:** 81 Chinese wheat cultivars{10919}. **c:** 5 pairs of primers{10919}.

There was a suggestion of a relationship between alleles and PHS response {10615}. *Vp-B1* allelic identifications for Chinese landraces, historical and current wheat cultivars are listed in {10621}.

17.2. Pre-harvest sprouting

Phs1{10500}. Semi-dominant {9960}. [*Phs*{9960}]. 4AL{9960}. **i:** Haruyokoi*6/Leader{10500}; Haruyokoi*6/Os21-5{10500}. **v:** Leader{10500}; Os21-5{10500}; Soleil{9960}. **ma:** Associated with *Xpsr1327-4A*{10346}; *Xhbe03-4AL* - 0.5 cM - *Phs1* - 2.1 cM - *Xbarc170-4AL*{10500}.

phs1. **v:** Haruyokoi{10500}.

QTL: Several QTL for falling number and alpha-amylase activity, two indicators for pre-harvest sprouting resistance, were identified in {0169}. The most significant were associated with *Xglk699-2A* and *Xsfr4(NBS)-2A*, *Xglk80-3A* and *Xpsr1054-3A*, *Xpsr1194-5A* and *Xpsr918-5A*, *Xpsr644-5A* and *Xpsr945-5A*, *Xpsr8(Cxp3)-6A* and *Xpsr563-6A*, and *Xpsr350-7B* and *Xbzh232(Tha)-7B* {0169}.

In cross AC Domain/Haruyutaka, one major QTL in chromosome 4AL and two lesser possibly homomeologous QTLs for dormancy in 4BL and 4DL {0226} were found.

Tolerance to preharvest sprouting (PHS) in the cross SPR8198/HD2329 was associated with *Xwmc104-6B* and *Xmst101-7D* {0032}. In AC Domain (red seeded, PHS resistant) / RL4137 (white seeded, PHS moderately resistant) most measures of PHS occurred as clusters at the *R* loci. However, *QSi.crc-5D* for sprouting index, R^2=0.44, was independent of seed colour {10626}.

QTL for preharverst sprouting were identified on chromosomes 3A (associated with

Xfbb293-3A at P=0.01), 3B (associated with *Xgwm403-3B* and *Xbcd131-3B* at P=0.001), 3D (associated with *Xgwm3-3D* at P=0.001) and 5A (associated with *Xbcd1871-5A* at P=0.001) in the population Renan/Recital {0347}. The resistant alleles on the group 3 chromosomes and on 5A were contributed by Renan and Recital, respectively. All QTL for preharvest sprouting co-located with QTL for grain colour {0347}. Zenkoujikomugi/CS: *Qphs.ocs-3A.1* on chromosome 3AS was associated with *Xbcd1380-3A* and *Xfbb370-3A* accounting for 38% of the phenotypic variation {10195}. Zenkoujikomugi/Spica: White seeded wheats with the dormancy-related QTL, *QPhs-3AS* from Zenkoujikomugi were more resistant to PHS than counterparts with the contrasting allele from Spica {10377}. White seeded wheats with contrasting alleles of *QPhs-4AL* were not different {10377}.

QPhs.ocs.3A-1 was localized to a 4.6 cM interval flanked by *Xbarc310-3A* and *Xbcd907-3A* {10245}. A weaker QTL, *Qphs.ocs-3A.2* in 3AL, was not associated with *TaVp1* {10195}, the wheat orthologue of the maize transcription factor Viviparous-1.
Qphs.ocs-4A.1 may be the same as a QTL in AC Domain/Haruyutaka due to tight linkage with *Xcdo785-4A* {10245}.
QPhs.ocs.4B.1, a CS allele contributing to dormancy, was located in the region of *Xgwm495-4B* {10245}.
In cross SPR 8198 (dormant)/HD2329, *QPhs.occsu-3A* was located in the *Xgwm155-3A* - *Xwmc153-3A* region with R^2=75% across 6 environments {10261}.
QTL analyses in several crosses {10275} indicated a common region in chromosome 4A associated with dormancy, dormant genotypes included AUS1408, SW95-50213 and Halberd. The location was consistent with Japanese and U.K. work even though different flanking markers were involved.
CN10955 (PHS resistant white seeded) / Annuello (PHS susceptible, white seeded) F8 RIL population: *QPhs.dpivic-4A.2* in the *Xgwm637-4AS* - *Xgwm937/Xgwm894-4AL* region and *QPhs.dpivic-4A.1* in the *Xwmc48-4AS* - *Xgwm397-4AS* region {10599}.

Rio Blanco (white seeded, PHS resistant) / NW97S186 (white seeded, PHS susceptible) RIL population: *QPhs.pseru-3AS*, R^2=0.41, *Xgwm369-3A* - *Xbarc12-3A*, and one minor QTL {10634}. This major QTL was confirmed in a Blanco / NW98S079 RIL population, R^2 up to 0.58 {10634}. *Qphs.psweru-3A* was fine mapped to a 1.4 cM region flanked by two AFLP markers and was tightly linked to *Xbarc57-3A* and seven other AFLP markers {10893}.

RL4452 (red seeded, low PHS tolerance)/AC Domain (red seeded, high PHS tolerance): DH lines: Genes associated with falling number, germination index and sprouting index contributing to PHS were locatged on chromosomes 3A, 4A (locus-2) and 4B in AC Domain and 3D, 4A (locus-1) and 7D in RL4452 {10671}.

SPR8198 (red seeded, PHS tolerance)/HD2329 (white seeded, PHS susceptible): RIL population: 7 QTL located on chromosomes 2AL, 2DL, 3AL and 3BL, the most important on 2AL and 3AL {10670}.

Sun325B (dormant white seeded)/QT7475 (semi-dormant white seeded), both parents with the chromosome 4A QTL: DH population: A QTL was located in the *Xgwm77-3B* - *Xwmc527-3B* interval (R^2=0.19) in the approximate region of the *R-B1* locus {10669}.

Diploid wheat

QTL:*T. monococcum* KT3-5 (non-dormant)/*T. boeoticum* KT1-1 (dormant): RIL population: QTL on chromosome $5A^m$L, *Xcdo1236c-5A* - *Xabc302-5A*), R^2=0.2-0.27. Weaker QTLs were found on $3A^m$(*TmAB18* - *Xwmc102-3A* and *Xrz444-3A* - *TmABF*) and $4A^m$(*Xrz261-4A* - *Xrz141-4A*) {0892}. The $3A^m$QTL co-located with *TmABF* and *TmAB18* {10417}, derived

from orthologous ABA signaling genes in *Arabidopsis*. The 5A QTL may be orthologous to the barley dormancy gene *SD1* {10417}.
Argent (non-dormant, white seeded) / W98616 (dormant, white seeded): 90 DH lines: Strong QTLs on chromosomes 1A, 3A, 4A and 7A and weaker QTLs on 2B, 5B, and 6B, all from W98616 {10740}.

18. Ear Emergence

QEet.ocs-4A.1{0047}. 4AL{0047}. **v:** CS/CS(Kanto107 4A) mapping population. **ma:** Associated with *Wx-B1*{0047}.

QEet.ocs-5A.1{0068}. 5AL{0068}. **v:** CS(*T. spelta* 5A)/CS(Cappelle-Desprez 5A) RI mapping population{9903}. **ma:** Associated with *Xcdo584-5A* and morphological locus *Q*{0068}.

QEet.ocs-5A.2{0026}. 5AL{0026}. **ma:** *Xcdo 412-5A* - *Xbcd9-5A* region{0026}.

QEet.inra-2B{10069}. 2B. **ma:** 2B linked to *Xgwm148* (LOD=5.7, R^2=11.9%.

QEet.inra-2D{10069}. 2D. **ma:** 2D linked to *XksuE3* (LOD=2.7, R^2=6.5%).

QEet.inra-7D{10069}. 7D. **ma:** 7D linked to *Pch1* (LOD=3.9, R^2=7.3%).

QEet.ipk-2D{0255}. *QEet.ipk-2D* coincides with a QTL for flowering time, *QFlt.ipk-2D*. Both QTLs may correspond to *Ppd-D1* {0255}. 2DS{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Lateness was contributed by W-7984{0255}. **ma:** Associated with *Xfba400-2D* and *Xcdo1379-2D*{0255}.

QEet.ipk-5D{0255}. *QEet.ipk-5D* coincides with a QTL for flowering time, *QFlt.ipk-5D*. Both QTLs probably correspond to *Vrn-D1* {0255}. 5DL{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Lateness was contributed by W-7984{0255}. **ma:** Associated with *Xbcd450-5D*{0255}.

19. Earliness Per Se

Genes for earliness *per se* {0023} affect aspects of developmental rate that are independent of responses to vernalization and photoperiod.

Eps-1A^m{0364}. [*Eps-A^{m}1*]. 1AL{0364}. **dv:** *T. monococcum* DV92 allele for late flowering, G3116 early flowering.{0364}. **ma:** 0.8 cM distal to *Xwg241-1A*{0364}; within a 0.9 cM region within the *VAtpC* - *Smp* region{10246}.

Eps-5BL.1{10075}. 5BL{10075}. **ma:** QTL mapped on chromosome 5BL, linked to *Xwmc73-5B* (this QTL explained 8% of the variance in flowering time, P<0.03{10075}.

Eps-5BL.2{10075}. 5BL{10075}. **ma:** QTL mapped on chromosome 5BL, linked to *Xgwm499-5B* (this QTL explained 6% of the variance in flowering time){10075}.

Eps-A1a{0024}. 3A{0023}.3AL{0024}. **v:** Chinese Spring{0024}.

Eps-A1b{0024}. **v:** Timstein{0024}.

epsCnn{0025}. **v:** Cheyenne{0025}.

EpsWi{0025}. 3A{0025}. **su:** Cheyenne*7/Wichita 3A{0025}. **ma:** Linked to QTLs for plant height, kernel number per spike, and 1,000-kernel weight in RSLs derived from CNN/CNN(WI3A){0025}.

QTL: Analysis in Courtot/CS {0132}. Two QTLs for narrow-sense earliness were detected on chromosome 2B in a CS/*T. spelta* var. *duhamelianum* KT19-1 RI population{10057}. These QTLs were associated with markers *Xpsr135-2B* and *Xabc451-2B* {10057}. For both QTLs, earliness was conferred by the CS allele.

QEet.fcu.5AL identified in *Xfcp359-5A* - *Xfcp231-5A* interval (R^2=0.38), at or near the *Q* locus in Grandin/BR34 {10256}. Grandin was the earlier parent.

20. Embryo Lethality

20.1. Embryo lethality in wheat x rye hybrids

The Chinese Spring (Omperial rye) addition lines 6R and 6RL crossed with different inbred rye lines (R2, R6, R7) produced hybrid seeds with different proportions of differentiated embryos. R2 with (*Eml-R1a*) gave only undifferentiated embryos; R6 and R7 (with *Eml-R1b*) gave 74-100% differentiated embryos {10748}. Cross of R2 with the CS nulli-tetrasomics gave differentiated embryos only with N6AT6B and N6AT6D, indicating the presence of a complementary factor *Eml-A1* chromosome 6A {10748}.

21. Flowering Time

The isolation of wheat genes orthologous to the Arabidopsis *Co* and rice *Hd1* genes was reported in {10054}. The genomic clones TaHd1-1, TaHd1-2 and TaHd1-3 originate from the long arms of chromosomes 6A, 6B and 6D, respectively. The orthology of the *TadHd1* genes with *Co/Hd1* was demonstrated by complementation of a rice line deficient in *Hd1* function with the TaHd1-1 genomic clone. It should be noted that the wheat *TaHd1* and rice *Hd1* genes are located in non-syntenic locations {10054}. To date, no variation for flowering time has been identified on the wheat group 6 chromosomes.

Winter wheat cross, Arina (149 days)/Forno (150 days): Six QTL were detected over six environments. The 3 most important, all from Arina, were in chromosomes 6DL (R^2=16%), 3DL (R^2=14%) and 7BL (R^2=13%); 3 others in 2AL, 5BL and 6DL were from Forno {10172}.

Winter wheat cross Ernie (early)/MO94-317 (late), days to anthesis (dta):
Qdta.umc-2D, linked to *Xbarc95-2D*, R^2 = 0.74 {10456}.
Spring wheat cross: Nanda 2419 / Wangshuibai: Seven QTLs for flowering time identified with earlier alleles for five coming from Nanda 2419: *QFlt.nau-1B* (closest marker *Xbarc80-1B*, R^2=11 %), *QFlt.nau-1D* (*Xbarc62-1D, Xgwm232-1D*, R^2=6.13 %), *QFlt.nau-2B* (*Xwmc35-2B*, R^2=10 %), *XFlt.nau-2D* (*Xwmc601-2D*, R^2=10 %), *XFlt.nau-4A.1* (*Xcfd2-4A, Xmag1353-4A*, R^2=10 %), *XFlt.nau-4A.2* (*Xmag3386-4A, Xwmc161-4A*, R^2=18-19 %), *XFlt.nau7B (Xmag2110-7B, Xmag1231-7B, Xgwm537-7B, Xwmc218-7B*, R^2=18 %) {10566}.

QFlt.ipk-3A{0255}. 3AL{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Lateness was contributed by W-7984{0255}. **ma:** Associated with *Xbcd451-3A*{0255}.

QFt.cri-3B.1{10567}. Nearest marker *Xbarc164-3B*; identified in croses of substitution lines of Ceska Presivka and Zlatka or Sandra {10567}.

Heading date QTL: CI 13227/Suwon 92 RIL population: AFLP marker - 2.6 cM - *QHd.pser-2DS* - 121.1 cM - *Xgwm261-2D* {10269}. This QTL could be *Ppd-D1* {10269}.
Karl 92*2/TA 4152-4 F2:F4 population: Two QTLs, *QHd.ksu-2D*, associated with *Xgwm261-2D* (R^2=0.17), and *QHd.ksu-3D,* associated with *Xgwm161-2D* 9 (R^2) {10273}.

22. Flour Colour

Loci controlling flour colour were identified and mapped in a recombinant inbred population derived from Schomburgk/Yarralinka {9936}. Regions in 3A and 7A accounted for 13% and 60% of the genetic variation, respectively, and *Xbcd828-3A*, *Xcdo347-7A* and *Xwg232-7A.1* were significantly associated with flour colour. The association was highly significant in all three replicates only for the 7A QTL. Symbols were not assigned to the flour colour loci. See also 29.2. Flour, semolina and pasta colour.

23. Free-threshing Habit

QFt.mgb-5A{0046}. 5AL{0046}. **tv:** Messapia/*T. dicoccoides* MG4343 mapping population{0046}. **ma:** Associated with *XksuG44-5A*{0046}.

QFt.mgb-6A{0046}. 6A{0046}. **tv:** Messapia/*T. dicoccoides* MG4343 mapping population{0046}. **ma:** Associated with *Xpsr312-6A*{0046}.

24. Frost Resistance

Fr1{1446}. 5AL{1446}. **v:** Hobbit{1446}. **ma:** Mapped to the mid-region of 5AL, 2.1 cM distal from *Xcdo504-5A* and *Xwg644-5A* and proximal to *Xpsr426-5A*{419}; Mapped 2 cM proximal to *Xwg644-5A* and *Vrn-A1*{0291}; and flanked by deletion points 0.67 and 0.68{0292}.

Studies using *Vrn-1* induced and natural mutants suggest that differences in frost tolerance previously associated to *Fr1* are actually pleiotropic effects of *Vrn-1* {10708}.

Fr2{0291}. 5DL{0291}. **s:** CS*7/Cheyenne 5D{0291}. **ma:** *Fr2* mapped 10 cM proximal to *Vrn-D1*{0291}.

Fr-A2{10079}. **dv:** *Triticum monococcum*. Frost tolerant parent G3116, frost susceptible parent DV92. **ma:** The QTL mapped on chromosome 5AL had a LOD score of 9 and explained 49% of the variation in frost tolerance. Closest markers: *Xbcd508-5A* and *Xucw90(Cbf3)-5A*. These markers are 30 cM proximal to *Xwg644-5A*, which is closely linked to frost tolerance locus *Fr-1*. Eleven different *Cbf* transcription factors were identified at the *Fr-A2* locus {10302}; QTLs for frost tolerance in the *Fr-2* region were also identified in wheat chromosome 5B (*Fr-B2* {10079}) and in barley chromosome 5H(*Fr-H2*{10083}.

Fr-B2. [*Fr-B1*{10075}]. **ma:** QTL mapped on chromosome 5BL, linked to *Xgwm639-5B* (this QTL explained 12-31% of the variance in frost tolerance) {10075}. *Xgwm639-5B* mapped close to *Xmwg914-5B,* and to *Xbcd508-5B*, a marker located at the peak of the *Fr-A2* QTL {10075}. This data suggests that this locus is more likely orthologous to *Fr-2* than to *Fr-1*.

QWin.ipk-6A. 6AS{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Winter hardiness was contributed by W-7984{0255}. **ma:** Associated with *Xfba85-6A* and *Xpsr10(Gli-2)-6A*{0255}.

Responses to cold exposure and their genetics are reviewed in {0020,0274}.

QTL:Norstar(tolerant)/Winter Manitou(non-tolerant): DH population: Norstar possessed major and minor QTL for tolerance on chromosomes 5A and 1D. The 5A QTL was 46 cM proximal to the *vrn-A1* locus (R^2=0.4); its peak co-incided with *Xwmc206-5A* and *Xcfd2-5A*, and expression of C-repeat Binding Factor genes with strong homology to *Cfb14* and *Cfb15* located at the *Fr-2* locus in *T. monococcum* {10414}.

25. Gametocidal Genes

25.1. Gametocidal activity

Gc1-B1a{1485}. [*Gc1a*{1490},*Gc1*{1487}]. 2B{1490}. **i:** CS*8/*Aegilops speltoides* subsp. *aucheri*{1487}.

Gc1-B1b{1485}. [*Gc1b*{1490}]. 2B{1490}. **i:** S*8/*Ae. speltoides* subsp. *ligustica*{1490}.

Gc1-C1{0188}. 2CL{0189}. **ad:** CS/2C{0189}. **su:** CS2C(2A), CS2C(2B), CS2C(2D){0189}.

Gc1-Sl1{1485}. [*Gc-S^{1}3*{1485}]. 2S^1{334}. **ad:** CS/*Ae. sharonensis*{334}.

Gc2-Sl1a{1485}. [*Gc-S^{1}1*{1485}]. 4S^1{866}. **ad:** CS/*Ae. longissima*{866}.

Gc2-Sl1b{1485}. [*Gc-S*^{1}*2*{1485}]. 4S^{1}{1013}. **ad:** S/*Ae. sharonensis*{1013}. **ma:** An EMS-induced *Gc-2* mutant was mapped to a wheat-*Aegilops sharonensis* T4B-4S^{sh}#1 translocation chromosome{10068}.

Gc3-C1{1485}. [*Gc-C*{1485}]. 3C{333}. **ad:** CS/*Ae. triuncialis*{338}.

Gc1-B1a, Gc1-B1b and *Gc1-S*^{1}, classified in the same functional group, are hypostatic to the genes *Gc2-S*^{1}*1a* and *Gc2-S*^{1}*1b*. *Gc3-C1* does not interact with the *Gc* genes in the other two groups.

In addition to these genes, chromosomes carrying gametocidal genes occur in *Ae. caudata* {337}, *Ae. cylindrica* {336} and other strains of *Ae. longissima* and *Ae. sharonensis* {335,1484}.

Gametocidal genes in chromosomes in the same homoeologous group have the same gametocidal action {0190}. In monosomic additions of chromosomes with gametocidal effects, chromosome deletions and translocations are produced in gametes not having the gametocidal genes. This feature has been exploited to isolate genetic stocks suitable for physical mapping of wheat {0191} chromosomes, and of rye {0192} and barley {0193,0194,0195} chromosomes in a wheat background.

Genes with gametocidal activity (*Sd1* {1647} and *Sd2* {1161}) in wheat are present in homoeologous group 7 chromosomes of *Thinopyrum elongatum* {653,1647}. A segment earlier believed to be derived from *Thin. distichum* {889,892} is probably the same as that from *Thin. elongatum* {1162}.

In the presence of both *Sd1* and *Sd2, Lr19* is transmitted preferentially in heterozygotes, the degree of distortion being determined by genetic background. In heterozygotes with the same background, and in the presence of only *Sd2, Lr19* shows strong self-elimination. Based on these results, it seems likely that the Sears' translocation 7D-7Ag#7 does not carry *Sd1* {939}. See also Pollen Killer.

Sd1{1647}. 7D{1647}. **v2:** Agatha *Sd2*{1647,1161}. **ma:** Proximal to *Lr19* and distal to *Xpsr165-7D*{10255}.

Sd2{1161}. 7BL{1163}. **v:** 88M22-149{1163,1161}.

Zhang et al. {10255} question the existence of this gene and alternatively suggest a duplication or deletion event influencing the transmission.

25.2. Suppression of gametocidal genes

Igc1{1489}. Causes suppression of the 3C chromosome gametocidal gene of *Ae. triuncialis*. This alien gametocidal factor also promotes chromosome breakage {1486}. 3B{1488}. **v:** Norin 26{1483,1488}; Nineteen wheats listed in{1483,1488}.

igc1. **v:** Chinese Spring{1483,1488}; Forty wheats are listed in{1483,1488}.

26. Gibberellic Acid Response (insensitivity)

Gai1. [*GAI1*{565,1246}]. 4B{406}.4BS{980}. **i:** See{408}. **v:** Norin 10 Der.{407,565}. **ma:** *Xpsr622-4B* (distal) - 1.9 cM - *Gai1* - 8.3 cM - *Xbcd110-4B* (proximal){9959}. **tv:** Messapia{9959}.

Gai2. [*GAI2*{565,1246}]. 4D{411}.4DS{980}. **i:** See{408}. **v:** Maris Hobbit{411}; Norin 10 Der.{565}; List in{407}.

Gai3. [*GAI3*{565,1246}]. 4B{413}.4BS{980}. **i:** See{408}. **v:** Minister Dwarf{413}; Selection D6899{359}; Tom Thumb{405}; Tom Thumb Der.{565,567}.

In wheats with *Gai3*, the aleurone layer fails to respond to applied GA {405}.

Two studies involving crosses between Tom Thumb derivatives and tall parents suggested that gibberellic acid insensitivity and reduced height were controlled by one gene, i.e., *Gai3* {359,413}. In a third study involving a Tom Thumb derivative, recombinants were isolated, indicating separate but linked genes, i.e., *Gai3* and *Rht-B1c* {565,567}. Further evidence was obtained for linkage between genes for gibberellic acid insensitivity and Norin 10 genes for reduced height in hexaploid {568} and durum {720} wheats. Hu & Konzak {567} reported 27% recombination between *Gai1* and *Rht-B1b* and 10% recombination between *Gai2* and *Rht-D1b* in hexaploid wheats involving Norin 10 and Suwon 92 derivatives. In durum derived from crosses involving Norin 10, 15% recombination was obtained between one of the genes for reduced height and gibberellic acid insensitivity {1246,1247}. Gale & Law {403} considered *Gai1* and *Rht-B1b, Gai2* and *Rht-D1b, Gai3/* and *Rht-B1c* to be pleiotropic genes.

27. Glaucousness (Waxiness/Glossiness)

Glaucousness refers to the whitish,wax-like deposits that occur on the stem and leaf-sheath surfaces of many graminaceous species. The expression of glaucousness depends on the arrangement of wax deposits rather than the amount of wax {603}. Non-glaucous variants also occur and genetic studies indicate that non-glaucousness can be either recessive or dominant. Recessive forms of non-glaucousness are apparently mutants of the genes that produce the wax-like deposits.

Dominant non-glaucous phenotypes (as assessed visually) appear to be due to mutations that affect the molecular structure, and reflectance, of the wax-like substances {10001}. The genes involved in wax production and the "inhibitors" are duplicated in chromosomes 2B and 2D. There appear to be independant genes for wax production and "inhibitors" {912,1493,10001}. In earlier issues of the gene catalogue the two kinds of genes were treated as multiple alleles {1432}. All forms of wild and cultivated einkorn are non-glaucous {10001}.

Orthologous loci occur in barley chromosome 2HS (*gs1, gs6, gs8*) {467}, rye chromosome 7RL (*wa1*) {725} and maize (*gl2*) {211}.

A gene for spike glaucousness, *Ws*, was mapped distally on chromosome 1BS in the cross *T. durum* cv. Langdon / *T. dicoccoides* acc. Hermon H52 {0171}.

27.1. Genes for glaucousness

W1. 2BS{267,1493}. **i:** Chinese Spring mono-2D/S615//10*wS615{10001}. **v:** Chinese Spring{1493}. **itv:** LD222*11/*T. turgidum* var. *pyramidale* recognitum{1546}. **v2:** S615 *W2*{10001}.

w1. Recessive allele for reduced glaucousness. 2BS{1432}. **v:** CS mono-4B mutant{1064}; Mentana{1432}; Salmon{1493}.

W2. **i:** Chinese Spring mono-2B/S615//11*wS615{10001}. **v:** *T. compactum* cv. No 44{10001}. **v2:** S615 *W1*{10001}.

W2a. **dv:** Glaucous forms of *Ae. tauschii*.

W2b. **v:** Chinese Spring - weak hypomorph recognized at increased dosage{1432}.

A non-glaucous spike phenotype in line L-592, a 7S(7A) substition line, is described in {0113}.

w1w2{10001}. **i:** w-S615 = S615*11/Salmon{10001}. **v:** Salmon{10001}; Mentana{1432}; CS mono-4B mutant{1064}.

27.2. Epistatic inhibitors of glaucousness

Each inhibitor inhibits all genes for glaucousness.

Iw1{10001}. [*W1*^{I}{1493},*I1-W*{1493}]. 2BS{10001}. **i:** S615/Cornell 5075//10*S615{10001}.

Iw2{10001}. [*I2-W*{1493},*Iw3672*{10510}]. 2DS{10001}. **bin:** 2DS5-0.47-1.00{10578}. **i:** S615/Golden Ball Synthetic//10-*S615{10001}. **v:** Golden Ball Synthetic{10001};

Synthetic hexaploid line 3672{10510}; Vernal Synthetic{10001}. **dv:** Non-glaucous forms of *Ae. tauschii*{1493}. **ma:** In *Ae. tauschii: Iw2* - 30.1 cM - *Xgdm35-2DS*{10227}; *Xbarc124-2D* - 0.9 cM - *Iw2* - 1.4 cM - *Xwe6(AL731727)*{10510}; *Xcfd56-2D* - 6 cM - *Iw2* - 10 cM - *Xcfd51-2D*{10578}.

Iw3{277}. [*IW3*{277},*I3-W*{277}]. 1BL{277}. **tv:** *T. turgidum* var. *dicoccoides*{277}. A non-glaucous spike phenotype in line L-592. A 7S(7A) substitution line, is described in {0113}.

A dominant gene (*Vir*) for non-glaucousness was located in chromosome 2BL of cv. Shamrock, a derivative of *T. dicoccoides* {10543}. This gene mapped 2 cM distal to *Xgwm614-2B* {10543} whereas the *W1/Iw1* locus was placed distal to *Xgwm614-2B* in {10189}. Lines with *Vir* had delayed senescence ('staygreen') and an average yield advantage over their glaudous sibs {10543}. Although maps constructed from three tetraploid crosses suggested that *w1*, *W1* and $Iw1^{DIC}$ = *Vir* remain unresolved {10815}.

27.3. Spike glaucousness

Spike glaucousness is recessive {10666}.

Ws{10666}. 1AS{10666}. **bin:** 1AS1 - 0.47 - 1.00{10666}. **v:** Svenno{10666}. **ma:** *BJ23702a* - 3.5 cM - *Tc95235* - 4.8 cM - *Bla*{10666}.

ws{10666}. **v:** Ciccio{10666}.

28. Glume Colour and Awn Colour

Black glumes are now included in the following homoeologous series with red/brown/bronze glumes.

28.1. Red (brown/bronze/black) glumes

The majority of studies report a single dominant gene for red glume colour. A few papers report two factors {1009,1477,1520}. Red glume colour in Swedish land cultivars is apparently associated with hairy glumes {1277} suggesting, because *Hg* is located in chromosome 1A, that a red glume factor different from *Rg1* is involved in the Swedish stocks. Nothing was known of the possible association of such a gene with *Bg,* another glume colour gene on chromosome 1A. See {1640} for review. A chromosome 1A gene, *Rg3,* was eventually identified by linkage with *Gli-A1* {1405} and shown to cosegregate with *Hg* {624}.

Rg-A1{10378}. [*Rg3*{562,924,923}]. 1AS{562,923,924,9906}.

Rg-A1a{10378}. **v:** TRI 542{10378}; White glumed genotypes. **dv:** DV92{282}; G2528{10378}.

Rg-A1b{10378}. [*Rg3*]. **i:** Saratovskaya 29*3//F2 CS mono 1/Strela{924}. **v:** CS/Strela Seln{9906}; Iskra{9906}; L'goskaya-47{1405}; Zhnitsa{9906,10378}. **v2:** Milturum 553 *Rg-B1b*{9906}; Milturum 321 *Rg-B1b*{9906}; Strela *Rg-B1b*{9906,924}; Sobko & Sozinov{1405,1406}; reported a further group of 30 international wheats which, by inference from their *Gli-A1* alleles, probably carry *Rg-A1b*. **ma:** A linkage order of *Glu-A1* - cent - *Hg* - *Rg-A1b*{1405}; *Xgwm1223-1A / Rg-A1 / Hg* - 2.2 cM - *Xgwm136-1A* - 4.2 cM - *Xgwm33-1A*{10635}.

Rg-A1c{10378}. [*Bg*{282,1304},*Bg(a)*{282}[3]]. 1A{282,1304}. **i:** ANK-22A{10378}; S29BgHg{10378}. **s:** CS*7/Indian 1A{1304}. **v:** TRI 14341{10638}. **v2:** Sears Synthetic *Rg-D1c*{10638}. **dv:** G1777{282}; G3116{282}. **ma:** *Rg-A1c(Bg)* and *Nor9* co-segregated in *T. monococcum* {282}[3]; *Xutv1391-1A* (distal) - 3 cM - *Rg-A1c(Bg)* - 1.6 cM - *Hg* - 2.4 cM - *Gli-A1* (proximal){9959}[2]; *Xgwm1223-A1* - 0&0.6 cM - *Rg-A1c*

- 4.7&4.6 cM - *Xgwm0136-1A*{10378}; Five of 6 wheats with *Rg-A1c* possessed a 264bp allele at *Xgwm0136-1A*{10378}; *Rg-A1c* - 0.7 cM - *Xgwm1223-1A*{10638}.

Rg-A1d. [*Bg(b)*{282}^{3}]. **dv:** G3116{282}.

At the diploid level *Rg-A1c (Bga)* and *Rg-A1d (Bgb)* were determinant and caused a solid black glume and a black line at the margins of the glume, respectively {282}.

A single factor for black glumes was reported in diploid, tetraploid and hexaploid wheats {1347}. Linkage with *Hg* was demonstrated at all levels of ploidy, indicating a common gene on chromosome 1A; *Bg* is epistatic to *Rg*.

Rg-B1{10378}. [*Rg1*,*Rg*]. 1B{1517}.1BS{369}.

Rg-B1a{10378}. **v:** TRI 542{10378}; White glumed genotypes. **dv:** *T. turgidum* ssp. *dicoccoides* acc. MG4343{9959}.

Rg-B1b{10378}. [*Rg1*]. **s:** CS*5/Red Egyptian 1B{1304}. **v:** Diamant I{9906}; Federation 41{1517}; Golubka{10635}; Highbury{1121}; Red Egyptian{1304}; *T. petrapavlovsky*{9906}. **v2:** Milturum 321 *Rg-A1b*{9906}; Milturum 553 *Rg-A1b*{9906}; Strela *Rg-A1b*{9906}. **tv:** Messapia{9959}; Ward{792}. **ma:** *Xutv1518-1B* (distal) - 7.7 cM - *Rg-B1b* - 0.8 cM - *Gli-B1* (proximal){9959}; *Xgwm1078-1B* - 1.5 cM - *Rg-B1b* - 3.1 cM - *Xgwm0550-B1*{10378}; *Xutv1518-1B* - (distal) - 7.7 cM - *Rg-B1b* - 0.8 cM - *Gli-B1* (proximal){9959}^{2}; *Xgwm1078-1B* - 4.6 cM - *Rg-B1* - 2.0 cM - *MW1B002(Gli-B1)* - 4.1 cM - *Xgwm550-1B*{10635}.

Rg-D1{10378}. [*Rg2*]. 1DL{769,1241}.1DS.

Rg-D1a{10378}. **v:** Novosibirskaya 67{10378}; L301{10378}; White glumed genotypes.

Rg-D1b{10378}. Derived from *Ae. tauschii* [*Rg2*]. **i:** Saratovskaya 29*5//*T. timopheevii* ssp. *timoppheevii/T. tauschii*{9906}. **v:** ITMI Synthetic W7984{10635}; Synthetic Hexaploid-11{10218}; (*Triticum turgidum* ssp. *dicoccoides/Ae. tauschii*){769}; (*Tetra Canthatch/Ae. tauschii* var. *strangulata* RL 5271); RL5404{1240}; (*Tetra Canthatch/Ae. tauschii* var. *meyeri* RL5289); RL5406{648,1240}. **v2:** Sears Synthetic *Rg-A1c*{10638}. **dv:** *Aegilops squarrosa* accessions. **QTL:** *QRg.ipk-1D* was mapped in the Opata/W-7984 (ITMI) mapping population{0255}; Linkage with *Gli-D1* implied *Rg2*. This QTL coincided with a QTL for awn colour, *QRaw.ipk-1D*{0255}. **ma:** *Xpsp2000-1D* - 9.3 cM - *Rg-D1b* - 21.2 cM - *Xgwm106-1D*{10128}; *Xgwm1223-1D* - 6.6 cM - *Rg-D1 / Xksud14-1D* - 13.9 cM - *Xgwm33-D1*{10635}; *Rg-A1c* - 3.9 cM - *Xgwm1223-1D*{10638}.

Rg-D1c{10378}. Brown or smokey-grey phenotype {729}. [*Brg*{729}]. **i:** ANK-23 = Novosibirskaya 67*10/K-28535{729}. **v:** Golubka{10378}; K-28535{729}; K-40579{729}; *T. aestivum* botanical varieties cinereum, columbina and albiglaucum{10378}. **ma:** *Xgwm1223-1D* - 1.5 cM - *Rg-D1c* - 13.1 cM - *Xbarc152-1D*{10378}; *Xbarc149-1D* - 6.3 cM - *Rg-D1c* - 26.5 cM - *Xbarc152-1D*{10378}.

Rg3{924,562}. 1AS{924,562,9906}. **i:** Saratovskaya 29*3 //F2 CS mono 1A/Strela{924}. **v:** CS/Strela Seln{9906}; Iskra{9906}; L'goskaya-47{1405}; L'govskaya-47{1405}; Zhnitstra{9906}. **v2:** Milturum 553 *Rg1*{9906}; Milturum 321 *Rg1*{9906}; Strela *Rg1*{9906,924}; Sobko & Sozinov{1405} reported a further group of 30 international wheats which, by inference from their *Gli-A1* alleles, probably carry *Rg3* . **ma:** A linkage order of *Glu-A1* - cent - *Hg* - *Rg3* was reported{1406].

Kovel {729} described a brown or smokey-grey glume phenotype in *T. aestivum* var *caesium* K-28535. This phenotype was also present in accession K-40579 and botanical varieties *cinereum, columbina* and *albiglaucum*. Close linkage to *Gli-D1* was shown and a gene designated *Brg* was assumed to be an allele of *Rg2* present in *Ae. tauschii* and synthetic hexaploid wheats. **v:** K-28535 {729}. **i:** ANK-23 = Novosibirskaya 67*10/ K-28535 {729}.

A 1B gene controlling red glume colour was mapped in a cross between durum wheat cv. Messapia and *T. turgidum* ssp. *dicoccoides* acc. MG4343. **ma**: *Xutv1518-1B* (distal) - 7.7 cM - *Rg1* - 0.8 cM - *Gli-B1* (proximal) {9959}.

QRg.ipk-1D{0255}. This QTL coincides with a QTL for awn colour, *QRaw.ipk-1D* {0255}. 1DS{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; The glume colour was contributed by W-7984{0255}. **ma:** Associated with *Gli-D1*{0255}.

28.2. Pseudo-black chaff

This is a blackening condition transferred from Yaroslav emmer to Hope wheat by McFadden at the same time as stem-rust resistance was transferred. The association of this condition with mature-plant stem-rust reaction (*Sr2*) has been noted in a number of papers. According to {742}, the condition is recessive. Pan {1102} considered linkage with stem-rust reaction could be broken, but this seems unlikely.

Pbc. 3B{742}.3BS. **s:** CS*6/Hope 3B{742}; CS*6/Ciano 5B{939}.

28.3. Black-striped glumes

This phenotype was reported in group *dicoccon*. **v:** E4225 {1417}.

28.4. Inhibitor of glume pigment

An inhibitor of glume pigment was reported on chromosome 3A {106}.

28.5. Chocolate chaff

cc{719}. 7B{719}.7BS{665}. **tv:** Langdon mutant{719}; PI 349056{665}. **dv:** CBC-CDd1{665}.

The chocolate chaff phenotype was suppressed by a gene(s) in chromosome 7D {719}.

28.6. Awn colour

The literature on awn colour is not clear. In general, awn colour is associated with glume colour {045}. Occasionally, however, awn colour and glume colour may be different. According to Panin & Netsvetaev {1103}, black awns were determined by three complementary genes designated *Bla1, Bla2, Bla3. Bla1* was located in chromosome 1A and linked with *Gld 1A* (= *Gli-A1*) and *Hg*.

QRaw.ipk-1A{0255}. 1AS{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; The awn colour was contributed by W-7984{0255}. **ma:** Associated with *Gli-A1*{0255}.

QRaw.ipk-1D{0255}. 1DS{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Awn colour was contributed by W-7984{0255}. **ma:** Associated with *Gli-D1*{0255}.

Bla1{10666}. 1AS{10666}. **bin:** 1AS1-0.47{10666}. **v:** Svenno{10666}. **ma:** *TC95235* - 4.8 cM - *Bla1*{10666}.

29. Grain Hardness/Endosperm Texture

Grain hardness or endosperm texture significantly influences flour milling, flour properties and end-use. The difference in particle size index between a hard wheat (Falcon) and a soft wheat (Heron) was reported by Symes {1452} to be due to a single major gene. Symes {1452} also found evidence for "different major genes or alleles" which explained differences amongst the hard wheats Falcon, Gabo and Spica. Using Cheyenne (CNN) substitution lines in CS and a Brabender laboratory mill, Mattern et al. {915} showed that the hard wheat milling and flour properties of Cheyenne were associated with 5D. Using Hope

5D substitution line in CS [CS(Hope 5D)] crossed to CS, and CS(Hope 5D) crossed to CS ditelosomic 5DL, Law et al. {777} showed that grain hardness was controlled by alleles at a single locus on 5DS. The dominant allele, *Ha*, controlling softness was present in Chinese Spring and the allele for hardness, *ha*, was present in the others. A similar study using CS (CNN5D)/CS recombinant inbred lines was reported by Morris et al. {03106}.

A pleiotropic result of hardness is the decreased level of a 15 kD starch granule protein, friabilin, on the surface of water-isolated starch {470}. In endosperm, soft and hard wheats have similar amounts of friabilin, consequently the distinction between the two textural types depends upon the manner in which the friabilin co-purifies with starch. Friabilin is also referred to by the name 'Grain Softness Protein' (GSP) {0384}, and was later shown to be comprised primarily of puroindoline a and puroindoline b {0295}. Grain hardness of reciprocal soft x hard F1 kernels was well correlated with friabilin occurrence on starch in triploid endosperm {0381}. See IV, Proteins: 5.8 Puroindoline. GSP-1 genes, which are closely related to puroindolines, are also listed in the Protein section.

Ha{777}. Soft phenotype. 5DS{777}. **i:** Falcon/7*Heron, Heron/7*Falcon{03109}; Paha*2//Early Blackhull/5*Paha{0203,0298}; Early Blackhull Derivative/5*Nugaines{0203,0298}. **v:** Chinese Spring {777,03106}; Cappelle Desprez {470}; Heron {1452,470}; Paha, Nugaines {0203,0298}; NY6432-18 {0241}.

ha{777}. Hard phenotype **i:** Falcon/7*Heron, Heron/7*Falcon {03109}; Paha*2//Early Blackhull/5*Paha {0203,0298}; Early Blackhull Derivative/5*Nugaines {0203,0298}. **s:** CS*6/Cheyenne 5D {915}; CS*6/Hope 5D {777}; Capelle Desprez*7/Besostaya 5D {470}. **v:** Falcon {1452,470}; Holdfast {470}; Early Blackhull, Early Blackhull Derivative{0203,0298}; Cheyenne {03106}; Clark's Cream {0241}. **ma:** *Ha* was closely linked to *Xmta9(Pui1)-5D* {1414}.

Single factor effects on hardness were found for chromosomes 2A, 2D, 5B and 6D, and interactive effects were found for chromosomes 5A, 6D and 7A {1414}.

The addition of King II rye chromosome 5R converted Holdfast wheat from hard to soft {470}. A 14.5 kD rye analogue was also isolated from 6x triticales which have soft texture {470}. All ryes are thought to have soft texture.

Two genes for grain hardness were reported in {055}.

Hard and soft NILs are listed in {0298}.

QTL: In a DH population of Courtot/CS a major locus in chromosome 5DS coincided with *Ha*; minor QTLs mapped in chromosomes 1A (associated with *Xfba92-1A*) and 6D (associated with *Xgwm55-6D*) {0141}.

Ten QTLs for kernel hardness (54% of the variation) were mapped in 'Forno'/ 'Oberkulmer' spelt {0280}. Two QTLs were detected for grain hardness in RILs of the ITMI population (Synthetic / Opata 85) {10051}. The QTL on the short arm of chromosome 5D was associated with *Xmta10-5D*, and increased hardness was contributed by Opata {10051}. The locus located proximally on the long arm of 5D was associated with *Xbcd450-5D* and increased hardness was contributed by the Synthetic allele {10051}.

Two QTLs, *QHa.ksu-3B*, associated with *Xksum9-3B* (R^2=0.09, and *QHa.ksu-5D(Ha),* associated with *Xcfd-5D* (R^2=0.3), were identified in Karl*2/TA 4152-4 {10273}.

Two QTLs were detected for grain hardness in RILs of the ITMI population (Synthetic / Opata 85) {10051}. The QTL on the short arm of chromosome 5D was associated with *Xmta10-5D*, and increased hardness was contributed by Opata {10051}. The locus located proximally on the long arm of 5D was associated with *Xbcd450-5D* and increased hardness was contributed by the Synthetic allele {10051}.

Two QTLs, *QHa.ksu-3B,* associated with *Xksum9-3B* (R^2=0.09, and *QHa.ksu-5D(Ha),* associated with *Xcfd-5D* (R^2=0.3), were identified in Karl*2/TA 4152-4 {10273}.

Using proteomic analysis of 2D-protein gels applied to 101 lines of the Opata/W-7984 (ITMI) RI mapping population, and after a preliminary study of a sub-group of these lines {10086}, 446 amphiphilic protein spots were resolved, 170 specific to either of the two parents and 276 common to both {10087}. An important category of these proteins comprises the puroindolines. Seventy-two loci encoding amphiphilic proteins were conclusively assigned to 15 chromosomes. At least one Protein Quantity Locus (PQL) was associated with each of 96 spots out of the 170 spots segregating; these PQL were distributed throughout the genome. The majority of the amphiphilic proteins were shown to be associated with plant membranes and/or play a role in plant defence against external invasions. Not only the puroindolines were associated with kernel hardness - a number of other amphiphilic proteins were also found to influence this trait.
Neixiang 188 (hard)/Yanshan 1 (medium hard) RIL population: *QGh.caas-1B.1* with hardness allele from Yanshan 1, R^2=0.28, *Xwms153-1BL - Xbarc81-1BL*{10640}

30. Grain Quality Parameters

In the comprehensive study of 46 quality-related traits in a RL4452/AC Domain RIL population, 99 QTLs involving 41 traits were located in 18 chromosomes {10361}; 14 QTLs clustered in the *Glu-1B* region (50cM), 20 QTLs occurred in the *Xwmc617-4D - Xwmc48-4D* region (30cM), 10 QTLs mapped to the *Xgwm130-7D - Xwmc405-7D* region (14cM) and 66 QTLs were dispersed {10361}. In a large study of 11 seed quality traits in a AC Karma/87E03-S2B1 DH population, 26 QTLs were detected in 7 chromosomes {10434}; 6 were clustered in the *Glu-D1* region and 5 were clustered in the *Rht-D1* region.

QTL analyses of 10 milling and baking quality traits (grain hardness, flour yield, grain and flour protein, alkaline water retention capacity (AWRC), sedimentation properties, cookie properties, lactic acid retention, dough strength, extensibility and mixograph properties) in the ITMI population grown in Mexico, France and USA (California) are reported in {10436}.
Neixing 188 / Yanshan 1 RIL population: 75 QTLs for 5 quality-related traits are reported in {10640}.

30.1. Sedimentation value

Qsev.mgb-6A{9920}. 6AL{9920}. **tv:** Nessapia/*T. dicoccoides* MG4343 mapping population{9920}. **ma:** Associated with *Xrsq805-6A*{9920}.

Qsev.mgb-7A{9920}. 7BS{9920}. **tv:** Messapia/*T. dicoccoides* MG4343 mapping population{9920}. **ma:** Associated with *Xpsr103-7A*{9920}. **QTL:** QTLs associated with *Glu-1* on chromosome arms 1AL and 1DL and *Gli-1/Glu-3* on 1BS in RSLs from the cross Cheyenne (high quality)/CS (low quality) {0251}. Cultivar Cheyenne contributed the higher SDS sedimentation values {0251}. The QTL on 1AL coincided with a QTL for bread loaf volume {0251}. The QTL on 1DL and 1BS coincided with QTL for bread mixing time{0251}.

30.2. Flour, semolina and pasta colour

QTL: A QTL was detected on chromosome 7A {9936}. Cultivar Schomburgk contributed the yellow colour allele in a cross Schomburgk/Yarralinka {9936}. Markers *Xcdo347-7A* and *Xwg232-7A* accounted for 60% of the genetic variation {9936}. A Sequence Tagged Site PCR marker is available {0180}.
A major QTL was detected in the distal region of chromosome 7BL in the cross Omrabi 5/ *T. dicoccoides* 600545. The QTL explained 53% of the variation and was completely linked to microsatellite marker *Xgwm344-7B*. Omrabi 5 contributed the allele for high yellow pigment level. Two additional small QTLs were detected on 7AL {0365}. Other references to flour

colour are given under Flour Colour, *Lr19*, and *Sr25*.

W9262-260D3 (low yellow colour)/Kofa (high colour): Four QTLs identified on chromosomes 2A (*Xgwm425-2A*), 4B (*Xgwm495-4B*), 6B (*Xgwm193-6B*) and *Psy-B1* (chromosome 7BL) {10230}. See also Enzymes Phytoene synthase.

Analysis of yellow flour pigment in a RIL population of PH82-2 (low)/Neixiang (high) revealed major QTL on chromosomes 7A co-segregating with marker *YP7A* (R^2 = 0.2 - 0.28) (see Phytoene synthase 1), and 1B (R^2 = 0.31 - 0.54) probably contributed by 1RS {10501}. Huapei 3 /Yumai 57: DH lines: 18 additive QTLs and 24 pairs of epistatic QTLs affected flour colour parameters; *qa-1B*, closely linked with *Xbarc372-1B* was associated with variation of a*, R^2=0.256 {10625}.

A further study confirmed major QTL on chromosome 1RS (R^2=0.319) and 7A (R^2=0.339), minor QTL occurred on 1A and 4A {10716}.

30.3. Amylose content

Amylose content has a significant effect on industrial quality; for example, reduced amylose wheats perform better in some types of noodles. The waxy protein genes have an important influence, but other genes are also involved.

QAmc.ocs-4A.1{0047}. 4AS{0047}. **v:** CS/CS(Kanto107 4A) mapping population{0047}.
ma: Associated with *Xbcd1738-4A* and *Xcdo1387-4A*{0047}.

30.4. Milling yield

QTL: A QTL was detected on chromosome 3A {0181}. Cultivar Schomburgk contributed an allele for the higher milling yield in cross Schomburgk/Yarralinka {0181}. RFLP markers *Xbcd115-3A* and *Xpsr754-3A* were associated with this QTL at LOD>3 {0181}.
A QTL associated with *Pinb* on chromosome arm 5DS was detected in RILs from the cross NY6432-18/Clark's Cream {0241}. Cultivar Clarks Cream contributed the higher flour yield allele {0241}. This QTL coincided with QTL for hardness, hydration traits (dough water absorption, damaged starch and alkaline water retention capacity (AWRC) and baked product traits (cookie diameter and cookie top grain) {0241}.

30.5. Alveograph dough strength W

QTL: QTLs for W were detected on chromosome arms 5DS (associated with *Xmta10-5D*), 1AS (associated with *Xfba92-1A*), and 3B (associated with *XksuE3-3B*) in cross Courtot/Chinese Spring {0141}. The first two QTLs coincided with those for hardness.
Ten QTL for W (39% of the variation), nine QTL for P (48% of the variation) and seven QTL for P:L (38% of the variation) were mapped in Forno/Oberkulmer spelt {0280}.

30.6. Mixograph peak time

QTL: A QTL associated with *Glu-Dy1* on chromosome arm 1DL was detected in RILs from the cross NY6432-18/Clark's Cream {0241}. Clark's Cream contributed the higher mixograph peak time allele {0241}. This QTL coincided with a QTL for bread mixing time {0241}.

30.7. Starch characteristics

The Isoamylase-1 gene from *Ae. tauschii (Iso-1)* complements the deficient rice sugary-1 mutant line {10295}.
QTL: QTLs for starch viscosity and swelling were associated with the *Wx-B1* locus in Cranbrook (*Wx-B1a*)/Halberd (null *Wx-B1b*). An additional QTL for starch viscosity was found on 7BL between markers *Xgwm344-7B* and *Xwg420-7B* in the first cross. This QTL disappeared when amylase activity was inhibited indicating that it was determined by the late maturing a-amylase activity contributed by Cranbrook. A QTL for starch viscosity was associated with the *Wx-A1* locus in the cross CD87/Katepwa {0362}.

30.8. Loaf volume

Lvl1{10312}. [*Lvl 1*{10312}]. 3A{10312}. **v:** Cappelle Desprez*7/Bezostaya 1 3A{10312}.
ma: *Xgwm720-3A - Lvl1* appeared to be located in the *Xgwm2-3A - Xgwm720-3A* region{10312}.

QTL: Loaf volume score consistent across three environments was scored in a RIL population Renan/Recital and revealed major QTL on chromosomes 3A (flanking markers *Xfbb250-3A, Xgwm666-3A,* positive effect from Renan) and 7A (flanking markers *Xcfa2049-7A, Xbcd1930-7A,* positive effect from Recital) {10536}.
A total of 30 QTLs were located on 12 chromosomes, each of which explained between 5.85 and 44.69% of the phenotypic variation; the QTLs of largest effect were located on chromosomes 6B and 6D {10659}.

30.9. Dough rheological properties

QTL: In a Cranbrook/Halberd DH population, environmental factors were a major determinant of dough extensibility whereas additive effects of alleles at the hight and low molecular weight glutenin loci determined dough strength {10247}.

30.10. Grain fructan content

Fructans are non-digestible carbohydrates considered to have health benefits to consumers.
QTL: Berkut (high fructan concentration) / Krickauff (low fructan concentration): QTL detected on chromosomes 2B, 3B, 5A, 6D, and 7A of which *QGfc.aww-6D.2* (R^2=0.17, nearest marker, *Xbarc54-6D*) and *QGfc.aww-7A.1* (R^2=0.27,*Xgwm681-7A*)had the largest effects {10631}.

30.11. Water absorption

Neixiang 188 / Yanshan 1 RIL population: *XAbs.caas-5D.1* with positive effects from Yanshan 1, R^2=0.3, *Xcfd18-5DS - Xcfd189-5DS* {10640}

30.12. Chinese dry noodle quality

Chuan 35050 / Shannong 483 RIL populations: 3 QTLs for noodle palate, elasticity and smoothness clustered near *Glu-D1* with beneficial effects associated with subunits 5+10 coming from Chuan 35050. A very significant taste QTL, *QStas.sdau-4A.1* and positive QTLs for stickiness and total score also on chromosome 4A came from Shannong 483 {10647}

31. Grass-Clump Dwarfness/Grass Dwarfness

Complementary dominant genes. Genotypes producing dwarfness: *D1-D2-D3-, D1-D2D2, D1-D4-D3-*, *D1-D2-D4* and *D1-D4D4*.

D1{534}. [*G*{972}]. 2D{534,939,1595}.2DS{942}. **s:** CS*7/Kenya Farmer 2D{1000}; CS*6/Timstein 2D{534}. **v:** Big Club{534}; Burt{1000}; Federation{942}; Mus{534}; Ramona 50{358}; Selection 1403{1000}. **v2:** Hermsen's pure-breeding dwarf *D2*{1000}; Falcon *D3*{1172}; Gabo *D3*{944}; Timstein *D3*{534}; Metzger's pure-breeding dwarf *D2 D3*{1000}.

D2{534}. [*Bi*{972}]. 2B{536,574}.2BL{944}. **s:** CS*7/Cheyenne 2B{1000}; CS*4/Red Egyptian 2B{1000}. **v:** Bezostaya 1{1595}; Crete-367{1029}; Desprez 80{1595}; Florence{1000}; Kenya W744{944}; Loro{1172}; Mara{1595}; Marquis{1000}; Poros{1595}; Redman{534,574,1001}; Riebesel{534}; Tobari 66{358}. **v2:** Hermsen's pure-breeding dwarf *D1*{534,1000}; Amby *D3*{358}; Cedar *D3*{1000}; Mendel *D3*{534}; Plantahof *D3*{534}; Spica *D3*{944}; Cappelle-Desprez *D4*{1595}; Brevor *D4*{1000}; Cheyenne *D4*{1000}; Metzger's pure-breeding dwarf *D1D3*{1000}.

D3{534}. [*A*{972}]. 4A{534,1595}.4AL{939}. **s:** CS*6/Timstein 4A{534,1000}; CS*7/Kenya Farmer 4A{534,1000}. **v2:** Amby *D1*{358}; Falcon *D1*{1172}; Gabo *D1*{944}; Kenya Farmer *D1*{1000}; Timstein *D1*{534}; Metzger's pure-breeding dwarf *D1 D2*{1000}.

D4{1000}. 2D{1000,1595}.2DL{1598}. **s:** CS*7/Cheyenne 2D{1000}. **v2:** Cappelle-Desprez *D2*{1595}; Cheyenne *D2*{1000}; Brevor *D2*{1000}.

d1d2d3d4. **v:** Chinese Spring{534,1000}.

Genotype lists in can be found in {358,534,972}. The effects of multiple allelism at *D2*, and possibly at *D1*, and modifying genes were demonstrated {1595}.

Knott {683} described a lethal dwarf condition controlled by a dominant gene closely linked with *Sr30* (chromosome 5D) in Webster and a complementary recessive gene in LMPG.

Phenotypes resembling grass clump dwarfs in hybrids carrying a 2BL.2RS translocation were reported in {916}. The complementary gene{s} in wheat was not *D1, D2 or D3*. The effect was suppressed at high temperature.

32. Grain Weight

QTL : Variation at locus *QGw1.ccsu-1A*, associated with *Xwmc333-1A*, accounted for 15% of the variation in a RIL population from RS111/CS {0165}.

Rye Selection 111 (high GW)/CS (low GW) RIL: two definitive QTLs *QGw.ccsu-2B.1* and *QGw.ccsu-7A.1* and one tentative QTL, *QGw.ccsu-1A.1*, were detected by CIM analysis {10363}. The chromosome 7A QTL co-located with a QTL for early heading {10363}.

QGw1.inra-2B{10071}. **v:** Renan/Recital; favourable allele from Renan {10071}. (R^2=10.7-19.7%){10071}. **ma:** *Xgwm374-2B - Xgwm388-2B*{10071}.

QGw1.inra-5B{10071}. **v:** Ranan/Recital; favourable allele from Recital {10071}. (R^2=4.9-10.4%){10071}. **ma:** *Xgwm639-5B - Xgwm604-5B*{10071}.

QGw1.inra-7A{10071}. **v:** Renan/Recital; favourable allele from Recital {10071}. (R^2=5.2 - 10.3%){10071}. **ma:** *Xcfa2049-7A - Xbcd1930-7A* {10071}.

33. Growth Rate and Early Vigour

QTL analyses in *Ae. tauschii*: chromosomes 1D, 4D, and 7D carried QTLs for relative growth rate, biomass allocation, specific leaf area, leaf area ratio, and unit leaf rate. Chromosome 2D had QTLs for rate and duration of leaf elongation, cell production rate, and cell length. Chromosome 5D harbored QTLs for total leaf mass and area, number, and growth rate of leaves and tillers {10293}.

34. Hairy/Pubescent Auricles

Pa{886,042}. 4BS{886,042}. **s:** Saratovskaya 29*9/Yanetzkis Probat 4B{886}; Saratovskaya 29*5/Shabati Sonora 4B{886}; Saratovskaya 29*4/Siete Cerros 4B{886}. **v:** Diamant 1{886}; Magali{886}; Pirotrix 28{886}; Shabati Sonora{886}; Siete Cerros{886}; Ulyanovka 9 {886}.

pa. **v:** Gabo{886}; Saratovskaya 29{886}; This phenotype is expressed in Diamant ditelo 4BL{886}.

35. Hairy Glume

Hg{1494}. 1A{1293}.1AS{947}. **i:** S-615*11/Jones Fife{1500}. **s:** CS*7/Indian 1A{1293}. **v:** A well-known, widespread and easily identified dominant marker - only a few examples will be listed. Indian{1293}; Jones Fife{1494}; Prelude{1494}. **itv:** LD222*11/*T. turgidum* var. *durum melanops*{1546}. **tv:** Golden Ball{1342,1494}. **dv:** *T. monococcum* lines{1494}. **ma:** *Xutv1391-1A* (distal) - 3 cM - *Bg* - 1.6 cM - *Hg* - 2.4 cM - *Gli-A1* (proximal){9959}; Tel.........*Hg/BG605525* - 3.8 cM - *Xpsp2999(Glu3)-1A*{10193}.

A 1A gene controlling hairy glumes was mapped in a cross between durum cv. Messapia and *T. turgidum* ssp. *dicoccoides* acc. MG4343{9959}.

Hg1{1405}. **v:** Ulyanovkn{1405}; Pionerskaya{715,1405}.

Evidence for multiple alleles in *T. monococcum* is given in {744}.

The likelihood of three alleles, *hg* (hairless), *Hg1* (weakly hairy) and *Hg* (very hairy), with *hg1* being recessive to *Hg* and causing a short (weak) hairy phenotype, was mentioned in {1405}.

36. Hairy Leaf

Hl1{0316}. Weakly hairy. [*Hl*{884}]. 4B{884}.4BL{760}. **v:** Artemovka{925}; Caesium 111{925}; Lutescens 53/12{925}; Lutescens 62{925}; Milturum 321{884}; Poltavka{925}; Pyrothrix 28{925}; Saratov 321{884}; Saratovskaya 29{884,760}; Sarrubra{925}. **ma:** *Xgwm375-4B* - 12.1 cM - *Hl1* - 2.1 cM{10516}.

Hl2{0316}. 7BS{0316}. **v:** Hong-mang-mai {0316}.

The hairy leaf gene (Hl^{Aesp}) in *Ae. speltoides* introgression line 102/00^I was allelic with *Hl2* {10516}.

hl1 hl2. **v:** Chinese Spring{884}.

Kuspira *et al.* {744} provided evidence for at least three alleles at an *Hl* locus in *T. monococcum.*

A QTL analysis of the ITMI population identified loci determining hairiness of leaf margins and auricles in regions of chromosomes 4B and 4D orthologous to *Hl1* {10516}.

37. Hairy Leaf Sheath

Levy & Feldman {795} concluded that complementary genes determined hairy leaf sheath in *T. dicoccoides*.

Hs{795}. [*Hls*{761}]. **v:** Certain hexaploid derivates of G25 produced in Israel{939}. **tv:** *T. dicoccoides* G25{761}.

hs. **v:** Most hexaploid wheats{939}. **tv:** *T. dicoccoides* G7{761}.

38. Hairy Neck/Pubescent Peduncle

Hp{275}. Derived from *Secale cereale*

4BL{T4B.5R}{274,275}. **i:** S-615*11/CS Derivative{1500}.

5BS{T5B-5R}{1298}. **v:** HN-2 (CS type){1298}.

6D{T6D-5R}{1298}. **v:** HN-1(CS type){1298}.

4BL{T4B.5R}{274,275}. **v:** CS Derivative{1304}.

39. Hairy Node/Pubescent Node

Inheritance of hairy (glabrous) node versus non-hairy node was attributed to a single, dominant gene difference {396,837,910,914} and the *Hn/hn* locus was shown to be linked with *B1* (awn inhibitor). Observations on 5A trisomics and telosomics of Chinese Spring confirmed this location. Love & Craig {837} studied a cross involving Velvet Node CI 5877, and Gaines & Carstens {396} studied an offtype single plant designated Velvet Node Wash. No. 1981.

Hn. 5AL. **v:** Aurore{722}; Fylgia{722}; Extra-Kolben II{722}; Marquis{910}; Tammi{765}; *T. vulgare erythrospermum*{910}. **tv:** *T. polonicum vestitum*{910}.

hn. **v:** Garnet{722}; Kimno{722}; Pika{722}; Timantii{722}.

Multiple alleles were reported in *T. monococcum*{744}.

40. Heat tolerance

QTL: QTLs contributing to grain-filling duration (GFD) under high temperatures were associated with *Xgwm11-1BS* (11% of variability) and *Xgwm293-5AS* (23% of variability) in Ventnor (tolerant) // Karl 92 (non-tolerant) {0327}.

41. Height

Ht is the general symbol.

41.1. Reduced Height : GA-insensitive

Rht-1{371,0019}.

The *Rht-1* homoeoloci are orthologous with the *D8* locus in maize and the *GAI* locus in *Arabidopsis*. They encode proteins resembling nuclear transcription factors and are involved in sensing gibberellin levels {0019}. Common wheat and durum NIL pairs are listed in {02102}.

Rht-A1a{0019}. **v:** Chinese Spring{0019}; All wheats are assumed to be monomorphic.

Rht-B1{116}. 4B{109,406,1040}.4BS{089,116}. **ma,tv:** *Gai1/Rht-B1b* - 1.8 cM - *Xpsr622-4B*{110}. **ma:** Co-located with *Xbarc10-4B*{10189}.

Rht-B1a{116}. **v:** Tall wheats{116}; e.g. Chinese Spring{0019}.

Rht-B1b{116}. Partially recessive {024}, recessive {357}, semi-dominant {408}. [*Rht1*{015},*Sd1*{015}]. **i:** See{408,414,02102}. **v:** Frontier{1597}; Guardian{1597}; Selection 14-53/Burt, 5{015}; Siete Cerros{407}; Wren{1174}; WW15{407}. **v2:** Norin 10-Brevor, 14 *Rht-D1b*{015}; Oleson *Rht-D1b*{357}; Selection D6301 *Rht-D1b*{357}; Shortim *Rht-D1b*{243}; See{407,415,1062,1386}. **tv:** Cocorit 71{109,416}; Creso{109,416,451}; Malavika{1442}; Mida{450}; Sansone{109}; Valgerado{109,416}; Valnova{450}; Valselva{450}.

The development of allele-specific primers for *Rht-B1b* was reported in {0378}.

QTL: QTL for reduced plant height, peduncle length and coleoptile length contributed by Cranbrook were associated with *XcsMe1-4B* (up to 49% of variability for plant height and peduncle length and 27-45% of variability for coleoptile length) in the cross Cranbrook (dwarf) / Halberd (tall). The dwarfing effect underlying the QTL was caused by the *Rht-B1b* allele {0379}.

Rht-B1c{116}. Semi-dominant {1040}. [*Rht3*{565},*Sd3*{565}]. **i:** Tom Thumb/7* Kharkov// Lancer{1040}; See{408}. **v:** Minister Dwarf{404}; Selection D6899 (Tom Thumb-Sonora 64/Tacuari){357}; Tom Thumb{405}; Tom Pouce Blanc{407,1634}; Tom Pouce Barba Rouge{407,1634}; Topo; Tordo. **ma:** *Xmwg634-4B* (distal) - 30.6 cM - *Rht-B1c* - 11.9 cM - *Xpsr144-4B* (proximal){117}.

Rht-B1d{116}. Semi-dominant {1599,116}. [*Rht1S*{1599}]. **v:** Saitama 27{1599}; Occurs frequently in Italian and Yugoslavian wheats{1599}; Argelato, Centauro, Chiarano, Etruria, Farnesse, Gallo, Gemini, Lario, Pandas, Produttore, Orlandi, Orso, Salvia, Sprint, Strampelli.

Rht-B1e{116}. [*RhtKrasnodari1*{452},*Rht1(B-dw)*{1600}]. **v:** Krasnodari 1 (a spontaneous GA-insensitive offtype of Bezostaya 1){1600}.

Rht-B1f{116}. Semi-dominant {116}. [*RhtT. aethiopicum*{116}]. **tv:** *T. aethiopicum* accessions W6824D{116}; W6807C{116}.

Rht-B1g{0019}. **v:** Highbury mutants M3 103-3 and M3 103-9{0019}; Allele *Rht-B1g* is a fast neutron-induced mutation of *Rht-B1b* and produces a tall gibberellin responsive phenotype{0019}.

Rht-B1^{IC2196}{10144}. **tv:** *T. turgidum* var. *polonicum* IC12195{10144}.

Rht-D1{116}. 4D{411,583,1544}.4DS{980,1266,116}. **i:** Common wheat and durum NIL pairs are listed in {02102}. **ma:** *Xpsr1871(Pki)-4D* - 4 cM - *Rht-D1* - 6 cM - *Xubc821(PhyA)-4D*{410}; *Rht-D1* - 2.8 cM - *Xglk578-4D*{9966}; *Xpsr1871* - 1 cM - *Rht-D1b* - 4 cM - *Xpsr821*(PhyA){0019}.

Rht-D1a{116}. **v:** Tall wheats{116}; e.g. Chinese Spring.

Rht-D1b{116}. Partially recessive {024}, recessive {357}, semi-dominant {408}. [*Rht2*{015},*Sd2*{015}]. 4D{411}.4DS{980}. **i:** See{408,414,02102}. **v:** Biscay{10574}; Combe{567}; Era{407}; Gaines Sib 2{015}; Jaral{407}; Kite{1174}; Maris Hobbit {411}; Pirat{10574}; Pitic 62 {567}; Rubens{10574}; Songlen{243}. **v2:** Oleson *Rht-B1b*{357}; Norin 10-Brevor, 14 *Rht-B1b*{015}; Selection D6301 *Rht-B1b*{357}; List in{1386}. **ma:** The development of allele-specific primers for *Rht-D1b* was reported in{0378}.

Rht-D1c{116}. Dominant {114}. [*Rht10*{1266}]. **v:** Ai-bian{1544,1266}. **ma:** *Xpsr921-4D* (4DS) - 0.8 cM - *Rht-D1c* - 28 cM - *Xgwm165-4D* (4DL){117}.

Rht-D1d{116}. Semi-dominant {116}. [*RhtAi-bian 1a*{115}]. **v:** Ai-bian 1a (spontaneous mutant of Ai-bian 1){115}.

The line XN004, earlier considered to have *Rht21*{0230}, was shown to carry an allele at the *Rht-D1* locus {0231}.

Various common wheat and durum N1Ls differing at the *Rht-B1* and *Rht-D1* loci are listed in {02102}. Genotype lists in {402,1382,1612,1613}.

Genotypes of Indian semi-dwarf wheats based on the Ellis et al. {0378} markers are given in {10404} and those for U.S. eastern and central and winter wheat cultivars are given in {10868}.

41.2. Reduced Height : GA-sensitive

Borner *et al*. {116} found no evidence of orthologous GA-sensitive genes in rye, but reviewed evidence for orthologous GA-insensitive genes. The close linkage of *Rht8* and *Xgwm261-2D* permitted the use of the microsatellite as a marker for the detection of allelic variants at the *Rht8* locus{9962}.

Rht4{568}. Recessive. 2BL{10249}. **v:** Burt *ert* 937, CI 15076{566,717}. **ma:** Associated with *Xwmc317-2B*{10249}.

Rht5{717}. 3BS{10249}. **v:** Marfed *ert* 1, M1, CI 13988{717,718,1593}. **ma:** Approximately 10 cM from *Xbarc102-3B*{10249}.

Rht6{718}. Recessive. **v:** Brevor{569}; Burt{569,718}. **v2:** Norin 10-Brevor, 14 *Rht-B1b Rht-D1b*{569}.

Rht7{1602}. 2A{1602}. **v:** Bersee Mutant A{1602}; Bersee Mutant C{1602}.

Rht8. 2D{772,1601,1598}.2DS. **s:** Cappelle-Desprez*/ Mara 2D{1601}. **v:** Chuan Mai 18{10249}; Novasadska Rana 1{1604}; Sava{1601,414}. **v2:** Akakomugi *Rht9*{1191}; Mara *Rht9*{1191}. **ma:** *Xgwm484-2D* (proximal) - 19.9 cM - *Rht8* - 0.6 cM - *Xgwm261-2D* (distal){727}; Close linkage with *Xwmc-2D*{10249}; A survey of Chinese cultivars showd 13 alleles of *Xgwm261-2D*{10284}.

The close linkage of *Rht8* and *Xgwm261-2D* permitted the use of the microsatellite as a marker for the detection of allelic variants at the *Rht8* locus{9962}. Allele sizes for *Xgwm261* in U.S. eastern and central wheat cultivars are given in {10868}.

Rht8a. Associated with a 165-bp fragment of WMS 261 {9962}. **v:** Autonomia{9962}; Bobwhite{9962}; Brevor{9962}; Chaimite{9962}; Ciano 67{9962}; Chris{9962}; Dugoklasa{9964}; Federation{9962}; Frontana{9962}; Glennson 81{9962}; Hope{0243}; Jupateco 73{9962}; Kenya{9962}; Klein 32{9962}; Lerma Rojo{9962}; Lusitano{9962}; Maringa{9962}; Marquis{0243}; Mentana{9962}; Michigan Amber{0243}; Nainari 60{9962}; Newthatch{9962}; Opata 85{9962}; Othello{9962}; Penjamo 62{9962}; Quaderna{9962}; Rex{9962}; Riete{9962}; Saitama 27{9962}; Spica{9962}; Veery S{9962}; Victo{9962}.

Rht8b. Associated with a 174-bp fragment of WMS 261 {9962}. **s:** Cappelle Desprez*/Mara 2D{1601}. **v:** Arthur{0243}; Balkan{9962}; Bunyip{9962}; Cappelle-Desprez{9962}; Carstens{0243}; Diakovchanka{0243}; Eureka{9962}; Festival{9962}; Fronteira{9962}; Fultz{9962}; Gabo{9962}; Heine VII{9962}; Inallettabile 95{9962}; Jena{9962}; Klein Rendidor{9962}; Leonardo{9962}; Lutescens 17{9962}; Mironovskaya 808{9962}; Norin 10{9962}; Norin 10/Brevor 14{9962}; Oasis{0243}; Odom{0243}; Podunavka{9962}; Purdue Abe{0243}; Record{9962}; Red Coat{9962}; Salzmunder Bartweizen 14/44{0243}; Soissons{9962}; Talent{9962}; Tevere{9962}; Timstein{9962}; Tp114/65{0243}; Wilhelmina{9962}; Wiskonsin 245 C/11226{0243}.

Rht8c. Associated with a 192 bp fragment of WMS 261 {9962}. **v:** Akakomugi{1191}; Alfa{9962}; Aquila{9962}; Ardito{9962}; Argelato{9962}; Avrora{9962}; Banija{9964}; Baranjka{9964}; Beauchamps{9962}; Bezostaya{9962}; Biserka{9962}; Campodoro{9962}; Centauro{9962}; Chikushi-Komugi (Norin 121){9962}; Chuanmai 18{10512}; Damiano{9962}; Djerdanka{9964}; Dneprovskaya{9962}; Duga{9964}; Etoile-de-Choisy{9962}; Etruria{9962}; Fakuho-Komugi (Norin 124){9962}; Farnese{9962}; Favorite{9962}; Fedorovka{0243}; Fiorello{9962}; Fortunato{9962}; Funo{9962}; Gala{9962}; Haya Komugi{9962}; Impeto{9962}; Irnerio{9962}; Jarka{9964}; Jugoslavia{9962}; Kavkas{9962}; Kaloyan{0243}; Khar'kovskaya 50{0243}; Khar'kovskaya 93{0243}; Khersonskaya 86{0243}; Kolubara{9964}; Kosava{9964}; Libellula{9962}; Lonja{9964}; Lovrin 32{9962}; Macvanka-2{9964}; Mara{119,9962}; Marzotto{9962}; Mv 03-89{0243}; Mv 06-88{0243}; Mv 17{0243}; Neretva{9962}; Nizija{9962}; Novasadska Rana 1{1604}; N.S. Rana 1{9962}; N.S. Rana 2{9962}; N.S. 649{9962}; N.S. 3014{9962}; Obrii{0243}; Odesskaya 51{0243}; Odesskaya 117{0243}; Odesskaya 132{0243}; Odesskaya Krasnokolosaya{0243}; Odesskaya Polukarlikovaya{0243}; Orlandi{9962}; Osjecanka{9964}; OSK 5 5/15{9964}; OSK 4 57/8{9964}; OSK 3 68/2; Partizanka{9962}; Partizanka Niska{9962}; Poljarka{9964}; Posavka 1{9964}; Posavka 2{9962}; Pomoravka{9962}; Produttore{9962}; Radusa{9962}; Roazon{0243}; Salto{9962}; Sanja{9962}; San Pastore{9962}; Sava{1601,414,9962}; Siete Cerros{9962}; Sinvalocho{9962}; Simvol Odesskii{0243}; Sivka{0243}; Strumok{0243}; Skopjanka{9962}; Skorospelka 3B{9962}; Slavonija{9964}; Somorka{9964}; Sremica{9964}; Superzlatna{9962}; Svezda{9962}; Tira{0243}; Tisa{9964}; Transilvania{9962}; Ukrainka Odesskaya{0243}; Una{9962}; Villa Glori{9962}; Vympel{0243}; Yubileinaya

75{0243}; Zagrebcanka{9964}; Zelengora{9964}; ZG 6103/84{9964}; ZG 7865/83{9964}; Zitarka{9964}; Zitnica{9962}; Zlatna Dolina{9964}; Zlatoklasa{9964}; Zolotava{0243}.

Although CS carries a 192 bp fragment, sequencing showed it was a different allele than other genotypes with *Rht8c* {02103}.

Although the 'diagnostic' association of *Rht8c* and *Xgwm261*$_{192}$ applied in many Strampelli derivatives and European wheats, there was no association between reduced height and this allele in Norin 10 and its derivatives {10512}. The pedigrees of a number of Chinese wheats postulated to have *Rht8c* on the basis of the marker trace to Italian sources {10515}.

Rht8d. Associated with a 201-bp fragment of WMS261 {9962}. **v:** Pliska{9962}; Courtot{9962}.

Rht8e. Associated with a 210-bp fragment of WMS261 {9962}. **v:** Chino{9962}; Klein Esterello{9962}; Klein 157{9962}.

Rht8f. Associated with a 215-bp fragment of WMS261 {9962}. **v:** Klein 49{9962}.

Rht8g. Associated with a 196-bp fragment of WMS261 [{0243}]. **v:** Mirleben{0243}.

Rht8h. Associated with a 206-bp fragment of WMS261 [{0243}]. **v:** Weihenstephan M1{0243}.

Rht9. 7BS{772,1601}.5AL{10249}. **v:** Acciao{718}; Forlani{718}; Mercia 12{10249}. **s:** Cappelle-Desprez*/Mara 5BS-7BS{1601}. **v2:** Akakomugi *Rht8*{1601}; Mara *Rht8*{1601}. **ma:** Close linkage with *Xwmc410-4A*{10249}.

Rht11{718}. **v:** Karlik 1{718}.

Rht12{718}. Dominant. 5A{1445,1606}. **bin:** 5AL-23, based on co-segregation with *B1*{1606}. **v:** Karcagi 522M7K{721}. **ma:** *Rht12* is located distally on 5AL cosegregating with *B1* and closely linked to *b-Amy-A1*{1606}; *Xgwm291-5A* - 5.4 cM - *Rht12*{726}.

Rht12 delayed ear emergence by 6 days{1606}.

Rht13{718}. 7BS. **v:** Magnif 41M1 CI 17689{718}. **ma:** Associated with *Xwms577-7B*{10249}.

Rht14{718}. Allelic with *XRht16* and *Rht18* {10767, 10818}. 6AS{10767}. **v:** Cp B 132 {123} = Castelporziano PI 347331{718}. **ma:** *Rht14* - 11.7 cM - *Xbarc3-6A*{10767}.

Rht15{718}. **tv:** Durox{718}.

Rht16{718}. Allelic with *Rht14* and *Rht18* {10767, 10818}. 6AS{10767}. **v:** Edmore M1{718}. **ma:** *Rht16* - 28.0 cM - *Xbarc3-6A*{10767}.

Rht17{718}. **v:** Chris Mutant CI 17241{1129}.

Rht18{718}. Allelic with *Rht14* and *Rht16* {10767, 10818}. 6AS{10767}. **tv:** Icaro{718}. **ma:** *Rht18* - 25.1 cM - *Xbarc3-6A*{10767}.

Rht19{718}. **tv:** Vic M1{718}.

Rht20{718}. **v:** Burt M860{718}.

Rht21{0230}. The existence of this gene was not confirmed {0231}.

Rht22{10857}. 7AS{10857}. **tv:** Aiganfanmai{10857}. **ma:** *Xgwm471-7A* - 29.5 cM - *Rht22* - 20.1 cM - *Xgwm350-7A*{10857}.

41.3. Reduced Height : QTL

In Courtot/CS:

QHt.fcu-4BL{10256}. **ma:** Associated with *Xbarc125-4B* (R^2=0.57){10256}. Reduced height allele in Grandin {10256}.

QHt.fcu-6AS{10256}. **ma:** Associated with *Xbarc23-6A* - *Xcp201-6A* (R^2=0.07){10256}. Reduced height allele in BR34 {10256}.

QHt.crc-2D{10287}. 2D{10287}. **ma:** Linked to BE497718-260 (LOD 4.2) in RL4452/AC Domain{10287}.

QHt.crc-4B{10287}. 4B{10287}. **ma:** Linked to *Rht-B1* (LOD 7.7) in RL4452/AC Domain{10287}.

Associated with QTLs for lodging and 1000-grain weight.

QHt.crc-4D{10287}. 4D{10287}. **ma:** Linked to *Rht-D1* (LOD 30.9) in RL4452/AC Domain{10287}.

Associated with QTLs for lodging 1000-grain weight, yield, height, and test weight.

QHt.crc-5B{10287}. 5B{10287}. **ma:** Linked to *Xwmc640-5B* (LOD 6.1) in RL4452/AC Domain{10287}.

QHt.crc-7A{10287}. 7A{10287}. **ma:** Linked to *Xwmc139-7A* (LOD 3.3) in RL4452/AC Domain{10287}.

QHt.crc-7B{10287}. 7B{10287}. **ma:** Linked to *Xgwm333-7B* (LOD 3.3) in RL4452/AC Domain{10287}.

QHt.fra-1A{9957}. **ma:** Linkage with *Xfba393-1A*{9957}.

QHt.fra-1B{9957}. **ma:** Linkage with *Xcdo1188-1B.2*{9957}.

QHt.fra-4B{9957}. **ma:** Linkage with *Xglk556-4B*{9957}.

QHt.fra-7A{9957}. **ma:** Linkage with *Xglk478-7A*{9957}.

QHt.fra-7B{9957}. **ma:** Linkage with *XksuD2-7B*{9957}.

QTLs for height detected in the cross Renan/Recital {10069}. LOD scores and percent of variation explained by the QTL(R^2 are averages of three years of field tests.

QHt.inra-2B{10069}. **ma:** Associated with *Xgwm249-2B* (LOD=5.8, R^2=15.4%){10069}.

QHt.inra-4A{10069}. **ma:** Associated with *Xfba243-4A* (LOD=6.5, R^2=15.0%){10069}.

QHt.inra-5A{10069}. **ma:** Associated with *Xgwm639b-5A* (LOD=5.7, R^2=10.8%{10069}.

QHt.inra-6D{10069}. **ma:** Associated with *Xcfd76-6D* (LOD=3.7, R^2=8.1%{10069}.

QHt.inra-7A{10069}. **ma:** Associated with *Xcdo545-7A* (LOD=3.2, R^2=7.7%){10069}.

QHt.ipk-4A{0255}. 4AL{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; the height is contributed by Opata{0255}. **ma:** Associated with *Xmwg549-4A*, *Xabg390-4A* and *Xbcd1670-4A*{0255}.

QHt.ipk-4A coincided with QTLs for ear length (*QEl.ipk-4A*), grain number (*QGnu.ipk-4A*) and grain weight per ear (*QGwe.ipk-4A*) {0255}.

QHt.ipk-6A{0255}. 6A{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; The height is contributed by W-7984{0255}. **ma:** Associated with *Xcdo29-6A* and *Xfba234-6A*{0255}.

QHt.ipk-6A coincided with QTLs for peduncle length (*QPdl.ipk-6A*) and ear length (*QEl.ipk-6A*) {0255}.

Two QTLs for plant height were assigned to chromosome 3A in RSLs from Cheyenne*7/ Wichita 3A substitution line{0025}.

Seven QTLs on chromosomes 1A, 1D, 2B, 2D and 4B affected plant height among RILs of CS/*T. spelta duhamelianum*. Effects linked with the CS alleles of *Xbcd1160-1A, Xksu127-1D* and *XksuF11-2D* increased height whereas those CS alleles associated with *Xpsr131-2B, Xpsr125-2B, Xpsr934-2D* and *Xcs22.2-4B* reduced it {0196}.

QHt.ocs-4A.1{0047}. 4AL{0047}. **v:** CS/CS(Kanto107 4A) mapping population{0047}. **ma:** Associated with *Xpsr119-4A* and *Wx-B1*{0047}.

QHt.ocs-4A.2{0047}. 4AS{0047}. **v:** CS/CS(Kanto107 4A) mapping population{0047}. **ma:** Associated with *Xbcd1738-4A* and *Hd*{0047}.

QHt.ocs-5A.1{0068}. [*Qt.ocs-5A.1*{0068}]. 5AL{0068}. **v:** CS(*T. spelta* 5A)/CS(Cappelle-Desprez 5A) RI mapping population{9903}. **ma:** Associated with the interval*Xcdo1088-5A - Xbcd9-5A*{0068}.

This QTL coincided with a QTL for culm length, *QCl.ocs-5A.1* {0068}.

QHt.riso-3A{10067}. **ma:** Mapped on the centromeric region between SSR markers *Xwmc505-3A* and *Xwmc264-3A* (LOD>6){10067}.

42. Herbicide Response

42.1. Difenzoquat insensitivity

Dfq1{1396}. Insensitive. 2B{1396}.2BL{789}. **v:** CS{1396}.

dfq1. Sensitive. **s:** CS*6/Ciano 67 2B{1396}; CS*7/Marquis 2B{789}; CS*/Sicco 2B{1396}. **v:** Ciano 67{1396}; Sicco{1396}.

Busch *et al.* {153} reported a single dominant gene for tolerance of Era and Marshall compared with the susceptibility of Eureka and Waldron, but its relationship to *Dfq1* is unknown.

42.2. 2,4-D tolerance

Randhawa *et al.* {1190} reported a single dominant gene in each of WL711, CPAN1874 and CPAN1922 controlling tolerance. HD2009 and PBW94 were described as susceptible.

42.3. Chlortoluron Insensitivity

Su1{1402}. Insensitive. 6B{1402}.6BS{799}. **v:** Cappelle-Desprez{1402}. **tv:** B-35{735}.

su1. Sensitive. **v:** Chinese Spring{1402}; Poros{1402}. **tv:** B-7{735}. **ma:** *Xpsr312-6B* - 5.3 cM - *Su1* - 6.8 cM - *Xpsr477(Pgk2)-6B*{736}. **ma,tv:** *Nor2* (6BS) - 2.7 cM - *Su1*{1401}; *Su1* - 5.2 cM - *Xpsr371-6B* (6BL){735}.

Su1 also controls insensitivity to metoxuron {1402}.

A single dominant gene for tolerance to isoproturon was found in tetraploid wheats derived from a tolerant *T. monococcum* source {1044}. This gene is presumably different from *Su1*.

42.4. Imidazolinone resistance

Resistance alleles found in mutagenized populations were incompletely dominant and additive in effect {10099}. Resistance is due to single base pair changes in acetohydroxyacid synthase.

Imi1{10099}. [*AhasL-D1*{10101},*Fs-4*{10100}]. 6DL{10101}. **v:** BW755 = Grandin*3/Fidel-FS-4{10099}; CDS Teal IMI 1A{10099}; CDC Teal IMI 9A{10099}; CDC Teal IMI 10A = Fidel-FS-2{10099}; Clearfield WHS Janz = Janz*4/Fidel-FS-2; Clearfield WHS Stiletto = Stiletto*3//Spear/ Fidel-FS-3; Fidel-FS-2 = ATCC40997{10100}. **v2:** CDC Teal IMI 15A = PTA 3955 *Imi3*{10099}.

Imi2{10099}. [*AhasL-B1*{10101}]. 6BL{10101}. **v:** CDC Teal IMI 11A=PTA 3953{10099}.

Imi3{10099}. [*AhasL-A1*{10101}]. 6AL{10101}. **v2:** CDC Teal IMI 15A *Imi3*{10099}. **dv:** *T. monococcum* mutant EM2 (mutant of susceptible line TM23 {10102}).

Mutant EM2 has a serine to asparagine substitution near the carboxyl end of the enzyme. The same change led to imidazolinone resistance in hexaploid wheat, rice and *Arabidopsis* {10102}.

43. Hybrid Weakness

43.1. Hybrid necrosis

[Progressive lethal necrosis {155}; Firing {971}].

Complementary dominant genes. Descriptive alleles *w* (weak), *m* (medium) and *s* (strong) were allocated by Hermsen {532}. Phenotype is affected by modifying genes (and/or genetic background) and environment {566}. According to Dhaliwal *et al.* {257} progressive necrosis is suppressed at 28C.

Ne1{530}. [*Le*{155,550},*F*{971},*Le1*{1491}]. 5B{1491}.5BL{1636}. **ma:** *Xbarc216-5B* - 8.3 cM - *Ne1* - 2 cM - *Xbarc74-5B*{10334}.

Ne1m{530}. **i:** S-615*11/Prelude{1500}. **v:** Carpo{532}; Eskisehir 220-39{532}; Garnet{532}; Klein Aniversario{532}; Koga{532}; Mus XII/80/22{532}; Prelude{532,1491}.

Ne1s{530}. **v:** Big Club{155,532,550}; C306{1475}; Felix{531}; Gaza 141 PI 220429 {532}; Luteseens 1163{1264}; Marquillo{115,532,550}; Ponca{532}; Spica{939}; Synthetics TA4152-19, TA4152-37, TA4152-44, TA4152-60{10334}. **tv:** Gaza 1E PI 133460; Gaza PI 189262{532}; Iumillo{532}; Kubanka{532}; PI 94587{155,532}; Quanah{532}.

Ne1s is common in tetraploid wheats {1080}.

Unknown ***Ne1*** allele. **tv:** HW75 {697}; HW178 {697}. Chinese Spring carries the weakest allele {532} and its effect can be observed in CS*7/Atlas 66 2B {939} relative to CS.

Ne1w{530}.

v: Bobin group {532}:Kenya Farmer {532}; The Bobin selection used in breeding Gabo {532}; and its sister selection, Timstein {532,1556} was in fact Gular. Hence Gular, not Steinwedel, is the presumed source. The Sydney University accession Bobin W39 was the parent of Gabo and Timstein, whereas "true" Bobin carried the accession number W360. The particular accession tested by Hermsen is not clear. According to Metgzer {1000} Steinwedel is a non-carrier; Federation group {532}:Cadia {532};Cleveland {971}; Minister group {532}; Rieti group {532}: Mentana {532}; Mara {532}.

Ne2. [*Le2*{155,550,1491},*F*{971}]. 2B{1491}.2BS{1085}. **ma:** *Xgwm148-2B* - 6.7 cM - *Ne2* - 3.2 cM - *Xbarc55-2B*{10334}.

Ne2m{530}. **v:** Alsen{10334}; Squarehead group{532}: European wheats{532}; Fronteira group{532}: Sonalika{1475}; South American wheats and derivatives, e.g. Atlas 40{532}: Wheats possessing *Lr13*{939}, e.g. Manitou{939}.

Ne2m?{530}. **v:** Barleta group{532}: South American wheats, e.g. Klein Titan{532}; La Prevision 25{532}; Lin Calel{532}.

Ne2ms{530}. **v:** Mediterranean group{532}: Dawson{155,550}; Fultz{550}; Fulcaster{550}; Fulhard{550}; Honor{550}; Jones Fife{1491}; Shepherd{550,971}; Trumbull{155}; Vermillion{530}; Wabash{155}. (Although placed in this group on basis of pedigree, the last three stocks, as well as Fultz selection of CI 19293, appear to have the stronger allele of the Crimean group{532}; Mironovskaya{10630}; Noe group{532}: Vilmorin 27{532}; Unknown ***Ne2*** allele{532}; Harvest Queen{532}. **tv:** Acme{532}; Arnautka{532}; Carleton{532}; Langdon{1498}; Mindum{532}; Stewart{532}.

However, *Ne2* was stated to be absent or rare in tetraploid wheats {1080}.

The Chinese Spring 2BS telosome carries an *Ne2* allele that is not present in Chinese Spring {1085}.

Ne2s{530}. **i:** S-615*11/Kharkov{1500}. **v:** Crimean group{532}: Blackhull{550}; Chiefkan{550}; Clarkan{550}; Kharkov{1491}; Michigan Amber{532}; Minhardi{155}; Red Chief{550}; Stepnaja 135{1264}; Turkey{532}.

Ne2w{530}. **v:** Vakka{532}; Varma{532}.

ne1 ne2. **v:** Chancellor{531}; Elgin{1491}; Gladden{155}; Leap{155}; Purkof{155}; Red Bobs{1491}; Red Egyptian{1491}; Steinwedel{1000}; S-615 {1491}; Wichita{531}.

Genotype lists in {531,532,535,640,696,698,1093,1135,1264,1381,1473,1474,1475,1492,1496,1497,1502,1503,1512,1505,1506,1507,1508,1509,1510,1630,1631,1632,1633,1637,1638,1639,0112}.

Rye line 1R136-2 carries *Ner1* {1210} that complements wheat gene *Ne2* {1289,1210} and rye gene *Ne2* {1210} to produce necrosis. Rye lines L155 and L256 carry *Ne2* {1210} that complements *Ne1* {630,1210} and *Ne1* {1210}.

Ner1{1210}. 5RL{1211}. **al:** *S. cereale* 1R136-2{1210}.

Ner2{1210}. 7RL{1211}. **al:** *S. cereale* L155, L256{1210}.

43.2. Hybrid chlorosis type 1

Ch1{535}. [m^a{1245}]. 2A{538,939}. **i:** Steinwedel*2/Khapli{939}; *T. macha* var. *colchicum*{535}. **v:** *T. macha* var. *subletschumicum*{1245,1493}. **tv:** Khapli{1080,1549}; *T. dicoccoides* var. *kotschyanum*{535}; *T. dicoccoides* var. *straussianum*{535}.

36 group dicoccon wheats are listed in {697}.

Ch2{535}. [m^b{1245},*Ne3*{1504}]. 3D{1495,1504}.3DL{692,939}. **v:** Chinese Spring{535,1504}; *T. vavilovi*.

Extremely widespread, very few wheats lack this gene.

Allelic variation at the *Ch2* locus was suggested {537,1000}. Prelude, Reward and Red Bobs were exceptional in producing severe symptoms and death at an early stage. Konosu 25 may carry a weak allele {1000}. Different alleles in C306 (strong) and Sonalika (medium) were suggested in {697}.

ch1 ch2. **v:** Albit{1000,1509}; Burt{1000,1509}; Chancellor{1000}; Garra{1549}; Kharkof{535}; Steinwedel{1549}. **su:** TAP 67 (= Pawnee 3Ag(3D)){1644}.

Lists appear in {535, 697, 1381, 1473, 1474, 1475, 1496, 1497, 1502, 1503, 1512, 1505, 1506, 1507, 1508, 1509, 1510}.

A gene, *Chr1,* in rye produces chlorosis symptoms in hybrids with wheats such as C306, HD2939 and NI5439 possessing *Ch2* {1472}. Evidence for multiple alleles of *Chr1* was also presented {1472}.

Chr1{1472}. **dv:** Cereal rye lines, EC179188 = WSP527A{1472}; EC143825 = WSP506A{1472}; EC338685 = Blanco{1472}; others{1472}.

chr1{1472}. **dv:** EC179178{1472}; EC179185 SAR/SWPY5{1472}.

43.3. Hybrid chlorosis type 2

Cs1{1511}. [*Chl*^{1}]. 5A{1498}. **v:** *T. dicoccum* cv. Hokudai{1511}.

Occurs at high frequency in the *T. paleocolchicum* group of emmers.

Cs2{1511}. [*Chl*^{2}{1501}]. 4G{1498}. **tv:** Many accessions of *T. timopheevii* and *T. araraticum*{637,1511}.

Multiple allelism at the *Cs2* locus is discussed in {637}.

43.4. Apical lethality

Apical lethality is caused by complementary recessive genes and is characterized by stunting and tiller death at the 4-5 leaf stage. The lethal genotype was designated *apd1 apd1 apd2 apd2* {10492}.

Apd1{10492}. **v:** WR95 = Kalyansona/Gigas//HD1999/Sonalika/3/*T. carthlicum*{10492}.

apd2{10492}. **v:** HD2009{10492}; HW2041{10492}; Lok-1{10492}; others{10492}.

Apd1 Apd2. **v:** Atila{10492}; Kalyansona{10492}; others{10492}.

apd1 apd2. Lethal genotype.

Uniculm plants occured as heterozygous segregates among progenies, but homozygous uniculm lines could not be established {10492}.

44. Iron Deficiency

Fe1{921}. 7DL{927}. **v:** Saratovskaya 29{921}.

Fe2{921}. 7BS{927}. **v:** CS{927}.

45. Lack of Ligules

The liguleless character is controlled by complementary recessive genes in hexaploid wheat {077,738,942} and by a single recessive in tetraploid wheat {047,050,939,10133}. One gene at the tetraploid level is allelic with one of those in the hexaploid {939,10133}. Evidence for orthology of *lg1* and *lg2* with *lg* of rice {170}, *lg1* of maize {004}, *li* of barley {1155} and *al* of rye was presented in {725}. **al:** Imperial rye chromosome 2R restored the liguled condition to a liguleless CS derivative {939}.

lg1{047}. 2B{942}.2BS{10767}. **i:** ANK33=Novosibirskaya 67*10/K59990{10061}. **v:** Eligulate W1342 *lg2 lg3*{942,10133}; K31289{10133}; K59990{10061}; K53660{10133}; Liguleless partial backcross derivative of CS{939}; Partial backcross derivative of CS{939}. **tv:** K17769{10133}; K17784{10133}.

lg2. 2D{942}. **i:** ANK33 = Novosibirskaya 67*10/K59990. **v:** Eligulate W1342 *lg1 lg3*{942, 10133}; Liguleless partial backcross derivative of CS{939}.
Because diploid wheats are liguled, polyploid wheats presumably carry a third recessive factor in chromosome 2A.

lg3{10133}. 2A{10133}. **i:** ANK33=Novosibirskaya 67*10/K59990{10061}. **v:** Present in all hexaploid cultivars.

Genotypes of selected tetraploid wheat {10133}

Lg1Lg1 Lg3 Lg3: *T. turgidum* var. *durum* Ldn - dic DS 2A: *T. turgidum* var. *dicoccum* Khapli and Vernal; *T. turgidum* var. *dicoccoides* Israel A; MG4343

Lg1Lg1 lg3 lg3: *T. turgidum* var. *durum*: Altaiskaya Niva; Castelpoziano; Langdon; Ldn-GB DS 2B; Golden Ball; Modoc; PI349056

lg1lg1 Lg3Lg3: None identified.

46. Leaf Erectness

QLer.ipk-2A{0255}. 2AS{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; The erect leaf phenotype was contributed by Opata{0255}. **ma:** Associated with *Xbcd348-2A*{0255}.
Mutants lacking ligules are known to have erect leaves. However, the QTL for leaf erectness reported here is not related to liguleless mutants {0255}.

47. Leaf Tip Necrosis

Ltn{1361}. 7D{1361}. **v:** Wheats with *Lr34/Yr18*{301,1361}; See *Lr34, Yr18*. **c:** Putative ABC transporter{10862}.

Ltn1{10281}. [*Ltn*{1361}]. **v2:** Parula *Ltn2*{10281}. **ma:** Associated with *Xgwm295-7D* and *Xgwm130-7D*{10281}. **c:** See *Lr34*.
This gene is identical to *Lr34, Sr57, Yr18, Pm38* and *Ltn* and reportedly has effects on response to other diseases and pathogens including BYDV and *Biploaris sorokiniana*.

Ltn2{10281}. 1B{10281}. **v:** Wheats with *Yr29/Lr46*{10281}; See *Yr29, Yr46*. **v2:** Parula *Ltn1*{10281}. **ma:** *Xwmc44-1B* - 1.4 cM - *Xbac24prot* - 9.5 cM - *Ltn2* - 2.9 cM -

Xbac17R........Xgwm140-1B{10281}; *Xgwm44-1B* - 3.6 cM - *Ltn2* - 2.1 cM - *XtG818/XBac17R.....Xgwm140-1B*{10281}.

According to Messmer et al. {0031} LTN may be caused by several QTLs and is affected by genetic background and environment.

QLtn.sfr-1B{0050}. 1BS{0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xgwm18-1B* and *Xglk483-1B*{0050}.

QLtn.sfr-3A{0050}. 3A{0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xpsr570-3A* and *Xpsr543-3A*{0050}.

QLtn.sfr-4B.1{0050}. 4B{0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xpsr921-4B* and *Xpsr593-4B*{0050}.

QLtn.sfr-4B.2{0050}. 4B{0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xpsr593-4B* and *Xpsr112-4B*{0050}.

QLtn.sfr-4D{0050}. 4DL{0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xpsr302-4D* and *Xpsr1101-4D*{0050}.

QLtn.sfr-5A{0050}. 5A{0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xpsr549-5A* and *Xglk163-5A*{0050}.

QLtn.sfr-6A{0050}. 6A{0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xpsr563-6A* and *Xpsr966-6A*{0050}.

QLtn.sfr-7B.1{0050}. 7B {0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xpsr350* and *Xbzh232(Tha)-7B*{0050}.

QLtn.sfr-7B.2{0050}. 7B{0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xglk750-7B* and *Xmwg710-7B*{0050}.

QLtn.sfr-7D{0050}. 7DS{0050}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0050}. **ma:** Associated with *Xpsr160-7D* and *Xgwm44-7D*{0050}.

48. Lesion Mimicry

Lesion mimics that resemble the response of plants to infection by pathogens occur in many species ({10743} for examples).

lm{10743}. 1BL{10743}. **bin:** C1BL6-0.32{10743}. **v:** Ning 7840{10743}. **ma:** Proximal to *Xgwm264.1-1B*{10743}.

Lm was positively associated with *QLr.pser.1BL* {10743}.

49. Lodging

QLd.crc-3D{10287}. 3D{10287}. **ma:** Linked to *Xgwm191-3D* (LOD 3.7) in RL4452/AC Domain{10287}.

QLd.sfr-1B{0052}. 1BS{0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr949-1B* and *Xgwm18-1B*{0052}.

This QTL coincided with QTL for reduced height, increased culm stiffness and broader leaf width {0052}.

QLd.sfr-2A{0052}. 2AS{0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr958-2A* and *Xpsr566-2A*{0052}.

This QTL coincided with QTL for reduced height, increased culm stiffness, broader leaf width, more erect growth habit, later ear emergence and increased culm thickness {0052}.

QLd.sfr-2D{0052}. 2D{0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr933-2D* and *Xglk529-2D*{0052}.

QLd.sfr-3A{0052}. 3AS{0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr598-3A* and *Xpsr570-3A*{0052}.

This QTL coincided with QTL for increased culm stiffness and reduced culm thickness {0052}.

QLd.sfr-4A{0052}. 4AS{0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xgwm397-4A* and *Xglk315-4A*{0052}.
This QTL coincided with QTL for reduced height, increased culm stiffness and more erect growth habit {0052}.

QLd.sfr-5A{0052}. 5AL{0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr918-5A* and *Xpsr1201-5A*{0052}.
This QTL coincided with QTL for reduced height, increased culm stiffness, reduced leaf width, more erect growth habit, later ear emergence and increased culm thickness{0052}.

QLd.sfr-5B{0052}. 5BL{0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr370-5B* and *Xpsr580-5B*{0052}.
This QTL coincided with QTL for increased culm stiffness, broader leaf width and more erect growth habit {0052}.

QLd.sfr-6B{0052}. 6BL{0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr964-6B* and *Xpsr142-6B*{0052}.

QLd.sfr-7B{0052}. 7BL{0052}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population{0052}. **ma:** Associated with *Xpsr927-7B* and *Xpsr350-7B*{0052}.
This QTL coincided with QTL for reduced height and later ear emergence {0052}.

50. Male Sterility

50.1. Chromosomal

Ms1376{10814}. Sterility is dominant **v:** TR1376A{10814}.
Male fertile counterpart: TR1376B {10814}. *Ms1376* was discovered among progenies of a transgenic family of Xinong 1376 containing leaf senescence-inhibiting gene P_{SAG12}-*IPT* {10814}.

ms1. Recessive alleles for sterility 4B{268}.4BS{064}.

ms1a{268}. **v:** Briggle's Chancellor Derivative{268}; Pugsley's Male Sterile{268}.

ms1b{268}. **v:** Probus mutant{268}.

ms1c{064}. **v:** Cornerstone{064}.

ms1d{0290}. **v:** Mutant FS2{0290}.

ms1e{0290}. **v:** Mutant FS3{0290}.

ms1f{0290}. **v:** Mutant FS24{0290}.

ms1g{10355,10546}. 4BS{10354}. **v:** Lanzhou Mutant 257A{10354,10355}; Male sterile line 257A{10546}.

ms2{806}. Dominant allele for sterility. [*Ta1*{240}]. 4DS{806}. **v:** Taigu = Line 223{240,807,806}; *ms2* confers sterility when present in octaploid triticale{597}.

ms3{872}. Dominant allele for sterility. 5AS{872}. **i:** Chris derivative{872}; KS87UP9{219}. **ma:** *Xwg341-5A* - 0.8 cM - *ms3*.......cent{0289}; *Xcdo-677-5A* and *Xbcd1130-5A* also cosegregated with *Xwg341-5A* but were located in a different region in the physical map{0289}.

ms4{0293}. Dominant allele for sterility, distinguished from *ms2* on the basis of different degrees of recombination with the 4D centromere. 4DS{0293}. **v:** Konzak's male sterile.

ms5{0290}. 3A{0290}. **v:** Mutant FS20{0290}.

50.2. Sterility in hybrids with wheat

Shw{0331}. [*1HL*{0331}]. **ad:** Additions of 1H and 1HL to wheat and certain translocation lines {0331}. **ma:** Located in a 16.4 cM interval flanked by *Xmwg800-1H* and *Xmwg943-1H*. A possible relationship with Ncc genes is discussed {0331}.

50.3. Photoperiod and/or temperature-sensitive male sterility (PTGMS)

wtms1{10332}. 2B{10332}. **v:** BNY-S{10332}. **ma:** E: AAG/M:CTA$_{163}$ - 6.9 cM - *wtms1* - 4.8 cM - *Xgwm374-2B*{10332}.

Described as a thermo-sensitive gene (TGMS), giving complete sterility at less than 10C, but fertile at higher temperatures {10332}.

wptms1{10333}. 5B{10333}. **v:** Line 337S wptms2{10333}. **ma:** *Xgwm335-5B* - 4.2 cM - *wptms1* - 24.4 cM - *Xgwm371-5B*{10333}.

wptms1 produces sterility only in the presence of *wptms2*.

wptms2{10333}. 2B{10333}. **v:** Line 337S *wptms1*{10333}. **ma:** *Xgwm374-2B* - 6.9 cM - *wptms2* - 20.9 cM - *Xgwm120-2B*{10333}.

wptms2 produces sterility only in the presence of *wptms1*. *wptms1* and *wptms2* were analysed and mapped under long photoperiod/high temperatures, but an earlier study indicated a single gene for male sterility under short photoperiod/low temperatures. Althought mapping data are different a possible relationship between *wtms1* and *wptms2* needs to be resolved.

51. Manganese Efficiency

QTL: Variation associated with *Xcdo583-4B* explained 42% of the variation for Mn efficiency in the durum cross Stojocri 2 (Mn efficient)/Hazar (MN inefficient) {0320}.

52. Maturity time

QMat.crc-3B{10287}. 3B{10287}. **ma:** Linked to *Xwmc231-3B* (LOD 3.0) in RL4452/AC Domain{10287}.

QMat.crc-4A{10287}. 4A{10287}. **ma:** Linked to *Wx-B1* (LOD 6.1) in RL4452/AC Domain{10287}.

QMat.crc-7D{10287}. 7D{10287}. **ma:** Linked to *Xgwm130-7D* (LOD 17.5) in RL4452/AC Domain{10287}.

53. Megasporogenesis

53.1. Control of megasporogenesis

Msg{625}. 7AS{625}. **tv:** Langdon{625}.

54. Meiotic Characters

54.1. Low-temperature pairing

ltp{527}. **v:** Chinese Spring{527}.

Expressed in the absence of chromosomes 5D at 12°C - 15°C, but not at 20°C. A contrasting allele, *Ltp*, for normal pairing at the lower temperature range was demonstrated in *T. dicoccum*.

54.2. Pairing homoeologous

Ph1{1537}. 5BL{1301}. **ma:** PCR-based assays for presence and absence of *Ph1* have been described{0214,0217,9965,0359}; The *Ph1* factor(s) was restricted to a region flanked by *Xrgc846-5B* and *Xpsr150-5B*{0219}; *Ph1* was physically mapped in 5BL to fraction length

0.55, bracketed by deletions 5BL-1 and *ph1b*{446}.

A complex *Ph1* candidate structure comprising at least one 5B-specific member of the *cdc2* complex multigenic cluster (involved in chromosome condensation), a unique repeat structure with similarities to repeats on chromosome 3B, and a heterochromatic sub-telomeric insertion from chromosome 3AL was identified {10240}.

ph1a. - Not applicable - see *ph2b* {1303}.

ph1b{1301}. **v:** Sears' high pairing mutant{1301}. **ma:** A PCR-based detection system for *ph1b ph1b* individuals is described in {9965}.

ph1c{593}. **tv:** Cappelli *ph1* mutant{449,593}; This mutant is deficient for a terminal portion of chromosome 5BL{449}. **ma:** Mutant lines with *ph1b* and *ph1c* carry deletions of the chromosome segment possessing *Ph1* in the respective parent lines{593,447}.

Several *ph1* mutants are described in {0219}.

Ph2{1302}. 3DS{1302}.

ph2a{1302}. **v:** Sears' intermediate pairing mutant{1301,1302}.

ph2b{1304,1303}. [*ph1a*{1537}]. **v:** Chinese Spring mutant 10/13{1537}.

54.3. Inhibitor of pairing homoeologous

Ph1^{I}. **al:** *Aegilops speltoides*{1218,439}.

55. Nitrate Reductase Activity

Nra{424}. **v:** UC44-111{424}.

nra{424}. **v:** Anza{424}.

56. Nuclear-Cytoplasmic Compatability Enhancers

scs{869}. Derived from *T. timopheevii* {869}. [*scs*^{ti}{10878}]. 1AL{870,027}. **v:** *T. timopheevii*{869}. **ma:** A number of completely linked RAPD makers were identified{044}; *Xbcd1449.2-1A* - 0.6 cM - *scs* - 2.3 cM - *Xbcd12-1A*{10878}.

Asakura *et al.* {044} used the symbol *Ncc* as a synonymn for *scs* pointing out that the effects of the gene are not limited to a single species.

57. Nucleolus Organizer Regions

57.1. 18S - 5.8S - 26S rRNA genes

NORs have been observed as secondary constrictions associated with nucleoli on satellited chromosomes {e.g., 221}, and by *in situ* hybridization to chromosome spreads {039,294,1014} of 18S-5.8S-26S ribosomal-DNA probes {038,433}. Allelic variation in gene number has been demonstrated at all wheat *Nor* sites and at *Nor-R1* by filter {367} and *in situ* hybridization {1012}. Allelic variants of the *Nor* loci are detected by hybridization of rDNA probes to restriction endonuclease-treated DNA on Southern blots {037,288,917,1399}. Alleles *Nor-B2a* to *Nor-B2f* were identified using *Taq1* digests of genomic DNAs hybridized to derivatives of the plasmid pTa250 {433} containing spacer-DNA fragments pTa250.4 {367,917} and pTa250.15 {288}.

Other variants may have been isolated {1399} using *BamH1/EcoR1* double digests and pTa71 {433}. The variants may or may not be equivalent to those described below.

Nor1a and Nor2a. **v:** Maris Huntsman{1399}.

Nor1b and Nor2b. **v:** Bezostaya 1{1399}.

Nor1c and Nor2c. **v:** Cappelle-Desprez, Maris Ranger{1399}.

Nor-A1. 1AS{221,367,835,1012}. **v:** *T. spelta*{221,367,835,1012}. **dv:** *T. monococcum*{658}.

Nor-B1. [*Nor1*{1120}]. 1B{037,288}.1BS{221,367,835,1041}. **v:** CS{288}.

Deletion mapping divided the *Nor-B1* in a proximal subregion *Nor-B1p* (short repeat) and a distal subregion *Nor-B1d* (long repeat) {0275}

Nor-B1a{918}. **v:** Cheyenne, Chinese Spring, Hope, Kite, Oxley, Teal, Timstein{037,288}; Vasco, 8 others{288}.

Nor-B1a-{918}. **v:** A derivative allele of *Nor-B1a* with a significantly reduced amount of spacer. Condor 64-1{918}; Sonora 64-1{918}.

Nor-B1b. **v:** Olympic, Robin, Shortim{917}.

Nor-B1c{918}. **v:** Banks{917}; Corella{917}; Warigal{917}; 5 others{917}.

Nor-B1c-{918}. **v:** Rosella{918}.

Nor-B1d{918}. **v:** Maris Huntsman{918}.

Nor-Ag^{i}1{374}. 1Ag^{i}{374}. **ad:** Vilmorin27/*Ag. intermedium*{374}.

Nor-H1. [*Nor-I1*{794}]. 1HS{794}. **dv:** Sultan barley{794}.

Nor-R1. 1RS{039}. **ad:** CS/Imperial{039}.

Nor-S1. 1SS{294}. **al:** *Ae. speltoides*{294}.

Nor-U1. 1U{906}. **su:** CS/*Ae. umbellulata*{906}.

Nor-V1{241}. 1V{241}. **ad:** CS/*D. villosum*{241}.

Nor-B2. [*Nor2*{1120}]. 6BS{1041,221,366,835}. **v:** CS.

Nor-B2a{918}. 6B{288}. **v:** CS{037,917}.

Nor-B2a-{918}. **v:** Blueboy{918}; Sonora 64-1{918}.

Nor-B2b. T6B{288}. **v:** Banks, Oxley, Shortim, Timstein{037}; 12 others{917}.

Nor-B2c. **v:** Corella, Robin, Teal, 1 other{917}.

Nor-B2d{918}. H6B{288}. **v:** Hope{037}; Olympic{917}; Warigal{917}.

Nor-B2d-{918}. **v:** Harrier{918}; Kite{917,918}.

Nor-B2e. **v:** Vasco{917}.

Nor-B2f. Ch6B{288}. **v:** Cheyenne{037,917}.

Nor-B2g{918}. **v:** Falcon; Gluclub; La Prevision{918}.

Nor-B2h{918}. **v:** Yaktana{918}.

Nor-B2i{918}. **v:** Maris Huntsman; Thatcher{918}.

Nor-E2. 6ES{294}. **ad:** CS/*E. elongata*{294}.

Nor-G2. 6G{578}. **tv:** *T. timopheevii* IPSR (PBI) No. 1{294}.

Nor-H2. [*Rnr1*{1248}]. 6H{1070,039,1248}.6HS{794}. **al:** Clipper barley{039}; Sultan barley{794}.

Nor-S2. 6SS{294}. **al:** *Ae. speltoides*{294}.

Nor-A3. 5AS{1014,658}. **dv:** *T. monococcum, T. urartu* IPSR (PBI) Acc. A.

Nor-D3. 5DS{221,835}. **v:** CS; most wheats{037,288,917}.

Nor-Ag^{i}3. 5Ag^{i}{374}. **ad:** CS/*Ag. intermedium*{374}.

Nor-E3. 5ES{294}. **ad:** CS/*E. elongata*{294}.

Nor-H3. [*Rnr2*{1248}]. 5H{1070,039,1248}.5HS{794}. **al:** Clipper barley{039}; Sultan barley{794}.

Nor-U3. 5U{906}. **ad,su:** CS/*Ae umbellulata*{906}.

Nor-D4{1042}. 7DL{1042}. **v:** CS{1042}. **dv:** *Ae squarrosa*{1042}.

Nor-H4. [*Nor-I4*{794}]. 7HS{794,793}. **al:** Sultan barley{794}.

Nor-H5. [*Nor-I5*{794}]. 2HS{794,793}. **al:** Sultan barley{794}.

Nor-B6{601}. 1BL{601}. **v:** CS; Cheyenne, Wichita{601}. **tv:** Langdon{601}.

Nor-A7{601}. 5AL{601}. **v:** CS; Cheyenne, Wichita{601}. **tv:** Langdon{601}.

Nor-D8{601}. 3DS{601}. **v:** Witchita{601}.

Nor-A9{00120}. [*Nor-A1*{221,367,835,1012}]. 1AS{282,276}. **v:** *T. spelta*{221,367,835,1012}.

Nor-A10{00120}. [*Nor-A3*{1014,658}]. 5AS{282,276}. **dv:** *T. monococcum*{282,276}; *T. urartu* IPSR (PBI) Acc. A.

More detailed listings for allelic variation at *Nor-B1* and *Nor-B2* are given in {917,918}. Two sites designated temporarily as *Nor-Ax* and *Nor-Ay* were identified in *T. monococcum* ssp. *boeoticum*, but were absent in ssp. *urartu*.

58. Osmoregulation

Osmoregulation is a specific form of solute accumulation regulating turgor pressure and hydration during periods of stress with positive effects on growth. Wheat lines selected for higher osmoregulation in the greenhouse have greater growth and seed yields under water limited conditions in the field.

Or{1030}. Low osmoregulation. **s:** CS (Red Egyptian 7A). **v:** Cappelle Desprez; Condor*4/3Ag14{1030}; Red Egyptian. **ma:** *Or* (proximal in 7AS) - 13 cM - *Xpsr119-7A*{1031}.

or{1030}. High osmoregulation. 7A{1030}.7AS{1031}. **v:** CS, Condor, Songlen, Takari{1030}.

59. Phenol Colour Reaction of Kernels

Wheat genotypes vary in response when caryopses are treated with weak solutions of phenol, a dark colour response being indicative of a positive response. This response is believed to be related to the action of tyrosinase. There seems to a genetic relationship with polyphenol oxidase activity which causes a darkening of flour, pasta and noodle products (see also Polyphenol Oxidase (PPO) activity).

Tc1{10130}. 2AL{10130,10131}. **su:** Various substitutions of chromosomes 2A into CS{10131}. **sutv:** Langdon*/dicoccoides 2A{10130}. **tv:** Golden Ball{10130}.

Tc2{10130}. 2BL{10130}. **sutv:** Langdon*/Golden Ball 2B{10130}. **tv:** Golden Ball{10130}.

Tc3{10131}. [*Tc*{10131}]. 2DL{10130}. **v:** Chinese Spring (intermediate response){10130}. **v2:** Timstein *Tc1*{10131}. **su:** CS/*Timstein 2D{10131}. **tv:** Cocorit 71{10130}; Langdon{10130}. **sutv:** Langdon*/CS 2D(2A); Langdon*/CS 2B(2D){10130}; *T. dicoccoides* Israel A {10130}. Lines with a negative phenol colour reaction.

60. Pollen Killer

Ki{1306}. Killing allele is dominant. 6BL{1306}. **v:** Chinese Spring{1306}; Mentana{929}.

ki. **v:** Probably the majority of wheats including Timstein, Gabo and Yalta{1306}.

Modifiers also appear to be involved as Luig {840, and unpublished} found variation among *kiki* parents. Some F2 and F3 *Sr11sr11* plants from Yalta/Chinese Spring crosses segregated with less than 50% *Sr11-* phenotypes among the progeny indicating that killing extended to eggs as well as pollen. See also, Gametocidal Activity.

Kato & Maeda {10164} reported both partial pollen and seed sterility in crosses involving certain landraces and Chinese Spring. They attributed sterility to recessive alleles of three complementary genes. The genes were designated *Ki2, Ki3* and *Ki4* {10164}, but the relationship of *Ki3* to the earlier designated *Ki* was not established. Some genotypes:

Ki2 Ki3 Ki4: **v:** Aka Kawa Aka {10165}; Hope {10165}; Marquis {10165}; Red Russian {10165}

ki2 Ki3 Ki4: **v:** Akadaruma {10165}; Canthatch {10165}; Norin 61{10165}; Pakistani Landrace IL159 {10164}

Ki2 ki3 Ki4: **v:** Gabo {10165}; Thatcher {10165}; Timstein {10165}; Zlatiborka {10165}
Ki2 Ki3 ki4: **v:** Kagoshima {10165}; Komugi Jingoro {10165}; Sakobore {10165}
ki2 ki3 Ki4: **v:** Finnish Landrace WAG4339 {10165}; Hungarian Landrace WAG4458 {10165}; Novosadska Jara {10165}
ki2 Ki3 ki4: **v:** Chinese Spring {10165}; Eshima Shinriki {10165}; Ethiopian Landrace IL70 {10164}; Norin 26 {10165}
Ki2 ki3 ki4: **v:** Cadet {10165}; Iraqi Landrace IL171 {10165}; Rex {10165}

61. Polyphenol Oxidase (PPO) Activity

3,4 dihydroxyphenylalanine (L-DOPA) was used as a substrate in a non-destructive test of polyphenol oxidase activity in seeds. Chromosome 2D was shown to carry PPO gene(s) based on Langdon/Chinese Spring (2D) substitution lines and nullisomic-tetrasomic analysis {0342}. An orthologous series of genes affecting PPO activity in both common wheat and durum was proposed in {10149}. See also, Phenol Colour Reaction of Kernels

Chara (mod high)/WW2449(low): DH population: PPO activity Associated with *Xgwm294b-2A* (R^2=0.82), *Xwmc170-2A*, *Xgwm312-2A* and *Xwmc178-2A* (R^2>0.7) {10410}.

Chara (medium high PPO)/WW2449 (low PPO): one QTL was located on chromosome 2A. Two markers (one SNP, one CAPS) based on BQ161439 were polymorphic between the parents and showed linkage or allelism with PPO loci *Xtc1* and *XPPO-LDOPA*. *Xtc1* - 0.6 cM - *XPPO-LDOPA/XPPO18/BQ161439* {10484}.

A QTL on 2D, associated with *Xfba314-2D* was identified in an M6 / Opata 85 population using the L-DOPA assay. The high PPO activity was contributed by M6 {0344}. Markers significantly associated with PPO activity were also detected on chromosomes 2A, 2B, 3B, 3D and 6B in the population NY18 / Clark's Cream {0344}.

A multiplex of markers *PPO33* and *PPO16* was reliable for selecting genotypes with low PPO activity {10418}.

Tetraploid wheat

Messopia/*T. dicoccoides*: RILs: Associated with RFLP *Xutv1427-2A* {10411}.

Jennah Khetifa (high)/Cham 1 (low): Associated with *Xgwm312-2AL* {10411}.
STS marker PPO18 based on a polyphenol oxidase (*PPO*) gene (GenBank AY596268) was closely linked to SSR markers *Xgwm312* and *Xgwm294* on chromosome arm 2AL. PPO18 explained 28-43% of the variation in PPO activity in the cross Zhongyou 9507/CA9632 {10290}.

62. Red Grain Colour

Red colour is probably due to the polyphenol compounds phlobaphene or proanthocyanidin, synthesized through the flavanoid pathway. Himi & Noda {10107} provided evidence that the R genes were wheat forms of Myb-type transcription factors (*Tamyb10-3A, Tamyb10-3B,Tamyb10-3D*). Genetic evidence is provided in {10838}.
Red colour is dominant to white. At each locus, the white allele is assigned *a* and the red allele, *b*. White-grained *T. aestivum* and amber-grained *T. durum* wheats carry recessive *a* alleles at each locus. White-grained CS*7/Kenya Farmer and CS*6/Timstein are considered near-isogenic to CS with *R-D1b*.

R-A1{548}. [*R2*{548}]. 3AL{957,1003}. **v:** Rio Blanco{10839}. **ma:** (Proximal) *Xpsr483(Cxp1)-3A* - 28 cM - *R-A1* - *Xpsr904-3A* {370} (distal); *Xwmc559-3A* - 16.3 cM - *R-A1/Xgwm155-3A* - 4.5 cM - *Xwmc153-3A*{10839}.

R-A1a. **ma:** Based on *Tamyb10-A1* sequences this allele in CS lacks the ability to bind DNA due to deletion of the first half of the R2 repeat of the MYB domain {10838}; The *R-A1a* allele in Norin 17 has a 2.2 bp insertion in the second intron that appears to prevent transcription{10838}.

R-A1b. [*R2*]. **i:** Novosibirskaya 67*9/Solo{730}. **v:** Baron{370}; Diamant 2{014}; Hustler{370}; Norin 10- Brevor, 14{017}; Maris Widgeon{370}; Mercia;{370}; Motto{370}; Red Bobs{1003}; Sapphire{370}; Slejpner{370}; Talent{370}; Wembley{370}.

R-B1{548}. [*R3*{548}]. 3BL{1003,370}. **ma:** *Xbcd131-3B* - 5 cM - *R-B1* - 5 cM - *Xabc174-3B*{410}; *Xwmc29-3B* - 5 cM - *R-B1* - 5 cM - *Xbarc84-3B*{10280}; *Xgwm4010-3B* - 1.6 cM - *R-B1* - 4.6 cM - *Xgwm980-3B*{10839}.

R-B1a. **ma:** Based on the *Tamyb10-B1* sequence this allele in CS has a 19 bp deletion of the CCG repeat region causing a frameshift mutation{10838}.

R-B1b. [*R3*]. **i:** Novosibirskaya 67*9/k-28536{730}. **v:** Canon{370}; Dollar{370}; Grana{370}; Supreme{370}.

R-D1{549}. [*R1*{548}]. 3DL{1291,1293}. **v:** CS. **ma:** *Xbcd131-3D* cosegregation with *R-D1* - 15 cM - *Xabc174-3D*{410}; *Xgwm2-3D* - 15.4 cM - *R-D1* - 3.2 cM - *Xgwm4306-3D*{10839}.

R-D1a. **ma:** No *Tamyb10-D1* sequence was detected in lines with this allele indicating that it may be a deletion{10838}.

R-D1b. [*R1*]. **i:** Novosibirskaya 67*9/CS{730}. **v:** Alexandria{370}; Apollo{370}; Axona{370}; CS{1293}; Dwarf A{370}; Fortress{370}; Jerico{370}; Longbow{370}; Luna{370}; Mardler{370}; Maris Huntsman{370}; Minaret{370}; NFC 75/93/27A; Rapier{370}; Pawnee{549}; Voyage{370}; Vuka{370}.

R-N1{1018}. 3N{1018}. **su:** CS/*Ae. uniaristata*{1018}.

R-R1{1011}. 6RL{1011}. **ad:** Holdfast/King II{1011}.

R-V1{1518}. 3VL{1518}. **ad:** Creso/*D. villosum*{1518}.

A *3Ag* chromosome from decaploid *Ag. elongatum* carries an allele for red grain colour which was transferred to Agent and the majority of Sears' 3D-3Ae#1 translocations {939}. Other studies have identified wheats carrying either one or two, unidentified *R-1* alleles: {056,437,549, 631,654,659,1078,1148,1333,1349,1454,370}.

See also Variegated Red Grain Colour.

R-A1b R-B1b R-D1a. [*R2,R3*]. **v:** Red Chief{548}; Avalon{370}; Bersee; Cappelle Desprez; Feuvert; Mission; Parade; Rendezvous; Yuri{370}.

R-A1b R-B1a R-D1b . [*R2,R1*]. **v:** Bezostaya 1{370}; Brigand{370}; Broom{370}; Brock{370}; Kronjuwel{370}.

R-A1a R-B1b R-D1b. [*R3,R1*]. **v:** Fenman{370}; Kharkov{1003}; Norman{370}; Pastiche{370}; Riband{370}; Sperber{370}; Squadron{370}; Urban{370}.

R-A1b R-B1b R-D1b. [*R1,R2,R3*]. **v:** Bowie; Frondoso{1148}; Frontiera{437}; Hope{204,206}; Japanese Bearded{1548}; Kanred{1078,1426}; Lin Calel{1078}.

Functional markers based on *Tamyb10* sequences are given in {10838}.

63. Reaction to Black-Point of Grain

Black-point, a common grain defect, is a dark discoloration of the embryo region of the kernels. Whereas black-point is often attributed to infection by a number of fungi, the presence of such fungi may be a consequence of saprophytic colonization of affected tissues rather than the cause (see {10148} for references). The condition may be triggered by high humidity {0845}.

QTL: Sunco/Tasman DH populaion: QTL located in chromosomes 2B (15% of phenotypic variation), 3D, 4A (from Sunco) and 1D, 5A and 7AS (from Tasman {10148}. The 2B gene was associated with the presence of *Sr36* {10148}.

Markers *Xgwm319-2B* and *Xgwm048-4AS* were confirmed in a Batavia/Pelsart (resistant) DH population {10494}.

Cascades/AUS1408 DH population: QTL from Cascades located in chromosomes 2D (5 cM from *Xgwm484-2D*, 18% of phenotypic variation), 2A (13%), and 7AS (12%) {10148}.

64. Response to Photoperiod

One-gene {1169} and two-gene {638,1137,1170} differences were reported in inheritance studies. In Chinese Spring/Hope substitution lines for chromosomes 1A, 4B and 6B greater sensitivity to short photoperiod was found, whereas substitutions of 3B and 7D were less sensitive {487}.

'a' alleles are dominant.

There is an orthologous gene series on the short arms of homoeologous group 2. The "a" alleles confer the insensitive response {0063}, the contrasting allele may be referred to as "b".

Ppd-A1{0063,10612}. [*Ppd3*{1141}]. 2AL{1268}. **v:** C591{0057}. **tv:** GS100, Kofa (1027-bp deletion in the promoter){10612}; GS105, Svevo (1117-bp deletion in the promoter){10612}; A survey of *Ppd-A1* allele is reported in {10915}. **ma:** *Xwmc177-2A* - *Ppd-A1*, 2.2 and 2.8 cM in GS100/GS101 and GS105/GS104, respectively{10612}.

GS100 and GS105 had different deletions relative to GS101 and GS104, respectively, and both were consistently a few days earlier flowering than their near-isogenic counterparts with *Ppd-A1b* {10612}.

Ppd-A1a{10612}. **tv:** GS100{10612}; GS105{10612}.

Ppd-A1a was present in 39% of Chinese landraces and 97% of improved cultivars {10622}. GS100 and GS105 had different deletions relative to GS101 and GS104, respectively and both were consistently a few days earlier flowering than their near-isogenic counterparts with *Ppd-A1b* {10612}

Ppd-A1b{10612}. **tv:** GS101{10612}; GS104{10612}.

Ppd-B1. **ma:** *Xwhs2002-2B/Xgwm257-2B* - *PpdB1* - *Xgwm148-2B*. Actual linkage value varied between crosses{10129}; *Xpsr666-2B* - 1.2 cM - *Xpsr109-2B* - 4.4 cM - *Ppd-B1* - 4.8 cM - *Xpsr804-2B* ...Cent{0062}.

According to {10611} the *Ppd-B1* allele from Japanese wheats has a stronger effect than the allele from CS.

Ppd-B1a{0063}. [*Ppd2*{1566}]. 2BS{1566, 1268, 1269}. **i:** H(C) = Haruhikari*5 / Fukuwasekomugi{10611}; H(D) = Haruhikari*/5/ Fukuwasekomugi *Ppd-D1a*{10611}. **s:** Cappelle-Desprez*/CS 2B{0058}. **v:** CS{1268}; Spica{557}; Timstein{1269}. **v2:** Fukuwasekomugi *Ppd-D1a*{10611}; Sharbati Sonora *Ppd-A1a*{887}. **c:** Varieties with the photoperiod insensitive allele have more than one *Ppd-B1* copy per chromosome 2B: two copies in Recital, three copies in Sonora 64, Timstein and C591, and 4 copies in Chinese Spring{10881}.

Ppd-B1b{10611,10881}. **v:** Beaver{10881}; Cappelle-Desprez{10881}; Cheyenne{10881}; Norstar{10881}; Paragon{10881}; Renan{10881}. **v2:** Haruhikari *Ppd-D1b*{10611}. **c:** Varieties with the photoperiod sensitive allele have a single *Ppd-B1* copy per chromosome 2B{10881}.

Ppd-B2{10628}. 7BS{10628}. **su:** Favorit (F26-70 7B){10628}. **v:** F26-70{0093}. **ma:** *Xgwm255-7B* - 20.7 cM - *Ppd-B2* - 4.4 cM - *Xgwm537-7B*{10628}.

This gene confers earlier flowering under long photoperiod conditions {10628}.

Ppd-D1. Comparative mapping showed that *Ppd-D1* was co-linear with barley *Ppd-H1* - a member of the pseudo-response regulator (PRR) gene family {10466}.

Jagger amplified the 414 bp band {10466} associated with daylength sensitivity whereas 2174 amplified the 288 bp band associated with insensitivity {10722}.

Ppd-D1a{0063}. [*Ppd1*{1566}]. 2DS{1268}. **i:** H(C) = Haruhikari*5 / Fukuwasekomugi{10611}; Haruhikari*5 / Saitama 27{10611}; H(D) Haruhikari*/5/Fukuwasekomugi *Ppd-B1a*{10611}. **s:** Capelle Desprez*/Ciano 2D{1598}; Capelle-Desprez*/Mara 2D{1598}; CS*/Ciano 2D *Ppd-B1a*{1268}. **v:** Akakomugi{1604}; Bezostaya 1{1604}; Festival{10466}; Kavkaz{0917}; Mara{1604}; Orqual{10466}; Recital{10466}; Saitama 27{10466}; Sava{1604}; Sideral{10466}; Soissons{10466}; Sonora 64{1566}; Talent{10466}; Texel{10466}. **v2:** Sharbati Sonora *Ppd-D1a*{887}; Fukuwasekomugi *Ppd-D1a*{10611}. **ma:** Stocks with *Ppd-D1a* had a 2,089bp deletion upstream of the coding region leading to mis-expression of the 2D PRR gene{10466}.

Ppd-A1b Ppd-B1b Ppd-D1b. **v:** Cheyenne{1141}; Diamont 1{887}; Lancer{638}; Saratovskaya 29{887}; Warrier{638}.

Two genes controlled photoperiod response in *T. turgidum* {788}.

Gene *Ppd-H2* on barley chromosome 2HS may be a member of the *Ppd-1* orthologous series {766}.

QTL : A QTL was detected in chromosome 4BS in Courtot/CS {0132}.

QTL: Trident (early)/Molineux (late): In addition to an effect associated with chromosome 2B, three QTLs were designated as follows: ***QPpd.agt-1AL*** *(Xwmc304 - Xgwm497),* ***QPpd.agt-7AS*** *(Xbarc154 - Xbarc108)* and ***QPpd.agt-7BS*** *(Xgwm46 - Xgwm333)* {10382}. The QTL in chromosome 1A is possibly orthologous to *Ppd-H2* in barley.

65. Response to Salinity

65.1. K+/Na+ discrimination

Variation in K+/Na+ discrimination ratios correlate with salt tolerance, high ratios being indicative of higher tolerance.

Kna1{290}. 4DL{290}.4BS.4BL-4DL{283}.4BS.4BL-4DL-4BL{849}. **v:** Hexaploid wheats{290}. **tv,su:** Langdon 4D(4B){283}. **tv,tr:** Various lines{290}; Selection 3*5-4{849}. **ma:** *Kna1* was completely linked with *Xabc305-4B, Xabc305-4D, Xbcd402-4B, Xbcd402-4D, Xpsr375-4D, Xpsr567-4B, Xpsr567-4D, Xwg199-4B and Xwg199-4D* in recombined *T. turgidum* 4B and *T. aestivum* 4D chromosomes{283,849}.

Lophopyrum elongatum chromosome arms 1ES, 7ES, and 7EL enhance K^+/Na^+ selectivity in wheat under salt stress {0065}.

Kna1 is a possible orthologue of *Nax2* and is the Na+ transporter *TaHKT1;5-D* {10455}.

65.2. Salt tolerance

QTL: Opata 85/W7984. 77 QTLs effective at different growth stages were mapped to 16 chromosome {10384}.

65.3. Sodium exclusion

Nax1{10452}. 2AL{10452}. **itv:** Tamaroi*6/Line 149 = P06306{10453}. **tv:** Line 149 *Nax2* = 126775b{10452}. **dv:** AUS 90382 *Nax2* = C68.101 {10455} = JIC *T. aegilopoides* no. 3. **ma:** *Nax1* was mapped as a QTL in the region *Xpsr102-2A* - 5.4 cM - *Xwmc170-2A* - 0.9 cM - *Xksud22-2A/Xksu16-2A* - 0.8 cM - *Xgwm312-2A* with $R^2 = 0.38$ in Tamaroi/Line 149{10452}; *TmHKT7-A2* was identified as a putative candidate Na^+ transporter{10454}. *Nax1* promotes withdrawal of Na^+ from xylem in leaf bases and roots {10453}.

Nax2{10453}. 5AL{10455}. **itv:** Tamaroi*6/Line 149 = P05603{10453}. **tv:** Line 149 *Nax1* = 126775b{10452,10453}. **dv:** AUS 90382 *Nax1* = C68.101 {10455} = JIC *T.*

aegilopoides no. 3. **ma:** Co-segregation with *Xgwm291-5A/Xgwm140-5A/Xgpw2181-5A*{10455}; *TmHKT1;5-A* was identified as a candidate for *Nax2*{10455}.
Nax2 is a likely orthologue of *Kna1* {10455}.

QTL for Na^+ exclusion and seedling biomass under salt stress were detected in the cross Berkut/Krichauff on chromosome 2A (*Nax1* region) and 6A (*Xcfd080-Xbarc171-6A*) {10917}.

66. Response to Tissue Culture

Qtcr.ipk-2B.1{084}. [*Tcr-B1*{084}]. **ma:** Weakly associated with *Xpsr102-2B*{084}.
Qtcr.ipk-2B.2{084}. [*Tcr-B2*{084}]. **ma:** Closely linked and distal to *Ppd-B1*{084}.
Qtcr:ipk-2B.3{084}. [*Tcr-B3*{084}]. **ma:** Linked with*Yr7/Sr9g*{084}.
QGpp.kvl-2A{0253}. 2AL{0253}. **v:** Ciano/Walter DH mapping population. The green plant percentage was contributed by Ciano{0253}. **ma:** Associated with *Xpsp3045-2A*{0253}.
QGpp.kvl-2B.1{0253}. 2BL{0253}. **v:** Ciano/Walter DH mapping population. The green plant percentage was contributed by Ciano{0253}. **ma:** Associated with *Xgwm388-2B*{0253}.
QGpp.kvl-2B.2{0253}. 2BL{0253}. **v:** Ciano/Walter DH mapping population. The green plant percentage was contributed by Ciano{0253}. **ma:** Associated with AFLP markers{0253}.

67. Response to Vernalization

The requirement for vernalization is particularly important for winter cereals to avoid cold injury of the sensitive floral organs during the winter. In wheat, vernalization requirement is controlled by four major genes designated *Vrn-1, Vrn-2, Vrn-3,* and *Vrn-4*. The first three genes were identified using map based cloning aproaches {10014, 10299, 10421}. The *Vrn-1* gene encodes a MADS-box transcription factor closely related to the Arabidopsis *AP1/FRUITFULL* family, responsible for the transition of the shoot apical meristem from the vegetative to reproductive stage in wheat {10014}.

Deletions in the promoter (*Vrn-A1a, Vrn-A1b*) {10198} or the first intron of this gene (*Vrn-A1c, Vrn-B1a, Vrn-D1a*) {10202} are the most common sources of spring growth habit among landraces and commercial cultivars of polyploid wheat worldwide {10617,10695,10709}.

The *Vrn-2* locus produces two linked and related proteins designated ZCCT1 and ZCCT2, characterized by the presence of a putative zinc finger and a CCT domain {10299}.

Deletions and mutations involving both the ZCCT1 and ZCCT2 genes are frequent in diploid wheat and are associated with recessive alleles for spring growth habit {10299}.

Among the cultivated tetraploid and hexaploid wheat species the *Vrn-B2* gene is generally functional whereas the *Vrn-A2* gene is not {10710}. At least one functional copy of *Vrn-2* combined with homozygous recessive alleles at all three *Vrn-1* loci is required to confer winter growth habit in hexaploid wheat.

The *Vrn-B3* locus (formerly known as *Vrn-5* or *Vrn-B4*) is homologous to the Arabidopsis *FT* gene {10421}. This dominant allele, found in the variety Hope, is associated with the insertion of a transposable element in the *Vrn-B3* promoter. Natural variation at the *Vrn-A3* and *Vrn-D3* loci has been also described in hexaploid wheat {10533}. *Vrn-3* promotes the transcription of *Vrn-1* and accelerates flowering {10421}.

The *Vrn-D4* allele for early flowering was originally identified in the Australian cultivar Gabo {671} and was backcrossed into Triple Dirk to develop the isogenic line TDF {1172}. This locus was mapped on the centromeric region of chromosome 5D between markers *Xcfd78* and *Xbarc205* {10711}. Natural variation for flowering time at the centrometric region of homoeologous group5 chromosomes has been found, so far, only in the D genome. Incorrect TDF seed stocks generated initial confusion about the existence of *Vrn-D4* but molecular markers are now available to separate the incorrect stocks {10711}. Using genetic analyses, Iwaki et al. {10003} found the *Vrn-D4* allele for spring growth habit occurred with a higher frequency in India and neighboring regions.

Vrn-1{1398}. Synonymous with *TaVRT-1* {10019}

Orthologous series in long arms of chromosomes of homoeologous group 5.

Vrn-1 is a MADS-box gene similar to Arabidopsis *APETALA1* {10014}. Spring types are associated with mutations in the promoter or the first intron {10014, 10198, 10202, 10288}. Reduction of *Vrn-1* transcripts in transgenic hexaploid spring wheat delays flowering {10300}.

A polymorphism between Jagger and 2174 was associated with *vrn-A1a*. A point mutation occurred in exon 4 {10695}; 17 of 19 genotypes surveyed, including Jagalene, carried the 2174 mutation and only Jagger and Overley carried the Jagger allele {10695}.

Vrn-1 genotypes in Pacific Northwest USA wheats are listed in {10695}.

Vrn-A1. **ma:** *Xgwm271-5A* - 6.5 cM - *Vrn-A1* - *Xbarc232-5A*{10880}.

Dominant spring habit alleles at the *Vrn-A1* locus

vrn-A1.

Copy number variation for *vrn-A1* was detected in IL369 (2 copies) {10202}, Malacca (2 copies) and Heeward (3 copies). Higher copy number was associated with later flowering or with increasing requirement for vernalization (i.e. longer exposure to cold is needed to achieve full vernalization) {10881}.

vrn-A1a{10198}. vrn-A1a {10198} **v:** Claire{10880}; Triple Dirk C{10880}. **v2:** Chinese Spring *Vrn-D1a*{10880}. **c:** GenBank AY616455{10198}.

vrn-A1b{10881}. **v:** IL369{10202}; Malacca{10881}. **c:** GenBank JF965396{10881}. This allele has two copies of the gene, possibly arranged in tandem although the physical structure is unknown. Both copies are distinguished from Chinese Spring *vrn-A1a* by a SNP in exon 7 (T in Malacca, C in Chinese Spring). One copy also has a SNP in exon 4 (T in Malacca, C in Chinese Spring). Sequenced cDNAs from Malacca show that both copies are expressed. {10881}.

vrn-A1c{10881}. **v:** Hereward{10881}. **c:** GenBank JF965397{10881}.

A comparison of Claire (*vrn-A1a*), Malacca (*vrn-A1b)* and Hereward (*vrn-A1c*) indicated that increasing gene copy number is associated with lateness {10881}. Two winter alleles were identified based on an SNP in exon 4 {10656}.

vrn-A1v{10916}. **v:** Don Ernesto INTA{10916}; Jagger{10916}; Norin 61{10916}; Opal{10916}.

vrn-A1w{10916}. **v:** Bezostaya{10916}; Bavicora M 92{10916}; Kavkaz{10916}; Gennson 81{10916}; Seri M 82{10916}; Wichita{10916}.

Vrn-A1a{1398}. [*Vrn1*{1172},*Sk*{002}]. 5AL{775,883}. **i:** Triple Dirk D (GenBank AY616458 & AY616459){1171,1172, 10198}. **s:** Kharkov 22MC*/Rescue 5A{358}; Winalta*8/Rescue 5A{876}; Rescue*/Cadet 5A *Vrn-D1a Vrn-B1a*{1221}. **v:** Cadet{1221}; Conley{1171}; Diamant II{885}; Falcon{1172}; Koga II{1611}; Kolben{001,1171,1172};

Konosu 25{460}; Marquis{001}; Reward{1171}; Saitama 27{460}; Saratov 29{883}; Saratovskaya 29{885}; Saratovskaya 210{883}; Shabati Sonora{885}; Thatcher{1171}; WW15{1172}. **v2:** Shortandinka *Vrn-B1a*{885}; Takari *Vrn-B1a*{253}; Triple Dirk *Vrn-B1a*{1173}; Hope *Vrn-B4a*{1424}. **ma:** *Vrn-A1* - 7.5 cM - *Xwg644-5A*{726}; Located mid 5A cosegregating with *Xcdo504-5A*, *Xwg644-5A* and *Xpsr426-5A*{419}; *Vrn-A1* - 0.8 cM - *Xbcd450-5A/Xrz395-5A* - 4.2 cM - *Xpsr426-5A*{9903}.

Cultivars possessing *Vrn-A1a* are insensitive to vernalization. *Vrn-A1a* is epistatic to other genes. According to {1221}, *Vrn-A1a* is not always fully dominant and not always epistatic. Kuspira *et al.* {745} attributed single gene variation in *T. monococcum* to the *Vrn-A1a* locus. Multiple recessive alleles were suggested {745}. *Vrn-A*^{m}*1* was mapped on the long arm of chromosome 5A^m closely linked to the same RFLP markers as *Vrn-A1* {279}. *Vrn-A*^{m}*1* was mapped to the *Xcdo504-5A* - *Xpsr426-5A* region {0312}. In the opinion of the curators this location may not be correct

Multiple alleles also were reported in {9930}, and the dominant allele of Novosibirskaya 67 and the weaker dominant allele of Pirotrix 28 were designated *Vrn1a* and *Vrn1b*, respectively.

Vrn-A1b{10198}. **v:** Marquis PI94548 (GenBank AY616461){10198}. **tv:** *T. turgidum* var. *durum* ST36{10198}.

Vrn-A1c{10198}. This allele has a promoter similar to recessive *vrn-A1a* from Triple Dirk C {10198} and a large deletion in intron 1 {10202}. **v:** IL162{10198}; IL369 {10198} has a 5.5 kb deletion in *Vrn-A1* intron 1{10202}. **tv:** Aldura PI 486150{10202}; Leeds CI 13796{10202}; Mexicali 75 PI 433760{10202}; Minos CI 15161 {10202}. Most durum genotypes have a 7.2 kb deletion in intron 1{10202}.

Vrn-A1d{10198}. **tv:** *T. turgidum* var. *dicoccoides* Amrim 34{10198}; FA15 (GenBank AY616462){10198}; Iraq 8736{10198}; Tabigha 15{10198}.

Vrn-A1e{10198}. **tv:** *T. turgidum* var. *dicoccum* ST27 = Vernal (GenBank AY616463){10198}.

Vrn-B1. **ma:** *Tsn1* - 14.8 cM - *Vrn-B1* - 0.7 cM - *Xwmc75-5B*{10880}.

vrn-B1. **c:** GenBank AY747604.1{10695}.

Vrn-B1a{1398}. [*Vrn4*{1173},*Vrn2*{1172},*Ss*{002},*Vrn2a* = *Vrn2*{921,920},*Vrn2b* = *Vrn2*{921,920}]. 5B{885}.5D{635}.5BL{885}.5B{921,920}.5BL or 7BL{635,0282}. **i:** Ank-18{921,920}; Triple Dirk B{1172}. **s:** Diamant 1*8/Mironovskaya 5A{920}; Diamant 1*8/Skorospelka 35 5A{920}; Rescue*/Cadet 5A *Vrn-A1 Vrn-D1a*{885}; Saratovskaya 29*8/Mironovskaya 808 5A{920}; Saratovskaya 29*8/Odesskaya 51 5A{920}. **v:** Bersee{557}; Brown Schlanstedt{001,002,1171,1172}; Cadet{1221}; Festiguay{1172}; Magali; Mara{1611}; Milturum 321{885,920}; Milturum 885{885,920}; Noe{002}; Pyrothrix 28{920}; Spica{557}; *T. spelta* var. *duhamelianum* KT19-1{10057}; Ulyanovka 9{920}. **v2:** Borsum *Vrn1-A1a*{001}; Dala *Vrn1-A1a*{001}; Diamant 1 *Vrn1*{001,920}; Gabo *Vrn4*{1172}; Halland *Vrn-A1a*{001}; Harukikari *Vrn-A1a*{883}; Rubin *Vrn-A1a*{001}; Saratovskaya 29 *Vrn-A1a*{920}; Shortandinka *Vrn-A1a*{1221}; Triple Dirk *Vrn-A1a*{1173}. **ma:** A dCAPS marker derived from *Xwg644-5B* was 1.7 cM from *Vrn-B1*{10006}; *Vrn-B1a* - 1.6 cM - *Xwg644-5B* - 2.5 cM - *Xgwm408-5B* {10004}; Closely linked to *Xgwm408-5B* in Diamant I*/Mironovskaya 808 5A // Bezostaya 1{10007}; A close association of *Vrn-B1* with *Xcdo1326-5B* was reported in{10057}. **c:** GenBank AY74603.1{10695}.

When mapped as a QTL *Vrn-B1* showed closest association with *Xgwm408-5B* {10007}.

All common wheat genotypes carrying *Vrn-B1a* studied so far have a 6.8 kb deletion in intron 1 (Triple Dirk B, Bersee, Festiguay, Mara, Milturum, Noe, Spica) {10202}.

Two variants of *Vrn-B1a* were distinguished in {920,921}. Carriers of an earlier designated *Vrn2b* (characterized by Diamant 1*8/Skorospelka 35 5A) showed accelerated flowering after 15 and 30 days of vernalization, whereas carriers of *Vrn-2a*, (characterized by Ank-18 and Saratovskaya 29*8/Mironovskaya 808 5A) did not respond to these periods of vernalization. This distinction was not made in the above list.

Vrn-B1b{10695}. **v:** Alpowa{10695}. **c:** GenBank FJ766015. Relative to *Vrn-B1a* (Triple Dirk B), *Vrn-b1b* has a G-C SNP at position 1656 and a 36 bp deletion at 1661-1696{10695}.
Vrn-B1c{10880}. **tv:** *T. turgidum* ssp. *carthlicum* PI 94749{10880}. **c:** GenBank JN817430 contains a 5,463 retrotransposons insertion in the 5' UTR region{10880}.
Vrn-D1{1398}. Vrn3{1172} 5DL{775,883}.
Vrn-D1a. **i:** Triple Dirk E{1172}. **s:** Rescue*/Cadet 5A Vrn-A1a{1221}. **v:** Chinese Spring{1172}; Loro{1172}; Norin 61{460}; Shinchunaga{460}; Shirasagi Komugi{460}; Ushio Komugi{460}. **v2:** Rescue *Vrn-B1a*{1221}.
All the common wheat genotypes carrying *Vrn-D1a* studied so far have a 6.8 kb deletion in intron 1 (Triple Dirk E, Chinese Spring, Norin 61, Shinchunaga, Shirasagi Komugi, Ushio Komugi) {10202}.

Stock:Genotype:Vernalization Response
Triple Dirk, Kolben: *Vrn-A1a Vrn-B1b Vrn-D1b*: No
Triple Dirk B, Festiguay :*Vrn-A1b Vrn-B1a Vrn-D1b*:Yes
Gabo:*Vrn-A1b Vrn-B1a Vrn-D1b*: Yes
Triple Dirk E, Chinese Spring:*Vrn-A1b Vrn-B1b Vrn-D1a*:Yes
Triple Dirk F: *Vrn-A1b Vrn-B1b Vrn-D1b Vrn-D5a:* Yes
Triple Dirk C: *Vrn-A1b Vrn-B1b Vrn-D1b Vrn-D5b*: Yes Winter type.

Vrn1{10014}. Spring type **v:** G2528{10014}.
vrn1{10014}. Winter type **v:** DV92{10014}; G1777{10014}; G3116{10014}. **ma:** *Vrn1* was completely linked to MADS-box genes *AP1* and *AGLG1*. *AP1* was considered a better candidate than *AGLG1* and differences between winter and spring genotypes appeared to be related to differences in the promoter region of *AP1*{10014}; The involvement of *AP1* in vernalization response conditioned by *Vrn-1* was also reported in{10019}.

Vrn-2{1398}.
Orthologous series in chromosomes of homoeologous group 4. *Vrn-A*^{m}*2* was located in *T. monococcum* {279} on chromosome 5A^m on the 4A^m translocated region. *Vrn-A*^{m}*2* was mapped to the distally located *Xwg114-5A - Xwec87-5A* region {0312}. *Vrn-H2*(sh/sgh1) occurs in barley chromosome 4H {1455} and is probably orthologous to *Vrn-A*^{m}*2* based on comparative maps {279,767}. *Vrn-2* is a zinc-finger/CCT domain transcription factor (*ZCCT1*) {10299}, and repressor of flowering down-regulated by vernalization and short days {10301}. Reduction of *Vrn-2* transcripts in transgenic hexaploid winter wheat accelerates flowering {10299}.
Vrn-A2a{279}. Winter habit, dominant in diploid wheat {279} **dv:** G1777{279}; G3116{279}.
Vrn-A2b{279}. Spring habit, recessive in diploid wheat. **dv:** DV92{279}; PI 355517{10299}; PI 345242{10299}; PI 352475{10299}; PI 277137{10299}.
Contains a non-functional mutation in the CCT domain {10299}.
Vrn-A2c{10299}. Spring habit, recessive in diploid wheat **dv:** PI 352484{10299}; PI 323437{10299}; PI 286068{10299}; PI 591871{10299}; PI 542474{10299}; PI 428175{10299}; PI 237659{10299}; PI 221329{10299}; PI 225164{10299}; PI 377662{10299}; PI 377648{10299}; PI 362610{10299}.
Complete deletion of the *ZCCT1* gene {10299}.

Vrn3{1398}. Orthologous series in chromosomes of homoeologous group 1 predicted from orthology with *Vrn-H3*(*Sh3*) in barley chromosome 1H {1455,1316}. Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization {773}.

Vrn-B3{10421}. [*Vrn-4B*{279},*Vrn5,eHi*{769,771,779}]. 7BS{768,769,771}. **s:** CS(Hope 7B) *Vrn-D1a*{768}. **v2:** Hope *Vrn-A1a*{1424}. **ma:** *Vrn-B3* is completely linked to *TaFT* and 1 cM distal to *Xabc158-7B* on the region of 7BS proximal to the translocation with homoeologous group 5{10421}.
The dominant *Vrn-B3* allele in Hope has a retrotransposon insertion in the *TaFT* promoter (GenBank DQ890165) {10421}. Transformation of winter wheat Jagger with the dominant *Vrn-B3* significantly accelerated flowering {10421}. Different Hope seed sources were heterogeneous for this insertion {10421}. The retrotransposon insertion in the *TaFT* promoter is present in the CS (Hope 7B) {10421}.
Vrn-H3{10421}. [*Sh3*]. **ma:** Completely linked to *HvFT* and 1 cM distal to *Xabc158* on 7HS. Originally mapped incorrectly on 1H based on loose linkage {1455,1316}.
vrn-B3. **v:** Chinese Spring *Vrn-D1* (GenBank DQ890162){10421}.
In both wheat and barley *Vrn-3* is completely linked with a flowering promoter gene homologous to Arabidopsis *FLOWERING LOCUS (FT)* {10421}. Polymorphisms in the A and D genome copies of *TaFT* are associated with variation of earliness components in hexaploid wheat {10533}.

Vrn4{279}. [*Vrn5*{771,769},*Vrn-D5*{10004}]. 5D{10002}.5DL{10004}. **i:** Triple Dirk F{10711}. **s:** CS (Hope 7B) *VrnD1a*{768}. **v2:** Gabo *Vrn-B1a*{1172}; IL47/*Vrn-A1a*{10005}. **bin:** Centromeric region. **ma:** *Xgdm3-5D* - 11.5 & 4.5 cM - *Vrn4*{10004}; Located in a 1.8 cM interval flanked by markers *Xcfd78-5D* and *Xbarc205-5D*{10711}.
Eight land races with only *Vrn4* were detected in {10003}; others combined *Vrn4* with other *Vrn* genes. Stelmakh {1424} doubted the existence of *Vrn4*. Goncharov {10108} confirmed the existence of *Vrn4* but failed to confirm its location on chromosome 5D. References to additional studies are given in {1424}.

Vrn4 was mapped on the centromeric region of 5D between markers. Incorrect TDF seed stocks generated confusion about *Vrn-D4* existence {10711}. Eight land races with only *Vrn4* were detected in {10003}; others combined *Vrn4* with other *Vrn* genes. Stelmakh {1424} doubted the existence of *Vrn4*. Goncharov {10108} confirmed the existence of *Vrn4* but failed to confirm its location on chromosome 5D.
Vrn-D5a{10004}. [*Vrn-D5*{10004},*Vrn4*{1172}]. 5D{10002}.5DL{10004}. **i:** Triple Dirk F{1172}. **v2:** Gabo *Vrn-B1a*{1172}; IL47 *Vrn-A1a*{10005}. **ma:** *Xgdm3-5D* - 11.5 & 4.5 cM - *Vrn-D5a*{10004}.
Eight landraces with only *Vrn-D5a* were detected in {10003}; others combined *Vrn-D5a* with other *Vrn* genes. Stelmakh {1424} doubted the existence of *Vrn-D5a*. Goncharov {10108} confirmed the existence of *Vrn-D5a* but failed to confirm its location on chromosome 5D. References to additional studies are given in {1424}.
QTL: Analysis in Courtot/CS {0132}.
A QTL on chromosome 5BL was linked to *Xgwm604-5B* (this QTL explained 11% of the variance in flowering time) {10075}.
Three genes up-regulated by vernalization were cloned from *T. monococcum* {10531}. These were VIN3-like genes similar to Arabidopsis VIN3.
Vil-1{10531}. GenBank DQ886919 {10531}. **ma:** *T. monococcum* chromosome 5A^{m}{10531}.
Vil-2{10531}. GenBank DQ886917 {10531}. **ma:** *T. monococcum* chromosome 6A^{m}{10531}.
Vil-3{10531}. GenBank DQ886918 {10531}. **ma:** *T. monococcum* chromosome 1A^{m}{10531}.

Allelic variations at the *Vrn-1* and *Vrn-B3* loci in Chinese wheat cultivars are summarized in {10617}.

Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization {773}.

Stem-elongation in winter wheat: In regions where wheat is used as a dual purpose crop for grazing and grain production a relatively long vegetative phase is required to maximize the vegetative tissue and to delay the stem elongation phase. Variation in this attribute occurs among winter wheats such as Jagger (early stem elongation) and 2174 (late elongation).

In a Jagger/2174 RIL population, QTL for stem elongation included *Qste.0cs-5A* (associated with the *Vrn-A1* locus, *Qste.ocs-1BL, Qste.ocs-2D* (associated with the *Ppd-D1* locus) and *Qste.ocs-6A* {1010}. In 2007 the respective R^2 values were 0.289, 0.155, 0.067 and 0.058. Jagger alleles on chromosome 5A, 1B and 6A promoted stem elongation whereas the allele on chromosome 2D had a delaying effect {10722}.

68. Restorers for Cytoplasmic Male Sterility

68.1. Restorers for *T. timopheevi* cytoplasm

Rf1{823}. 1A{1224,1619,873}.1AS{868}. **v:** L22{868}; (*T. timopheevii/Aegilops squarrosa)//* 3*Dirk{1619}. **v2:** *T. timopheevii*/3* Marquis *Rf2*{823}; R113 *Rf4*{873}.
The second gene referred to as *Rf4*{1619} in the last stock was located in chromosome 7D, but its relationship to *Rf2* in {823} is unknown.

Rf2{823}. 7D{871}. **v:** *T. timopheevii*/3*Marquis *Rf1*{823}.

Rf3{1453}. 1B{1453}.1BS. **v:** R18{10222}; R9034{10222}; *T. spelta* var. *duhamelianum*{1453}. **ma:** *Xcdo388-1B* - 1.2 cM - *Xabc156-1B*{9934}; RFLP markers *Xcdo442-1B* and *Xbcd249-1B* were found to be associated with *Rf3* on 1BS{860}; Mapped as a QTL in the region *Xbarc207-1BS - Xgwm131-1BL - Xbarc61-1BL* in crosses R18/ND36 and R9034/ND36{10222}.

Rf4{1619}. [*Rf2*{1619}]. 6B{1619,873}.1BS{868}. **v:** L3{868}; (*T. timopheevii/Aegilops squarrosa*) / 3*Canthatch *Rf5*{1619}; R113 *Rf1*{873}.

Rf5{1619}. [*Rf3*{1619}]. 6D{1619}. **v:** (*T. timopheevii/Aegilops squarrosa*)/ 3*Canthatch *Rf4*{1619}.

Rf6{865,859}. 6AS [T6AL.6AS-6U]{865}.6BS [T6BL.6BS-6U]{865}. **tr:** Line 2114{865}; Lines 040-5; 061-1{865}; 061-4{865}.
Genes *Rfc3* in chromosome 6RL and *Rfc4* in chromosome 4RL were reported in {225}.
Novel *Rf* genes were identified on 5AL linked to *Xcdo786-5A* and *XksuH1-5A*{860}.

Minor restorer effects were associated with *Xbarc330-5A* in R18 and *Xgdm130-7D* in R9034 {10222}. The relationships of these QTL with previously located restorers in chromosomes 5A {860} and 7D (*Rf2*) are unknown.

68.2. Restorers for *Aegilops longissima* cytoplasm

Vi{867}. 1B{870}.1BS{027}. **v:** *T. turgidum*{867}.
Probably derived from a cv. Selkirk (*T. aestivum*) line with *Ae. cylindrica* cytoplasm {867}.

68.3. Restorers for photoperiod-sensitive *Aegilops crassa* cytoplasm

Morai & Tsunewaki {1047} described photoperiod sensitive CMS caused by *Ae. crassa* cytoplasm in wheat cv. Norin 26. Almost complete sterility occurred when plants were grown in photoperiods of 15h or longer.

Rfd1{1047}. 7BL{1047}. **v:** Chinese Spring{1047}.
A different system of restoration occurs in cv. Norin 61 where at least four chromosomes, 4A,

1D, 3D and 5D, appear to be involved {1046}. Several Japanese wheats carry a similar or equally effective gene combination {0335}.

69. Ribosomal RNA

The *5S-Rrna-1* loci were physically mapped in 1AS, 1BS, and 1DS and the *5S-Rrna-2* loci were physically mapped in 5AS, 5BS and 5DS of Chinese Spring using deletion lines {1043}. Table 1 in {276} lists the chromosome or chromosome arm locations of rRNA loci in 12 Triticeae species.

69.1. 5S rRNA genes

Within the Triticeae there are basically two sets of 5S rRNA loci. One set, identified by repetitive units 320-468 bp in length, is located on group 1 chromosomes. The other set, identified by repetitive units 469-500 bp in length, is on group 5 chromosomes. Within species the repetitive units at a locus are extremely uniform in size and sequence. They remain stable in foreign genetic backgrounds.

5S-Rrna-A1. [*5SDna-A1*{295}]. 1AS{295,658}. **v:** CS{1043}.

5S-Rrna-B1. [*5SDna-B1*{295}]. 1BS{039,295}. **dv:** *T. monococcum*. **ma:** A PCR marker specific *5S-Rrna-B1* was developed{9974}.

5S-Rrna-D1. [*5SDna-D1*{295}]. 1D{295,758}.1DS{295}. **v:** CS{295,758}. **dv:** *Ae. tauschii*{758}. **ma:** A PCR marker specific for *5S-Rrna-D1* was developed in {9974}.

5S-Rrna-E1. [*5SDna-E1*{960}]. 1E{1290}. **dv:** *L. elongatum*.

5S-Rrna-R1. [*5SDna-R1*{1206}]. 1RS{039,1206}. **al:** *S. cereale*. **ma:** A PCR marker specific for *5S-Rrna-R1* was developed in {9974}.

5S-Rrna-Sc1. [*5SDna-Sc1*{960}]. 1S^{c}{1290}. **al:** *Elymus ciliaris*.

5S-Rrna-S^{t}1. [*5SDna-S^{t}1*{960}]. 1S^{t}{1290}. **al:** *E. trachycaulus*.

5S-Rrna-Y1. [*5SDna-Y1*{960}]. 1^{Y}{1290}. **al:** *E. ciliaris*.

5S-Rrna-A2. [*5SDna-A2*{295}]. 5AS{295,658}. **v:** CS{295}. **dv:** *T. monococcum*{295,658}.

5S-Rrna-B2. [*5SDna-B2*{295}]. 5BS{295}. **v:** CS.

5S-Rrna-D2. [*5SDna-D2*{295}]. 5D{295,758}.5DS{758}. **v:** CS{295,758}. **dv:** *Ae. tauschii*{758}.

5S-Rrna-R2. [*5SDna-R2*{1206}]. 5RS{1206}. **al:** *S. cereale*.

5S-Rrna-H^{t}2. [*5SDna-H^{t}2*{960}]. 5H^{t}{1290}. **al:** *E. trachycaulus*.

5S-Rrna-U2. [*5SDna-U2*{295}]. 5U{295}. **al:** *Ae. umbellulata*.

5S-Rrna-V2. [*5SDna-V2*{960}]. 5V{1290}. **al:** *D. villosa*.

5S-Rrna-H3. [*5SDNA-H3*{793}]. 2H{710}.2HL{793}. **al:** Betzes Barley; Sultan barley.

5S-Rrna-H4. [*5SDNA-H4*{793}]. 3HL{793}. **al:** Betzes barley; Sultan barley.

5S-Rrna-H5. [*5SDNA-H5*{793}]. 4HL{793}. **al:** Betzes barley; Sultan barley.

5S-Rrna-H6. [*5SDNA-H6*{793}]. 4HS{793}. **al:** Betzes barley; Sultan barley.

70. Seedling Leaf Chlorosis

sc{149}. 3BS{149}. **s:** CS*/Hope3B{149}. **v:** Hartog{149}; Suneca{149}; wheats with *Sr2*{149}.

Leaf chlorosis is affected by temperature and light and is enhanced by infection with pathogens. *sc* is completely linked with *Pbc* (pseudo-black chaff) and *Sr2* (reaction to *Puccinia graminis*).

71. Segregation Distortion

See also, Gametocidal Genes.

QSd.ksu-1D{9931}. 1DL{9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704{9925}. **ma:** Association with *Xcmwg706-1D*{9931}.

QSd.ksu-3D{9931}. 3DS{9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc TA1704{9925}. **ma:** Association with *Xwg177-3D*{9931}.

QSd.ksu-4D{9931}. 4DS{9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691/var. *typica* acc. TA1704{9925}. **ma:** Association with *XksuF8-4D*{9931}.

QSd.ksu-5D.1{9931}. 5D{9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704{9925}. **ma:** Association with *Xcdo677-5D*{9931}.

QSd.ksu-5D.2{9931}. 5DL{9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704{9925}. **ma:** Association with *Xglk614-5D* (synonym '*Xtag614-5D*'){9931}.

QSd.ksu-5D.3{9931}. 5DL{9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704{9925}. **ma:** Association with *Xwg1026-5D*{9931}.

QSd.ksu-7D{9931}. 7DS{9931}. **dv:** *Ae. tauschii* var. *meyeri* acc. TA1691; *Ae. tauschii* var. *typica* acc. TA1704{9925}. **ma:** Association with *Xglk439-7D* (synonym '*Xtag439-7D*'){9931}.

72. Soft Glumes

Sog{10555}. **dv:** *T. monococcum* ssp. *boeoticum* ID49{10555}; *T. monococcum* ssp. *aegilopoides* TA4342-96{10769}.

sog{10555}. 2AS{10555}. **bin:** C-2AS5-0.78. **dv:** *T. monococcum* ssp. *monococcum* var. *sinskajae* (syn. *aegilopoides*) UD69{10555}; Tm-9, a mutant of TA4342-96{10769}. **ma:** Co-segregation with AFLP loci *Xe4232041* and *Xe373311*{10555}; *Xgwm71-2A* - 3.3 cM - *sog* - 3.5 cM - *Xbcd120-2A*{10769}.

sog was considered to be an homologue of *Tg1* and *Tg2*. See Tenaceous glumes.

73. Sterol Esterification in Kernels - Synthesis of b-Sitosterol Esters

Two sterol-ester phenotypes, p-L (palmitate + linoleate) and L (linoleate) are inherited as alleles at a single locus.

Pln{428}. [*P-L*{428}]. 7DS{1476}. **v:** Aradi{428}; Aragon 03{428}.

pln{428}. [*L*{428}]. L{428}. **v:** Mara{428}; Pane 247{428}.

74. Stem solidness

Solid stem, caused by increased pith in normally hollow stem regions, is associated with resistance to wheat stem sawfly, *Cephus cinctus*. Solid stem confers resistance to wheat stem sawfly. See also Reaction to *Cephus* spp.

Qsst.msub-3BL. 3BL{10206}. **v:** Rampart PI 59388{10206}. **ma:** Linked to microsatellite markers *Xgwm247-3B*, *Xgwm340-3B*, and *Xgwm547-3B*. These markers explained 76% of the total variation for stem solidness in Rampart/Jerry{10206}.

Stem solidness in chromosome 3B of Golden Ball was verified in Langdon-Golden Ball disomic substitution lines {10730}.

Qsst.msub-3DL. [*Qss.msub-3DL*{10395}]. 3DL{10395}.

Associated with *Xgwm645-3DL* (R^2=0.31), *Xwmc656-3DL* (R^2=0.1), and *Xcfd9-3DL* (R^2=0.13) {10395}. This gene acted as an enhancer of *Qsst.msub-3BL* {10395}.

Qsf.spa-3B{10351}. **tv:** .

Kyle*2/Biodur (solid stem)//Kofa (hollow) DH population: *Qsf.spa-3BL* was located to a 21.3cM interval flanked by *Xgwm247-3B* and *Xgwm114-3B* {10351}. Mapped as a single gene, *Xgwm247-3B* - 6.9cM - *Qsf.spa-3B* - 14.4cM - *Xgwm114-3B* {10351}. This location was confirmed in two other crosses involving G9580B-FE1C and Golden Ball as the solid stem parents {10351}.

75. Temperature-Sensitive Winter Variegation

This phenotype involves reduced vigour and chlorotic patches on leaves of certain genotypes in *Ae. umbellulata* cytoplasm when grown at low temperatures {1596}.

Vgw. Variegation is dominant {1596}. [*Vg*{1021}]. 5BL{1021}. **v:** Bersee{1596}; Cappelle-Desprez{1596}; Hobbit Sib{1596}; Mara{1596}.

vgw{1021}. **v:** Besostaya I{1596}; CS{1596}; Poros{1596}; Sava{1596}; *T. spelta*{1596}.

76. Tenacious Glumes

Tg1{1240}. Derived from *Ae. tauschii*. Dominant. [*Tg*{1240}]. 2DS{1240}. **bin:** 2BS-3 1.00-0.84. **v:** Synthetic ABD wheats{652}. **ma:** Placed in a 12 cM interval between *Xwmc112-2D* and *Xbarc168-2D*{10497}.

Tg2{0046}. Derived from *T. dicoccoides* 2BS{0046}. **v:** TA 3419 = *Tetra Canthatch / Ae. tauschii* ssp. *meyeri* TA1599{10769}. **ma:** *Tg2* is associated with *Xrsq805(Embp)-2B* and *Xpsr899-2B*{0046}; *Xgwm261/Xwmc503-2D* - 2.3 cM - *Tg2* - 5.9 cM - *Xfba88/Xfbc400-2D*{10769}.

Soft Glume locus is not an orthologue of Tenacious Glumes {10769}.

A QTL analysis of the relationship of glume tenacity (*Gt*) with threshability (*Ft*) and the size of the glume base scar (*Gba*) after glume detachment in two crosses, viz. the ITMI population and CS*/CS (*Ae. tauschii* 2D), was undertaken {10497}. In the first cross *QFt.orst-2D.1* and *QGt.orst-2D.1* were closely associated with *Xgwm261-2D*, and *XFt.orst-2D.2* and *XGt.orst-2D* were associated with *Xgwm455-2D*, in the second population only the first pair along with *Xba.orst-2D* were detected; these appeared to correspond with *Tg1* {10497}.

77. Tiller Inhibition

tin1{1212}. Restricted tiller number is recessive{1212} [*Tin*{1212}]. 1AS{1212}.1A{10193}. **v:** Israel Uniculm 494{1212}; Banks + *tin*{10193}; Oligoculm 390{10193}; Uniculm 492{10193}. **ma:** *Xpsp2999(Glu3)-1A* - 3.9 cM - *tin1/Xgwm136-1A* - 2.4 cM - *Xwhs179-1A*{10193}; the 350 bp allele of *Xgwm136-1A* was diagnostic of *tin1*{10193}.

tin2{1212}. Tiller-reducing affect of this allele was dominant {9909}. [*Tin*{9909}]. 2A{9909}. **v:** 88 F2 185{9909}.

tin3{10329}. 3A^{m}L{10329}. **dv:** *T. monococcum* TA4443 = TA4342-96 mutant{10329}. **ma:** *Xbcd131/Xbcd1431-3A* - 9.6 cM - *tin3/Xpsr1205-3A* - 4.7 cM - *Xcfa2076-3A*{10329}.

A QTL of large effect on spike number per plant in a DH population of Fukuho-Komugi/Oligoculm mapping to the *Hg - Xpsp2999(Glu3)-1A* region {10218} probably corresponds to *Tin1*.

78. Uniculm Stunt

Stunting is favoured by a combination of long days and low night temperatures {581}. Caused by duplicate recessive genes, *us1* and *us2*, located in chromosomes 4A and 5B, respectively {200}.

Genotypes: Normal **v**: *Us1 us2*: Alfa {581}; Jaral {581}.
Normal **v**: *us1 Us2*: Mabruk {581}.
Stunted **v**: *us1 us2*: Line 492 {581}.

79. Variegated Red Grain Colour

vg{498}. **v:** Line 10859{498}.

vgvg genotypes in Line 10859 are variegated. The *Vg/vg* locus was independent of the single red gene locus in Line 10859. In a cross to Selkirk (*R-A1b, R-B1b, R-D1b) vgvg* was expressed only in plants with one *R* gene{498}. Variegated red pericarp was also studied in crosses of cv. Supreme. In this case, two red colour genes were present{0136}.

80. Yield and Yield Components

80.1. Grain number per spike

QGnu.ipk-4A{0255}. 4AL{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Higher grain number was contributed by Opata{0255}. **ma:** Associated with *Xmwg549-4A*, *Xabg390-4A* and *Xbcd1670-4A*{0255}.

QGnu.ipk-4A coincides with QTL for height (*QHt.ipk-4A*), spike length (*XEl.ipk-4A*) and grain weight per ear (*QGwe.ipk-4A*) {0255}.

QKps.unl-3A.1{10044}. 3AS{10044}. **v:** Cheyenne/Cheyenne(Wichita 3A) RI mapping population{10044}; a higher kernel number of 0.3 kernels was contributed by Wichita and the QTL explained 15.5% of the phenotypic variation{10044}; The QTL coincided with QTLs for grain yield, kernel number per square metre and 1000-kernel weight{10044}. **ma:** Associated with *Xbarc12-3A*{10044}.

Qkps.unl-3A.2{10044}. **v:** Cheyenne/Cheyenne(Wichita 3A) RI mapping population{10044}; a higher kernel number of 0.3 kernels was contributed by Cheyenne and the QTL explained 9.5% of the phenotypic variation{10044}. **ma:** Associated with *Xbcd141-3A*{10044}.

QTL: Three QTLs for kernel number per spike were assigned to chromosome 3A in RSLs from Cheyene*7/Wichita {0025}.

80.2. Grain volume weight

QGvwt.unl-3A.1{10044}. 3A{10044}. **v:** Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}; higher grain volume weight (+23 kg/hL) was contributed by Wichita and the QTL explained 43.1% of the phenotypic variataion {10044}; the QTL coincided with a QTL for spikes per square metre{10044}. **ma:** Associated with *Xbcd1380-3A*{10044}.

80.3. Grain weight

80.3.1. 50-grain weight

QFgw.ocs-4A.1{0047}. 4A{0047}. **v:** CS/CS(Kanto107 4A) mapping population{0047}. **ma:** Associated with *Xbcd265-4A* and *Xbcd1738-4A*{0047}.

80.3.2. 1000-grain weight

QTL: Two QTLs for 1,000-kernel weight were assigned to chromosome 3A in RSLs from Cheyenne*7/Wichita 3A {0025}. QTLs for grain size were identified on chromosome arms 1DS, 2DL and 6BL in a RIL population from RS111/CS {0236}. Eight QTLs for 1,000-kernel weight (54% of the variation) were mapped in Forno/ Oberkulmer spelt {0280}.

TaCwi-A1{10812}. **ma:** *Xbarc15* - 10.9 cM - *TaCwi-A1* - STS markers Cwi21 and Cwi22 - 17.6 cM - *Xgwm71-2AL*{10812}.

Based on the rice *GIF1* gene encoding a cell wall invertase (GenBank accession EU095553), common wheat *TaCwi-A1* was cloned, and two STS markers Cwi21 and Cwi22 were developed from the polymorphisms between two allelic variants. On average, *TaCwi-A1a* had 1,000 grain weights 2.4 g higher than *TaCwi-A1b* {10812}.

TaGW2-6A{10781}. **ma:** *Xcfd80-6AS.2* - 0.6 cM - *TaGW2-CAPS* - 0.5 cM - *Xbarc146-6A.1/Xwms132.4-6A*{10781}.

Based on its *OsGW2* orthologue in rice this gene was characterized and mapped as a CAPS marker in wheat {10781}. SNPs in the promoter region allowed distinction of two haplotypes. Hap-6A-A was mainly present in southern Chinese wheats; Hap6A-G was present in varieties from central and eastern Europe. On average Hap-6A-A had 1,000 grain weights more than 3g higher than Hap-6A-G {10781}.

QGw1.ccsu-1A{0165}. 1AS{0165}. **v:** RS111/CS mapping population{0165}. **ma:** Associated with *Xwmc333-1A*{0165}.

QGwt.crc-3D{10287}. 3D{10287}. **ma:** Linked to *Xgwm341-3D* - *Xwmc552-3D* (LOD 4.3) in RL4452/AC Domain {10287}.

QGwt.crc-4A{10287}. 4A{10287}. **ma:** Linked to *Xgwm494-Xgwm162* (LOD 6.7) in RL4452/AC Domain{10287}.

QGwt.crc-6D{10287}. 6D{10287}. **ma:** Linked to *Xgwm325-6D* - *Xgwm55-6D* (LOD 3.9) in RL4452/AC Domain{10287}.

QTgw.ipk-5A{0255}. 5AL{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; The higher yielding allele was contributed by W-7984{0255}. **ma:** Associated with *Xfba351-5A* and *Xcdo1312-5A*{0255}.

QTkwt.unl-3A.1{10044}. 3AS{10044}. **v:** Cheyenne/Cheyenne(Wichita 3A) RI mapping population {10044}; a higher kernel weight of 0.27% was contributed by Cheyenne and the QTL explained 12.7% of the phenotypic variation{10044}; The QTL coincided with QTLs for grain yield, kernel number per square metre and kernels per spike{10044}. **ma:** Associated with *Xbarc12-3A* and *Xtam55-3A*{10044}.

80.3.3. Test weight

QTwt.crc-1B{10287}. 1B{10287}. **ma:** Linked to *Xgwm374.1-1B* (LOD 3.9) in RL4452/AC Domain{10287}.

QTwt.crc-1D{10287}. 1D{10287}. **ma:** Linked to *Xgdm126-1D* (LOD 5.8) in RL4452/AC Domain{10287}.

QTwt.crc-2D{10287}. 2D{10287}. **ma:** Linked to *Xgwm349-2D* - *Xbarc59-2D* (LOD 5.2) in RL4452/AC Domain{10287}.

QTwt.crc-3B{10287}. 3B{10287}. **ma:** Linked to *Xwmc625-3B* - *Xbarc164-3B* (LOD 15.4) in RL4452/AC Domain{10287}.

QTwt.crc-3D{10287}. 3D{10287}. **ma:** Linked to *Xbarc71-3D* (LOD 5.2) in RL4452/AC Domain{10287}.

QTwt.crc-5D{10287}. 5D{10287}. **ma:** Linked to *Xgdm63-5D* - *Xwmc765-5D* (LOD 5.3) in RL4452/AC Domain{10287}.

80.4. Grain weight/ear

QGwe.ocs-4A.1{0047}. 4AS{0047}. **v:** CS/CS(Kanto107 4A) mapping population{0047}. **ma:** Associated with *Xbcd1738-4A*{0047}.

QGwe.ipk-2D{0255}. 2DS{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Higher grain weight was contributed by Opata{0255}. **ma:** Associated with *Xcdo1379-2D* and *Xbcd1970-2D*{0255}.

QGwe.ipk-4A{0255}. 4AL{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Higher grain weight was contributed by Opata{0255}. **ma:** Associated with *Xmwg549-4A*, *Xabg390-4A* and *Xbcd1670-4A*{0255}.

QGwe.ipk-4A coincided with QTLs for height (*QHt.ipk-4A*), spike length (*XEl.ipk-4A*) and grain number (*QGnu.ipk-4A*) {0255}.

80.5. Grain yield

Non-glaucous (virescent) lines from a Shamrock/Shango DH population had higher yields than glaucous sibs {10543}; see Glaucousness, subsection Epistatic inhibitors of glaucousness.

QGyld.unl-3A.1{10044}. 3AS{10044}. **v:** Cheyenne/Cheyenne(Wichita 3A) RI mapping population{10044}; a higher grain yield of 32 kg/ha was contributed by Wichita and the QTL explained 6.6% of the phenotypic variation{10044}; The QTL coincided with QTLs for kernel number per square metre, 1000-kernel weight and kernels per spike{10044}.

QGyld.unl-3A.2{10044}. 3A{10044}. **v:** Cheyenne/Cheyenne (Wichita 3A) RI mapping population{10044}; a higher grain yield of 82 kg/ha was contributed by Wichita and the QTL explained 28.1% of the phenotypic variation{10044}; The QTL coincided with a QTL for kernel number per square metre{10044}. **ma:** Associated with *Xbarc67-3A* and *Xbcd366-3A*{10044}.

QYld.crc-2A{10287}. 2A{10287}. **ma:** Linked to *Xgwm339-2A* (LOD 3.0) in RL4452/AC Domain{10287}.

QYld.crc-2B{10287}. 2B{10287}. **ma:** Linked to *Xgwm257-2B* (LOD 9.4) in RL4452/AC Domain{10287}.

QYld.crc-4A{10287}. 4A{10287}. **ma:** Linked to *Xgwm130-4A* (LOD 4.4) in RL4452/AC Domain{10287}.

QYld.inra-7D{10071}. **v:** Renan/Recital{10071}. **ma:** *Xcdf69-7D* (R^2=3.7-15.7%).

QYld.ndsu-5B{10161}. [*QGy.ndsu-5B*{10161}]. **v:** LDN (DIC5B)/LCN, contributed by LDN{10161}. **ma:** Mapped to the *Xbcd1030-5B* - *Xgwm604-5B* interval{10161}.

QYld.ocs-4A.1{0047}. 4AS{0047}. **v:** CS/CS(Kanto107 4A) mapping population{0047}. **ma:** Associated with *Xbcd1738-4A*{0047}.

Grain yield under drought stress

QTL: Dharwar Dry (drought tolerant)/Sitta: SSR locus *Xwmc89-4AL* was the marker most closely associated with QTL for grain yield, grain fill rate, spike density, grains/m^2, biomass and drought susceptibility index covering a genetic distance of 7.7 cM {10488}.

80.6. Kernel number per square metre

QKpsm.unl-3A.1{10044}. 3AS{10044}. **v:** Cheyenne/Cheyenne(Wichita 3A) RI mapping population {10044}; higher kernel number (170 kernels) was contributed by Wichita and the QTL explained 14.6% of the phenotypic variation{10044}; The QTL coincided with a QTL for grain yield{10044}. **ma:** Associated with *Xbarc12-3A*{10044}.

QKpsm.unl-3A.2{10044}. 3A{10044}. **v:** Cheyenne/Cheyenne (Wichita 3A) RI mapping population {10044}. **ma:** Associated with *Xbarc67-3A*{10044}.

80.7. Spikelet number/ear

QSpn.ocs-4A.1{0047}. 4AS{0047}. **v:** CS/CS(Kanto107 4A) mapping population{0047}. **ma:** Associated with *Xbcd1738-4A*{0047}.

80.8. Spike number per plant

QSn.sdau-BL{10784}. **ma:** *Xwmc657-4B* - 4.6 cM - *QSn.sdau-4B* - 1.6 cM - *Xgwm495-4B*{10784}.

QSn.sdau-BL was resolved as a single gene in Line 05210/Laizhou 953 {10784}. It was associated with decreased spike length and grain number per spike.

80.9. Spike number per square metre

QTL: A QTL for spike number per square metre was assigned to chromosome 3A in RSLs from Cheyenne*7/Wichita 3A {0025}.

80.10. Spike length

QEl.ipk-1B{0255}. 1BL{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Longer ear was contributed by Opata{0255}. **ma:** Associated with *Xbcd388-1B* and *Xwg605-1B*{0255}.

QEl.ipk-4A{0255}. 4AL{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Longer ear was contributed by Opata{0255}. **ma:** Associated with *Xmwg549-4A*, *Xabg390-4A* and *Xbcd1670-4A*{0255}.

This QTL is likely to be a pleiotropic effect of the gene underlying the height QTL, *QHt.ipk-4A* {0255}.

QEl.ipk-5A{0255}. 5AL{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Longer ear was contributed by W-7984{0255}. **ma:** Associated with *Xmwg522-5A*{0255}.

QTL: Five QTLs for spike length were detected in Courtot/Chinese Spring{0114} but only one on chromosome arm 5AL was consistent for at least two years.

80.11. Tiller number/plant

QTn.ocs-4A.1{0047}. 4AS{0047}. **v:** CS/CS(Kanto107 4A) mapping population{0047}. **ma:** Associated with *Xpsr163-4A*{0047}.

81. Yellow Berry Tolerance

QTL : A QTL for yellow berry tolerance, contributed by RS111, was associated with *Xgwm190-5D* and *Xgwm174-5D* in a RIL population from RS111/CS {0237}. A tolerance QTL contributed by CS, the susceptible parent, was detected on 6B {0237}.

Proteins

82. Proteins

82.1. Grain protein content

Thirteen QTLs for grain protein content were identified in a RI population from the cross WL711 (low protein content)/PH132 (high grain content) {10055}. The QTLs that were identified using more than one method or in more than one environment are listed below. Also listed is a QTL that was identified in the mean over the four environments and was therefore deemed important {10055}.

Gpc-B1a. [*QGpc.ndsu-6Ba*{623}].
This allele, fixed in cultivated durum, is a non-functional frame-shift mutation {10438}. A similar non-functional allele, or a complete deletion of *Gpc-B1*, is fixed in hexaploid wheat {10438}.

Gpc-B1b{10296}. [*QGpc.ndsu-6Bb*{632,10071},*Gpc-6B1*{10299}]. 6BS. **ma:** Mapped to a 0.3 cM interval flanked by *Xucw79-6B* and *Xucw71-6B*{10229}; *Xcdo365-6B* - 1.5 cM - *Gpc-B1* - 1.2 cM - *Xucw67-6B*{10296}; A high-throughput codominant marker, *Xuhw89-6B*, was then mapped less than 0.1 cM from *Gpc-B1*{10297}.
Gpc-B1b, the functional allele {10438} in *T. dicoccoides*, affects senescence and maturity in addition to grain protein content, accelerating senescence and maturity {10298}. *Gpc-B1* is a NAC transcription factor designated *Nam-B1* {10438}. A paralogous copy of this gene is present in homologous group 2 (*Nam2*).

Pro1{777}. 5DL{777}. **s:** CS*6/Hope 5D{777}.
May be identical to *Vrn-D1*.

Pro2{777}. 5DS{777}. **s:** CS*6/Hope 5D{777}.

QGpc.ccsu-2B.1{10055}. 2BL{10055}. **v:** WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 13.4% of the phenotypic variation {10055}. **ma:** Associated with *Xgwm1249-2B*{10055}.

QGpc.ccsu-2D.1{0015.10055}. 2DL{0015, 10055}. **v:** WL711/PH132 RI mapping population {0015,10055}; higher protein content was contributed by PH132 and the QTL explained 19% {0015} and 14% {10055} of the phenotypic variation . **ma:** Associated with *Xgwm1264-2D*{10055}.

QGpc.ccsu-3D.1{10055}. 3DS{10055}. **v:** WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 16.3% of the phenotypic variation {10055}. **ma:** Associated with *Xgwm456-3D*{10055}.

QGpc.ccsu-3D.2{10055}. 3DS{10055}. **v:** WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 14% of the phenotypic variation {10055}. **ma:** Associated with *Xgwm892-3D*{10055}.

QGpc.ccsu-7A.1{10055}. 7AS{10055}. **v:** WL711/PH132 RI mapping population {10055}; higher protein content was contributed by PH132 and the QTL explained 32.4% of the phenotypic variation {10055}. **ma:** Associated with *Xgwm1171-7A*{10055}.

QGpc.ipk.7B{10628}. **v:** F26-70{10628}; Closely associated with *Ppd-B2*{10628}. **su:** Favorit(F26-70 7B){10628}.
See Response to Photoperiod.

QGpc.ndsu-5B.1{10161}. 5B{10161}. **v:** LDN (DIC5B)/LDN, contributed by DIC5B{10161}. **ma:** Nearest marker, *Xgwm604-5B*{10161}.

QGpc.ndsu-5B.2{10161}. 5B{10161}. **v:** LDN (DIC5B)/LDN, contributed by DIC5B{10161}. **ma:** Nearest marker, *Xabc310-5B*{10161}.

QGpc.ndsu-5B.3{10161}. 5B{10161}. **v:** LDN (DIC5B)/LDN, contributed by DIC5B{10161}. **ma:** Nearest marker, *Xwg909-5B*{10161}.

QGpc.ndsu-6B{623}. 6BS{623}. **tv:** Langdon{623}.

QGpc.ndsu-6Ba{623}. **tv:** Langdon{623}.

QGpc.ndsu-6Bb{623,0071}. **tv:** Langdon-*T. dicoccoides* 6B{623}. **v:** Glupro{0179}. **ma:** *QGpc.ndsu-6B* was associated (LOD score = 18.9) with the interval *Xmwg79-6B* - *Xabg387-6B*. These loci were mapped in 6BS: *Xmwg79-6B* - 5.9 cM - *Xabg387-6B* - 9.0 cM - centromere{623}; Located in the 4 cM interval flanked by *Xmwg79-6B* and *Xcdo365-6B*{0244}; Flanking microsatellite markers and PCR-specific markers for Glupro are available{0179}.

QPro.inra-2A{10071}. 2A{10071}. **v:** Renan/Recital{10071}. **ma:** *XksuD18-2A* - *Xgwm614-2A* (R^2=4.4 - 8.9%){10071}.

QPro.inra-3A{10071}. 3A{10071}. **v:** Renan/Recital{10071}. **ma:** *Xcfd79-3A* - *Xfbb250-3A* (R^2=4.1-8.3%){10071}.

QPro.inra-4D{10071}. 4D{10071}. **v:** Renan/Recital{10071}. **ma:** Linked to *Xcfd71-4D* (R^2=4.6-10.3%){10071}.

QPro.inra-7D{10071}. 7D{10071}. **v:** Renan/Recital{10071}. **ma:** *Xcfd69-7D* - *Pch1* (R^2=6.4-10.4%){10071}.

QPro.mgb-4B. Associated with *Gai1* and *Xpsr622-4B* {110}^{2}.

QPro.mgb-5A. Associated with *Xpsr911-5A* {110}^{2} and *Xcdo412-5A*{0343}*.

QPro.mgb-6A.1. Associated with *Xpsr167-6A* and *XksuG8-6A* {110}^{2}.

QPro.mgb-6A.2. Associated with *Xmgb56-6A* {110}^{2} and *Xpsr627-6A*{0343}*.

QPro.mgb-6B. Associated with *Gli-B2-6B* {110}^{2} and *Nor-2*{0343}*. **ma:** *QGpc.ndsu-6B* was associated (LOD score =18.9) with the interval *Xmwg79-6B* - *Xabg387-6B*. These loci were mapped in 6BS: *Xmwg79-6B* - 5.9 cM - *Xabg387-6B* - 9.0 cM - centromere{623}.

Qpro.mgb-7A. Associated at P<=0.01 with *Pan2*{0343}*.

QPro.mgb-7B. Associated with *Xpsr490(Ss1)-7B*, *Pc* {110}^{2} and *Xutv913-7B*{0343}*.

QTLs for grain protein content were detected on chromosome arms 6AS (associated AFLP marker, *XE38M60*$_{200}$) and 1BL (associated RFLP marker, *Xcdo1188-1B*) in Courtot/Chinese Spring {0141}.
Nine QTLs (51% of the variation) were mapped in cross 'Forno'/ 'Oberkulmer' spelt {0280}.
A QTL for grain and flour protein content, contributed by CS, was associated with *XTri-1D*/Centromere in a RSL population from the cross Cheyenne (high quality wheat)/CS (low quality wheat) {0251}.
For QTLs conferring grain protein content detected in the cross Renan/Recital {10071}, only QTLs stable over at least 4 of 6 locations are presented. Renen contributed the four alleles for high grain protein content.

Ning 7840/Clark: RILs: QTLs from Ning 7840 were detected on chromosomes 3AS (*Xwmc749-3AS* - *Xgwm369-3AS*; R^2=0.09-0.11) and 4B (*Xgwm368-4B* - *Xwmc617-4B*, R^2=0.08-0.11) {10702}.
Durum: In 3BIL-85 (high protein introgressed from *T. dicoccoides*/Latino QTL were detected in chromosomes 2AS (associated with *Xcfa2164-2A*, R^2=17%), 6AS (*Xp39M37*$_{250}$*-6A*, R^2=17%) and 7BL (*Xgwm577-7B*, R^2=9%) {10338}.

82.2. Enzymes

82.2.1. Acid phosphatase

Acph-A1{504}. [*Acph2*{516},*Acph3*{516},*Acph-B1*{936}]. 4AS{504,516}. **v:** CS.

Acph-B1{504}. [*Acph4*{516},*Acph8*{516},*Acph-A1*{936}]. 4BL{504,516}. **v:** CS.

Acph-D1. [*Acph5*{516},*Acph6*{516}]. 4DL{504,516}. **v:** CS.

Acph-H1{1153}. 4H{1153}. **ad:** CS/Betzes.

Acph-M^{v}1{237}. [*Aph-v*{237},*Acph-M^{v}1*{985}]. 4M^v{237}. **tr:** H-93-33{984}.

Acph-R1. 7R{1457}.7RS{506}. **ad:** CS/Imperial.

Acid phosphatase gene loci were reported for 7RL in *S. cereale* {1251}, chromosomes L1 (= 7Ag^i) and L4 (= 4Ag^i) of *Thin. intermedium* {361}, and chromosome E of *Ae. umbellulata* {69}. Two loci on 7R were separated by 25 +or- 5.2cM {1534}.Wehling {1559} identified four acid phosphatase loci in *S. cereale*, three of which were located in 7R.

Acph-S^{s}1{1140}. 4S^s{1140}. **ad:** CS/*T. searsii.*

Acph-D2{10309,10407}. [*Acph1*{10309}]. 2DL{10309}. **dv:** *Acph-D2*$_{100}$ and *Acph-D2*$_{95}$ alleles distinguished accessions of *Ae. tauschii* ssp. *tauschii* and *strangulata*, respectively{10309}. **tv:** *Ae. tauschii*{10407}. **ma:** Cent ... *Acph-D2* - 4 cM - *Xgwm157-2D*{10309}.

82.2.2. Alcohol dehydrogenase (Aliphatic)

Adh-A1{502}. [*Adh*$_B${502},*Adh-B1*{504}]. 4A{502}.4AL{504,516}. **v:** CS.

Adh-B1{501,502}. [*Adh*$_1${501},*Adh*$_A${502},*Adh-A1*{504}]. 4B{502}.4BS{504,516}. **v:** CS.

Adh-B1a{1442}. [*Adh*$_{11}${501},*Adh-A1a*{1442}]. **v:** CS. **tv:** PI 226951{501}; Malavika{1442}.

Adh-B1b{1442}. [*Adh*$_{12}${501},*Adh-A1b*{1442}]. **v:** Rageni derivative{1443}. **tv:** CI 4013{501}; Bijaga Yellow{1442}.

Adh-B1b was the only variant *Adh-1* allele detected in study of a large number of *T. aestivum* and *T. turgidum* accessions {503}.

Adh-C1{1278}. [*G*{1278}]. **ad:** *T. aestivum* cv. Alcedo / *Ae. caudata* line G.

Adh-D1{504}. [*Adh*$_D${502}]. 4D{502}.4DS{504,516}. **v:** CS. **ma:** *Adh-D1* [*Adh1*, *Adh2*] was mapped 4 cM distal to *Xpsr163-4D* and closely proximal to *Xcsiha114-4D.1* [*XcsIHA114-1a*']{757}.

Adh-Ag^{i}1{560},{374}. [*Adh-X1*{361}]. 4Ag^i{560}. **ad:** Vilmorin 27/*Th. intermedium*; Caribo/*Th. intermedium.*

Adh-E1{518}. 4ES{518}. **ad:** CS/*E. elongata.*

Adh-H1{520}. 4H{520}. **ad:** CS/Betzes.

Adh-M^{v}1{984}. [*ADHmu*{984},*Adh-M^{v}1*{985}]. 4M^v{984}. **v:** H-93-33.

Adh-R1{1457}. [*AdhR2*{582}]. 4R{582,1457}.4RS{506}. **ad:** CS/Imperial{1457,506}; FEC28/Petkus{043}; Holdfast/King II{582}.

Adh-V1{1026,242}. 4V{1026}. **ad:** CS/*D. villosum.*

Three *Adh* genes were identified in *Hordeum vulgare* and *H. spontaneum* {144,490,493,520}. Two of these were tightly linked at the *Adh-H1* locus {144}. The third gene was tentatively located in 5H {490}.

A low-level of aliphatic alcohol dehydrogenase activity is commonly observed on zymograms in the absence of added substrate {513}; this may account for the observation of wheat lactate dehydrogenase that was reported in {1465}.

The gene series formerly designated *Adh-2* and *Adh-3* appear under Aromatic Alcohol Dehydrogenase

82.2.3. Aminopeptidase

Amp-A1{504}. 6AS{504,516}. **v:** CS.

Amp-A1a. **v:** CS{1533}.

Amp-A1b. **v:** Vitka{1533}.

Amp-B1{504}. 6BS{504,516}. **v:** CS.

Amp-B1a. **v:** CS{1533}.

Amp-B1b. **v:** Iskra{1533}.

Amp-B1c{703,1244}. Null allele **v:** *T. spelta* IPSR 1220017{703}; Sinvalocho M.A{1244}.

Amp-C1{1278}. 6D{1278}. **ad:** Alcedo/*Ae. caudata* line D.
Amp-D1{504}. 6DS{504,516}. **v:** CS.
  Amp-D1a{703}. **v:** CS.
  Amp-D1b{703}. **v:** Sears' Synthetic IPSR1190903.
Amp-Ag^{e}1{1575}. 6Ag^{e}{1575}. **ad,su:** Rescue/*Th. elongatum*.
Amp-Ag^{i}1{703}. 6Ag^{i}{703}. **ad:** Vilmorin 27/*Th. intermedium*.
Amp-E1{518}. 6E{518}. **ad:** CS/*E. elongata*.
Amp-H1{520}. 6H{520}. **ad:** CS/Betzes.
Amp-R1{1457}. 6R{1457,1280}. **ad:** CS/Imperial{1457}; Holdfast/King II{1280}.
Amp-A2{703}. 4AL{703}. **v:** CS.
  Amp-A2a{703}. **v:** CS.
  Amp-A2b{703}. **v:** *T. spelta* IPSR 1220017.
Amp-B2{703}. 4BS{703}. **v:** CS.
  Amp-B2a{703}. **v:** CS.
  Amp-B2b{703}. **v:** Timstein.
  Amp-B2c{703}. **v:** Hope.
Amp-D2{703}. 4DS{703}. **v:** CS.
  Amp-D2a{703}. **v:** CS.
  Amp-D2b{703}. **v:** Sears' Synthetic IPSR 1190903.
  Amp-D2c{703}. **v:** Bersee.
Amp-Ag^{i}2{703}. 4Ag^{i}{703}. **ad:** Vilmorin27/*Th. intermedium*.
Amp-E2{703}. 4E{703}. **ad:** CS/*E. elongata*.
Amp-H2{703}. 4H{703}. **ad:** CS/Betzes.
Amp-H^{ch}2{703}. 4H^{ch}{703}. **ad:** CS/*H. chilense*.
Amp-J2{703}. 4J{703}. **ad:** CS/*Th.junceum*.
Amp-M^{v}2{235}. 4M^{v}{235}. **su:** H-93-33{235}.
Amp-R2{703}. 4R{703}.4RS{702,093}. **ad:** CS/Imperial.
Amp-S^{l}2{703}. 4S^{l}L{703}. **ad:** CS/*Ae. sharonensis*{180}. **tr:** 4DS.4DL-4S^{l}L{660}.
Amp-V2{703}. 4V{703}. **ad:** CS/*D. villosum*.
Amp-A3{703}. 7AS{703}. **v:** CS.
  Amp-A3a{703}. **v:** CS.
  Amp-A3b{703}. **v:** Timstein.
Amp-H3{703}. 7H{703}. **ad:** CS/Betzes.

82.2.4. Alpha-amylase

a-Amy-A1{007}. [*Amy6*$_{A}${1082}]. 6AL{412,1082}. **v:** CS.
  a-Amy-A1a{007}. [*Amy 6A1*{1084}]. **v:** CS.
  a-Amy-A1b^{5}{007}. **v:** Bezostaya 1; Kavkaz.
  a-Amy-A1c^{5}. [*Amy 6A1^{m}*{1084}]. **v:** Aka.
a-Amy-B1{007}. [*Amy6B*{1082}]. 6BL{412,1082}. **v:** CS.
  a-Amy-B1a{007}. [*Amy 4*{1084},*Amy 6B1*{1084},*Amy 6B2^{o}*{1084}]. **v:** CS{007}; Rare.
  a-Amy-B1b{007}. [*Amy 4^{m}*{1084},*Amy 6B1^{o}*{1084},*Amy 6B2*{1084}]. **v:** Mara{007}.
  a-Amy-B1c{007}. [*Amy 4*{1084},*Amy 6B1*{1084},*Amy 6B2*{1084}]. **v:** Sava{007}; Rare.
  a-Amy-B1d{007}. [*Amy 4^{m}*{1084},*Amy 6B1^{o}*{1084},*Amy6B2^{o}*{1084}]. **v:** Sicco{007}; Rare.
  a-Amy-B1e{007}. [*Amy 4^{m}*{1084},*Amy 6B1$^{4'}$*{1084},*Amy 6B2^{o}*{1084}]. **v:** Cappelle-Desprez{007}.
  a-Amy-B1f {007}. [*Amy4^{m}*{1084},*Amy 6B1^{4}*{1084},*Amy 6B2^{o}*{1084}]. **v:** Sappo{007}.
  a-Amy-B1g{007}. [*Amy 4*{1084},*Amy 6B1^{4}*{1084},*Amy 6B2^{o}*{1084}]. **v:** Cheyenne{007}.
  a-Amy-B1h{007}. [*Amy 4*{1084},*Amy 6B1^{o}*{1084},*Amy 6B2^{o}*{1084}]. **v:** *T. macha* Line 1{007}; Rare.

Two types of nomenclature were assigned to the genes encoding the a-AMY-1 isozymes. In one, allelic states were defined for individual isozymes {1084} whereas in the other, several isozymes were considered to be the products of compound loci {007,412}. This listing shows the 'alleles' described in {1084} which are assumed in {007} to be synonymous with the a-*Amy-B1a* through *a-Amy-B1h* nomenclature. Amy 4 and Amy 4^1 are unmapped alternatives {1084} which appear to be identical to zymogram bands [bands 9 and 9b {007}] forming part of the *a-Amy-B1*phenotype. *Amy 6B1* [with forms *Amy 6B1*^{o}, and *Amy 6B1*$^{4'}$, considered to be mutually exclusive {1084}] and *Amy 6B2* [with forms *Amy 62* and *Amy 6B2*^{o} {1084}] describe further aspects of *a-Amy-B1* {007}. See *a-Amy1* below for further consideration of *Amy 6B2* {1084}.

a-Amy-D1{007}. [*Amy6D*{1082}]. 6DL{412,1082}. **v:** CS.

a-Amy-D1a{007}. [*Amy6D1*{1084},*Amy 6D2*{1084}]. **v:** CS.

a-Amy-D1b{007}. [*Amy6D1*{1084},*Amy 6D2*{1084}]. **v:** Prelude{1082}; Capelle-Desprez{007}.

a-Amy-D1c. [*Amy6D1*^{m}{1084},*Amy 6D2*{1084}]. **v:** *T. spelta* var. *duhamelianum*.

a-Amy-Ag^i***1***{374}. 6Ag^i{374}. **ad:** Vilmorin 27/*Th. intermedium*.

a-Amy-E1{013}. 6E{013}. **ad:** CS/*E. elongata*.

a-Amy-H1. [*a-Amy1*{146}]. 6H{146,1051}. **ad:** CS/Betzes.

a-Amy-R1{013}. 6RL{013}. **su,ad:** CS/Imperial; CS/King II; Holdfast/King II.

a-Amy-R^m***1***{013}. 6R^{m}L{013}. **ad:** CS/*S. montanum*.

a-Amy-S1{598}. 6SS{598}. **v:** Wembley derivative 31. **al:** *Ae. speltoides*.

It was estimated {902} that there are two *a-Amy-1* genes in 6A and five or six in both 6B and 6D, and three or four *a-Amy-2* genes at each of the 7A, 7B, and 7D loci.

a-Amy-A2{007}. [*Amy*$_{7A}${1082}]. 7AL{412,1082}. **v:** CS.

a-Amy-B2{007}. [*Amy*$_{7B}${1082}]. 7BL{412,1082}. **v:** CS.

a-Amy-B2a{412}. [*Amy 7B1*{1084},*Amy 7B2*{1084}]. **v:** CS.

a-Amy-B2b{412}. [*Amy 7B1*{1084},*Amy 7B2*^{m}{1084}]. **v:** Hope.

The alternative states of *Amy 7B2*, namely, *Amy 7B2* and *Amy 7B2*^{m} {1084}, are identical to the variation in band 2 {412}. The complete description of the *a-Amy-B2* variation also includes variation in band 11 {412}.

a-Amy-D2. [*Amy*$_{7D}${1082}]. 7DL{412,1082}. **v:** CS.

a-Amy-D2a{412}. [*Amy 7D1*{1084}]. **v:** CS.

a-Amy-D2b{417}. [*Amy 7D1*^{o}{1084}]. **v:** Largo{007}; Sears' Synthetic{007}; VPM1{417}.

a-Amy-Ag^i***2***{374}. 7Ag^i{374}. **ad:** Vilmorin 27/*Th. intermedium*.

a-Amy-E2{013}. 7EL{013}. **ad:** CS/*E. elongata*.

a-Amy-H2. [*a-Amy2*{146}]. 7HL{146,1051,793}. **ad:** CS/Betzes.

a-Amy-H^{ch}***2***{1015}. 7H^{ch}beta{1015}. **su,ad:** CS/*H. chilense*.

a-Amy-R2{013}. 7RL{013}. **su,ad:** CS/Imperial; CS/King II; Holdfast/King II.

a-Amy-S^b***2***{013}. 7S^b{013}. **ad:** Holdfast/*Ae. bicornis*.

a-Amy-U2{013}. 7U{013}. **ad:** CS/*Ae. umbellulata*.

Three other *a-Amy* loci, namely, *Amy 6B2, Amy 6D2, and Amy 7B2*, were reported {1084}. No variation was observed for the products of *Amy 6D2 and Amy 7B2*, although nullisomic analysis located the genes in 6DL and 7B, respectively. In accordance with the Guidelines, these genes are assumed to be part of the *a-Amy-D1* and *a-Amy-B2* loci, respectively. *Amy 6B2* was observed to produce alternative phenotypes {1084}. In a test of the segregation of these phenotypes relative to two alternative products of *Amy 6B1*, the two loci were found to be linked with a recombination frequency of 20.6% {1084}. However, an attempt to confirm the presence of more than one *a-Amy* locus in 6BL was unsuccessful {007}.

a-Amy1{1084,1083}. [*Amy 6B2*{1084},*Amy-B2*{1083}]. 6BL{1084,1083}. **v:** CS.

a-Amy1a{1083}. [*a-Amy-B1a*]. **v:** CS.

a-Amy1b{1083}. [*a-Amy-B1b*]. **v:** CS.

a-Amy1c{1083}. [*a-Amy-B4*]. **tv:** *T. durum* ssp. *georgicum*.

The presence of *a-Amy1* reported in {1084} was confirmed by segregational tests in a CS/Jones Fife population and in a population derived from a tetraploid cross {1083}. The recombinations with *a-AmyB1* were 9.3% and 22.3%, respectively.

A further set of a-amylase genes, *Xa-Amy-5* [*a-Amy3*], was identified in 5A, 5B and 5D by cross-hybridization with a-AMY-1 and a-AMY-2 probes {080}. Only one gene copy appears to be present at each locus. In rye, evidence was obtained for three *a-Amy-1* genes, two or three *a-Amy-2* genes and three *a-Amy-3* genes {907}.

Synthesis of a-amylase isozymes controlled by *a-Amy-1* genes on chromosomes 6A and 6D is reduced in DT6BS compared to euploid CS. This result suggests the presence of a gene(s) on the long arm of chromosome 6B, which is (are) required for GA-induced alpha-amylase synthesis in the aleurone {0072}.

82.2.5. Beta-amylase

b-Amy-A1{008,227}. [*b-Amy-A2*{008},*b-Amy-B1*{1331}]. 5AL{008,227}. **v:** CS{008}. **s:** CS/Federation{227}.

b-Amy-A1a{008}. [*b-Amy-A2a*{008},*b-B1a*{936}]. **v:** CS.

b-Amy-A1b{008}. [*b-Amy-A2b*{008},*b-B1b*{936}]. **v:** Koga II..

b-Amy-A1c{008}. [*b-Amy-A2c*{008},*b-B1c*{936}]. **v:** *T. macha* IPSR 1240005.

b-Amy-A1d{008}. [*b-Amy-A2d*{008},*b-B1d*{936}]. **v:** Holdfast.

b-Amy-A1e{008}. [*b-Amy-A2e*{008},*b-B1e*{936}]. **v:** Bezostaya I.

b-Amy-B1{628}. [*b-Amy-A1*{008}]. 4BL{008,628}. **v:** CS.

b-Amy-B1a{1330}. [*b-Amy-A1a*{008,1330}]. **v:** CS.

b-Amy-B1b{1330}. [*b-Amy-A1b*{008,1330}]. **v:** Sears' Synthetic IPSR 1190903.

b-Amy-B1c{1330}. [*b-Amy-A1b*{008},*b-Amy-A1c*{1330}]. **v:** Ciano 67.

b-Amy-B1d{1330}. [*b-Amy-A1c*{1330,400}]. **v:** Manella.

b-Amy-C1{1278}. B{1278}. **ad:** *Aestivum* cv. Alcedo /*Ae. caudata* line B.

b-Amy-D1{008}. 4DL{008,628}. **v:** CS.

b-Amy-D1a{008}. **v:** CS.

b-Amy-D1b{008}. **v:** Bersee.

b-Amy-D1c{008}. **v:** Sears' Synthetic. Rare.

Previously listed alleles *b-Amy-D1d* and *-D1e* were found to be *b-Amy-B1* alleles {400}. Two *b-Amy-D*^{t}*1* alleles were predominant in 60 accessions of *T. tauschii* {1578}.

b-Amy-Ag*^{i}*1{168,013}. 4Ag^{i}{168}. **ad:** Vilmorin27/*Th. intermedium*.

b-Amy-E*^{b}*1{661}. 5E^{b}L{661}. **tr:** 5AS.5E^{b}L.

b-Amy-H1. 4H{1153}. **ad:** CS/Betzes.

b-Amy-H*^{ch}*1{013}. 4H^{ch}{013}. **ad:** CS/*H. chilense*.

b-Amy-R1. [*b-Amy-R2*{013},*b-AmyR1*{043}]. 5R{103,1280}.5RL{043}. **ad:** FEC 28/Petkus{043,82}; Holdfast/King II{043,1280}. **tr:** CS/Imperial 5BL-5RL{043}.

b-Amy-S*^{l}*1{013}. 4S^{l}{013}.D{013}. **ad:** CS/*Ae. sharonensis* D{013}. **su:** CS/*Ae. sharonensis*. **ad:** CS/*Ae. longissima*.

b-Amy-U1{013}. [*b-Amy-U2*{013}]. 5U{013}. **su:** CS/*Ae. umbellulata*.

A second set of loci with homology to *b-Amy-1* genes was identified in 2AS, 2BS and 2DS and designated the *Xb-Amy-2* [*b-Amy-2* {1331}] set. Evidence for these genes derives from cross-hybridization with a b-AMY-H1 cDNA probe {1331}. Further members of the same set were identified in 2H {732}, and 2R and 2U {1331}.

Sixty *Ae. tauschii* lines revealed two *b-Amy-D*^{t}*1* alleles {1578}.

82.2.6. Endopeptidase

Ep-A1{516}. 7AL{516}. **v:** CS.

Ep-A1a{516,708}. **v:** CS.

An EP isozyme encoded by *Ep-A1a* of CS is visible on zymograms following starch gel electrophoresis {516}. The product of this allele is not observable, however, on zymograms following isoelectric focusing {708}.

Ep-A1b{708}. **v:** Cappelle-Desprez{708}; Hobbit{704}; Rendezvous{1603}.

Ep-A1c{708}. **v:** Sears' Synthetic.

Ep-A1d{894}. Isozyme 6. **v:** PI 294994{894}.

Ep-B1{516}. [*Ep1*{516}]. 7BL{516}. **v:** CS.

Ep-B1a{708}. **v:** CS.

Ep-B1b{708}. **v:** Cappelle-Desprez.

Ep-B1c{708}. **v:** Ciano 67.

Ep-B1d{708}. **v:** Bersee.

Ep-B1e{708}. **v:** Sears' Synthetic.

Ep-D1{516}. 7DL{516}. **v:** CS.

Ep-D1a{708}. **v:** CS.

Ep-D1b. [*EP-V1*{973}]. **v:** 5L 219{1521}; H-93-70{1521}; Hyak{021}; Madsen{020}; Rendezvous{708}; VPM1{973}.

Assuming that *Ep-D1* encoded an oligopeptidase G, comparative genetics were applied to develop a STS marker for identifying resistance gene *Pch1* {10513} (see Reaction to *Tapesia yallundae*.

Ep-D1c{708}. **v:** Sears' Synthetic.

Ep-D1d{1587}. Null allele. **v:** Wheats with *Lr19*{1587}.

Ep-D1e{894}. Isozyme 5. **v:** PI 294994{894}.

Ep-E1{518}. 7EL{518}. **al:** CS/*E. elongata*.

Ep-H1{520}. 7HL{520}. **al:** CS/Betzes.

Ep-H^{ch}1{708}. 7H^{ch}{708}. **su:** CS/*H. chilense*.

Ep-H^{t}1{1037}. 7H^{t}S{1037}. **ad:** CS/*E. trachycaulus*.

Ep-M^{v}1{985}. [*Ep-M^{v}1*{985}]. 7M^{v}L. **su:** 7M^{v}{7D}.

Ep-R1{092,266,708}. 6RL{092}. **ad:** CS/Imperial.

Ep-S^{b}1{708}. 7S^{b}{708}. **su:** Holdfast/*Ae. bicornis*.

Ep-S^{l}1{517}. 4S^{l}{517}. **ad:** CS/*Ae. longissima*.

Ep-S^{s}1{1140}. 7S^{s}{1140}. **ad:** CS/*T. searsii*.

Ep-U1{708}. 7U{708}. **su:** CS/*Ae. umbellulata*.

Ep-V1{708}. 7V{708}. **ad:** CS/*D. villosum*.

Ep-B2{599}. 6BS{599}.

An *Ep* locus was located in 4RS in King II {1280}, using Holdfast/King II addition lines and in 4R in Imperial {266} using Chinese Spring/Imperial addition lines.

82.2.7. Esterase

Genetic control of esterases [carboxylic ester hydrolases (E.C.3.1.1.1)] was the subject of a comparative study {814}.

82.2.7.1. EST-1

EST-1 is a dimeric enzyme that electrofocuses around pH4.0 and is expressed in all tissues except endosperm {814}.

Est-A1. [*Est*$_{A}${061}]. 3AS{060}. **v:** CS.

Est-B1. [*Est*$_{B}${061}]. 3B{060}.3BS{100}. **v:** CS.

Est-D1. [*Est*$_{D}${061}]. 3D{060}.3DS{100}. **v:** CS.

Est-E1{518}. 3ES{518}. **ad:** CS/*E. elongata*.

Est-H1{814}. 3H{814}. **ad:** CS/Betzes.

Est-R1. [*Est*$_R${061}]. 3R{060,1254}. **ad:** CS/Imperial{060}; Holdfast/King II{100}; Kharkov/Dakold{100}.

Est-S^{1}1{814}. 3S^1{814}. **ad:** CS/*Ae. longissima*.

Each of 208 hexaploid accessions carried the same *Est-1* alleles except accessions of *T. compactum* var. *rubriceps*, each of which carried an *Est-B1* or *Est-D1* electrophoretic mobility variant {585}.

82.2.7.2. EST-2

EST-2 is a coleoptile-specific monomeric enzyme that electrofocuses at low pI.

Est-A2. [*Est-2*$_A${585}]. 3A{585}. **v:** CS.

Est-B2. [*Est-2*$_B${585}]. 3BL{585}. **v:** CS.

Est-D2. [*Est-2*$_D${585}]. 3DL{585}. **v:** CS.

Among 208 hexaploid accessions, an apparent *Est-B2* null allele occurred frequently in accessions of *T. macha* and *T. sphaerococcum* and occasionally in accessions of *T. compactum*. The allele was not observed in *T. aestivum* and *T. spelta* accessions {585}.

82.2.7.3. EST-3

EST-3 is a monomeric enzyme that is expressed in young seedlings (this enzyme was not observed in {814}.

Est-B3. [*Est-3*$_B${585}]. 7BS{585}. **v:** CS.

Est-D3. [*Est-3*$_D${585}]. 7DS{585}. **v:** CS.

Est-H3{520}. 7H{520}. **ad:** CS/Betzes.

One accession carrying an apparent *Est-B3* null allele and one carrying an apparent *Est-D3* null allele were found among 208 hexaploid accessions {585}.

A 7AS locus encodes three esterase isozymes in immature grains {009}.

82.2.7.4. EST-4

EST-4 is a monomeric, leaf-specific enzyme that electrofocuses around pH 4.5.

Est-A4. [*Est-4*$_A${585}]. 6AL{585,919}. **v:** CS.

Est-B4. [*Est-4*$_B${585}]. 6BL{585,919}. **v:** CS.

Est-D4. [*Est-4*$_D${585}]. 6DL{585,919}. **v:** CS.

Probable *Est-A4* and *Est-D4* null alleles were detected in several accessions of *T. compactum* var. *rubriceps* {585}; otherwise, no *Est-4* variant occurred among 208 hexaploid accessions {585}.

An esterase gene was located in chromosome L7 (= 6Ag^i) of *Th. intermedium* {361}.

82.2.7.5. EST-5

EST-5 consists of 20 or more monomeric, grain-specific isozymes that electrofocus between pH 5.6 and 7.0.

Est-A5{009}. 3AL{009}. **v:** CS.

  Est-A5a{009}. **v:** CS.

  Est-A5b{009}. **v:** Kalyansona{009}; *T. compactum* AUS12084{756}.

Est-B5{009}. 3BL{009}. **v:** CS.

  Est-B5a{009}. **v:** CS.

  Est-B5b{009}. **v:** Big Club.

  Est-B5c{009}. **v:** Timstein.

  Est-B5d{009}. **v:** Sears' Synthetic.

Est-D5{009}. 3DL{009}. **v:** CS.

Est-D5a{009}. **v:** CS.

Est-D5b{009}. **v:** *T. macha*.

Est-D5c{009}. **v:** Hobbit 'S'.

Est-D5d{009}. **v:** *T. macha* Line 1.

Est-D5e{756}. **v:** *T. macha* WJR 38548.

Encoding of the endosperm esterases of hexaploid wheat by 12-15 genes in five compound loci located in 3AL, 3BL, 3DL, 3AS and 3DS was postulated in {1204}. Three and six alleles at *Est-D*^{t}*5* (in *Ae. tauschii*) were reported in {756} and {1578}, respectively.

In *S. cereale*, in addition to *Est-R1*, genes encoding leaf esterases were located in three chromosomes {1561}. These included a gene designated *Est8* in 6R in cvs. Imperial and King II, a gene designated *Est2* and two genes, designated *Est6* and *Est7*, which are part of a separate compound locus {1560}, in 5RL in Imperial, and a gene designaged *Est10* in 4R of King II and 4RL of Imperial. In *Hordeum vulgare*, genes encoding leaf esterases were located in 3H {1071; see also, 520,580} and 7H {520}.

Est-Ag^{i}***5***{374}. 3Ag^{i}{374}. **ad:** Vilmorin 27/*Th. intermedium*.

Est-H5{010}. 3H{010}. **ad:** CS/Betzes.

Est-H^{ch}***5***{010}. 3H^{ch}{010}. **ad:** CS/*H. chilense*.

Est-R5{010}. [*EstA*{737}]. 6R{043,1280}. **ad:** CS/Imperial{010,043}; Kharkov/ Dakold 6RL{010,1280}; CS/King II{010}; Holdfast/King II{043,1280}.

A second *S. cereale* gene encoding grain esterases, designated *EstB*, was located in 4RL in King II and Petkus and in 7RS in Imperial {737}.

Est-R^{m}***5***{010}. [*EstB*{737}]. 6R^{m}{010}.6R^{m}L{737}. **ad:** CS/*S. montanum*.

Est-S^{b}***5***{010}. 3S^{b}{010}. **su,ad:** CS/*Ae. bicornis*.

Est-S^{l}***5***{010}. 3S^{l}{010}. **ad:** CS/*Ae. longissima*.

Sixty *Ae. tauschii* lines revealed six *Est-D*^{t}*5* alleles {1578}.

82.2.7.6. EST-6

EST-6 is a dimeric enzyme that electrofocuses around pH 7.6 and is specific to endosperm.

Est-A6{1130}. 2AS{1130}. **v:** CS.

Est-A6a{1130}. **v:** CS.

Est-A6b{1130}. **v:** Ceska Previvka.

Est-B6{1130}. 2BS{1130}. **v:** CS.

Est-B6a{1130}. **v:** CS.

Est-B6b{1130}. **v:** Hope.

Est-D6{1130}. 2DS{1130}. **v:** CS.

Est-D6a{1130}. **v:** CS.

Est-D6b{1130}. **v:** Sears' Synthetic IPSR 1190903.

Est-M6{1130}. 2MS{1130}. **su:** CS/*Ae. comosa*.

Est-R6{370}. 2RS{370}. **al:** DS2 x RxL10 rye popn.

A group of leaf esterase isozymes controlled by the long arms of the homoeologous group 3 chromosomes were reported {919}. The relationship of these esterases to EST-2 and to the leaf esterase designed EST-6 reported in {629} has not been determined.

82.2.7.7. EST-7

EST-7 is a monomeric enzyme that electrofocuses in the same region as EST-6 but is specific to green tissues.

Est-A7{812}. 2AL{812}. **v:** CS.

Est-B7{812}. 2BL{812}. **v:** CS.

Est-D7{812}. 2DL{812}. **v:** CS.

Est-D7a{812}. **v:** CS.

Est-D7b{812}. **v:** Synthetic {IPSR 1190903}.

Est-E7{812}. 2E{812}. **ad:** CS/*E. elongata*.

Est-H7{812}. 2HL{812}. **ad:** CS/Betzes.

Est-R7{812}. 2RL{812}. **ad:** CS/Imperial. **su:** Holdfast/KingII.

Est-R^{m}7{812}. 2R^{m}alpha{812}. **ad:** CS/*S. montanum*.

Est-U7{812}. 2U{812}. **ad:** CS/*Ae. umbellulata*.

Est-V7{812}. 2V{812}. **ad:** CS/*D. villosum*.

82.2.7.8. EST-8

EST-8 consists of about 10 isozymes that electrofocus between pH 4.5 and 6.5 and are expressed only in vegetative tissues. EST-8 is likely to be the enzyme previously described in {919} and {629}.

Est-A8{629,814}. [*Est-A6*{629}]. 3AL{629}. **v:** CS.

Est-B8{613,814}. [*Est-B6*{629}]. 3BL{629}. **v:** CS.

Est-D8{629,814}. [*Est-D6*{629}]. 3DL{629}. **v:** CS.

Est-R8{613,814}. 6RL{629}. **ad:** CS/Imperial, CS/King II.

82.2.7.9. EST-9

EST-9 is a monomeric enzyme that electrofocuses around pH 5.0 and is expressed only in embryos.

Est-A9{814}. 3AS{814}. **v:** CS.

Est-B9{814}. 3BS{814}. **v:** CS.

Est-D9{814}. 3DS{814}. **v:** CS.

EST-2, EST-5 and EST-8 are controlled by genes on 3L and where a recombination test was possible between *Est-D5* and *Est-D8*, no segregation was observed. The different gene symbols were retained because of the different tissue specificities and polymerisation profiles of the enzymes. The same arguments surround the EST-1 and EST-6 genes located in the 3S arms {814}.

The *Est-6* gene of rye was mapped {249}. The *Est-6* genes of wheat were mapped comparatively in the proximal regions of chromosomes 2S {256}. The *Est-2, Est-5 and Est-8* were mapped to the extreme distal regions in the 3L arms {247}.

82.2.8. Glucosephosphate isomerase

Gpi-A1{507}. 1AS{195,507}. **v:** CS.

Gpi-B1{507}. 1BS{195,507}. **v:** CS.

Gpi-D1{507}. 1DS{195,507}. **v:** CS.

Gpi-D1a{195}. **v:** CS.

Gpi-D1b{195}. **v:** CS variant and certain CS aneuploids. Rare.

Varietal differences in GPI zymograms were noted in {1127}.

GPI zymogram phenotypes observed in *Triticum* and *Aegilops* species are reported in {456,457}.

No allelic variation at *Gpi-D^{t}1* was found in 60 accessions of *Ae. tauschii* {1578}.

Gpi-Ag^{i}1{361},{374}. [*Gpi-X1*{361}]. 1Ag^{i}{361}. **ad:** Vilmorin 27/*Th. intermedium*..

Gpi-E1{518}. 1ES{518}. **ad:** CS/*E. elongata*.

Gpi-H1{1153}. 1HS{1153}. **ad:** CS/Betzes.

Gpi-H^{ch}1{195}. 1H^{ch}{195}. **ad:** CS/*H. chilense*.

Gpi-R1{195}. 1R{195}.1RS{779}. **ad:** CS/King II{195}. **al:** 2a, 2b, and R14{779}.

Gpi-R^{m}***1***{195}. 1R{195}. **ad:** CS/*S. montanum.*
Gpi-S^{l}***1***{1228}. 1S^{1}{517}.1S^{1}S{1228}. **ma:** In *Ae. longissima 2 x Ae. longissima 10, Gpi-S*^{l}*1*, two glutenin loci, and three gliadin loci were mapped relative to one another as follows: *Glu-S*^{l}*1* - 15.9 cM - *Gpi-S*^{l}*1* - 38 cM - *Gli-S*^{l}*4* - 7.1 cM - *Glu-S*^{l}*3* - 0.9 cM - *Gli-S*^{l}*1* - 5.6 cM - *Gli-S*^{l}*5*{1228}; *Glu-S*^{l}*1* is located in 1S^{l}L and the other loci are in 1S^{l}S.
Gpi-S^{s}***1***{1140}. 1S^{s}{1140}. **ad:** CS/*Ae. searsii.*
Gpi-U1{195}. 1U{195}. **ad:** CS/*Ae. umbellulata.*
Gpi-V1{1026}. 1V{1026,241}. **ad:** CS/*D. villosum.*

82.2.9. Glutamic oxaloacetic transaminase

Got-A1{505}. 6AS{505}. **v:** CS.
Got-B1{505}. 6BS{505}. **v:** CS.
Got-D1{505}. 6DS{505}. **v:** CS.
Got-A2{505}. 6AL{505}. **v:** CS.
Got-B2{505}. 6BL{505}. **v:** CS.
Got-D2{505}. 6DL{505}. **v:** CS. **ma:** Cent - *Got-D2* - 2 cM - *Xpsr154-6D*{757}.
Got-Ag^{e}***2***{1575}. 6Ag^{e}{1575}. **ad,su:** Rescue/*Th. elongatum.*
Got-E2{518}. 6EBeta{518}. **ad:** CS/*E. elongata.*
Got-H2{520}. 6H{520}. **ad:** CS/Betzes.
Got-R2{1457}. [*Got3*{1559}]. 6R{1457}.6RL{1280}. **ad:** CS/Imperial 6R{1457}; Holdfast/King II 6RL{1280}.
Got-V2{1026,242}. 6V{1026}. **ad:** Creso/*D. villosum.*
Got-H^{t}***2***{1037}. 6H^{t}{1037}. **ad:** CS/*E. trachycaulus.*
Got-A3{505}. 3AL{505}. **v:** CS.
Got-B3{505}. 3BL{505}. **v:** CS.
Got-C3{1278}. F{1278}. **ad:** *T. aestivum* cv. Alcedo /*Ae. caudata* line C.
Got-D3{505}. 3DL{505}. **v:** CS.
Got-Ag^{e}***3***{521}. 3Ag^{e}L{521}. **ad:** CS/TAP 67. **su:** CS/TAP 67. **tr:** Certain CS 3D/Ag lines.
Got-E3{518}. 3EL{518}. **ad:** CS/*E. elongata.*
Got-H3. [*Got-b3*{090}]. 3H{090}. **ad:** CS/Betzes.
Got-H^{ch}***3***{351}. 3H^{ch}{351}. **ad:** MA/*H. chilense.*
Got-R3{1457}. [*Got3*{1559}]. 3R{1457}. **ad:** CS/Imperial{1457}; Holdfast/ King II{1253}; Kharkov/Dakold{1253}.
Got-S^{s}***3***{1140}. 3S^{s}{1140}. **ad:** CS/*Ae. searsii.*
Got-V3{1518,242}. 3VL{1518}. **ad:** Creso/*D. villosum.*
Got-R4. [*Got1/7R*{1203},*Got2*{1559}]. 7RL{1203}. **al:** *S. cereale.*

Wehling {1559} identified a GOT locus designated *Got1* in 4RL of *S. cereale.*

82.2.10. Hexokinase

Hk-B1{006}. 1BS{006}. **v:** CS.
Hk-D1{006}. 1DS{006}. **v:** CS.
Hk-A2{810}. 3A{810}. **v:** CS.
  Hk-A2a{810}. **v:** CS.
  Hk-A2b{810}. **s:** CS*/Sears' Synthetic 3A. **v:** Sears' Synthetic IPSR 1190903.
Hk-B2{006}. 3BS{006,810}. **v:** CS.
Hk-D2{810}. 3DS{810}. **v:** CS.
  Hk-D2a{810}. **v:** CS.
  Hk-D2b{810}. **v:** Sears' Synthetic IPSR 1190903.
Hk-E2{006}. 3ES{006}. **ad:** CS/*E. elongata.*

Allelic variation was observed in three of 55 hexaploid accessions {006}.

82.2.11. Lipoxygenase

The wheat *Lpx-1* gene in wheat corresponds to barley *LoxA* (GenBank L35931). The *Lpx-B1* locus is duplicated, with the *Lpx-B1.1* and *Lpx-B1.2* loci corresponding to GenBank sequences DQ474240 and DQ474241, respectively. The *Lpx-B1b* allele corresponds to a deletion associated with a 4.5-fold reduction in lipoxygenase activity. The *Lpx-2* gene in wheat corresponds to the barley *LoxC* gene (GenBank L37358) whereas the *Lpx-3* gene in wheat corresponds to the barley *LoxB* gene (GenBank L37359).

Lpx-A1{516}. [*Lpx-B1*{516}]. 4AL{516}. **v:** CS{516}. **ma:** *Xksu919(Lpx-1)-4A*{0091}.

Lpx-B1{516}. [*Lpx-A1*{516}]. 4BS{516}. **v:** CS{516}. **ma:** *Xcn110(Lpx-1)-4B*{0269,0367}.

Lpx-B1a{1533}. [*Lpx-A1a*{936}]. **v:** CS.

Lpx-B1b{1533}. [*Lpx-A1b*{936}]. **v:** Bosanka{1533}.

Lpx-B1.1{10303}. 4BS{10303}. **ma:** *Xksm62-4B* - 8 cM - *LpxB1.1* - 13 cM - *Xwmc617b-4B*{10303}.

Lpx-B1.1a{10303}. **tv:** UC1113{10303}.

Lpx-B1.1b{10303}. **tv:** Kofa, deletion{10303}.

Lpx-B1.2{10303}. 4B{10303}. **v:** CS.

Lpx-D1{516}. 4DS{516}. **v:** CS.

Lpx-E1{518}. 4ES{518}. **ad:** CS/*E. elongata*.

Lpx-H1{716}. 4H{716}. **ad:** CS/Betzes.

Lpx-A2{516}. 5AL{516,10303}. **v:** CS. **ma:** *Xksu919(Lpx-2)-5A*{0091}.

Lpx-B2{516}. 5BL{516,10303}. **v:** CS. **ma:** *Xksu919(Lpx-2)-5B*{0091}; *Xcn111(Lpx-2)-5B*{0269}.

Lpx-D2{516}. 5DL{516}. **v:** CS.

Lpx-E2{518}. 5EL{518}. **ad:** CS/*E. elongata*.

Lpx-H2{716}. 5H{716}. **ad:** CS/Betzes.

Lpx-S^s2{1140}. 5S^s{1140}. **ad:** CS/*Ae. searsii*.

Lpx-V2{242}. 5V. **ad:** CS/*D. villosum*.

Lpx-A3{10303}. 4AL{10303}. **tv:** UC1113 (GenBank DQ474244) and Kofa (GenBank DQ474242){10303}. **ma:** *Xwmc617a-4A* - 10 cM - *Lpx-A3* - 15 cM - *Xgwm192b-4A*{10303}.

Lpx-B3{10303}. 4B{10303}. **tv:** UC1113 and Kofa (GenBank DQ474243){10303}.

82.2.12. Malate dehydrogenase

Mdh-A1. [*Mdh2A*{087}]. 1AL{087}. **v:** CS.

Mdh-B1. [*Mdh2B*{087}]. 1BL{101,087}. **v:** CS.

Mdh-D1. [*Mdh2D*{087}]. 1DL{087}. **v:** CS.

Mdh-H1{1153}. 1HL{1153}. **ad:** CS/Betzes.

Mdh-H^{ch}1{352}. 1H^{ch}{352}. **ad:** MA/*H. chilense*.

Mdh-R1. [*Mdh2-1*{1252}]. 1RL{1252}. **ad:** CS/Imperial 1R; Kharkov/Dakold 1R; Holdfast/King II 1RL.

Mdh-S^s1{1140}. 1S^s{1140}. **ad:** CS/*T. searsii*.

Mdh-H2. [*Mdh2-b2*{090}]. 3H{090}.

Mdh-R2. [*Mdh2-2*{1252}]. 3R{1252}. **ad:** CS/Imperial.

A third set of dimeric MDH isozymes identified in mature grain are separable from MDH-1 and MDH-2 by their higher pI's in IEF {811}.

Mdh-A3{811}. 5AS. **v:** CS.

Mdh-A3a{811}. **v:** CS.

Mdh-A3b{811}. **v:** Bersee.
Mdh-B3{811}. 5BS. **v:** CS.
Mdh-B3a{811}. **v:** CS.
Mdh-B3b{811}. **v:** Hope.
Mdh-D3{811}. 5DS. **v:** CS.
Mdh-D3a{811}. **v:** CS.
Mdh-D3b{811}. **v:** Sears' Synthetic.
Mdh-E3{811}. 5ES. **ad:** CS/*E. elongata*.
Mdh-H3{811}. 5H. **ad:** CS/Betzes.
Mdh-U3{811}. 5U. **ad:** CS/*Ae. umbellulata*.
Mdh-R4{360}. 1RL{360}. **v:** Various crosses.

82.2.13. Peroxidase

Peroxidase (EC1.11.1.7) isozymes have high tissue specificity. Staining and electrophoretic systems are reviewed in {118}. PER-1, -2, -3, -4 and -5 are all reported in {816}.

82.2.13.1. PER-1

PER-1 is expressed in leaf {012} and coleoptile {816} tissues.

Per-B1{012}. 1BS{012,919}. **v:** CS.
Per-D1{012}. 1DS{012,919}. **v:** CS.
Per-D1a{012}. **v:** CS.
Per-D1b{012}. **v:** Sears' Synthetic.
Per-H^{ch}1{012}. 1H^{ch}{012}. **ad:** CS/*H. chilense*.
Per-R1{012}. [*Prx*{1561}]. 1RS{012,1561}. **ad:** CS/King II{012}; Holdfast/King II{1561}. **tr:** Veery 'S'{012}.
Per-V1{241}. 1V{241}. **ad:** Creso/*D. villosum*.

82.2.13.2. PER-2

PER-2 is expressed in young leaf {118}, coleoptile and root {816} tissues.

Per-A2. 2AS. **v:** CS.
Per-A2a{816}. **v:** CS.
Per-A2b{816}. **v:** Timstein.
Per-B2{118}. 2BS{118}. **v:** CS.
Per-B2a{816}. **v:** CS.
Per-B2b{816}. **v:** Sears' Synthetic IPSR1190903.
Per-D2{118}. 2DS{118}. **v:** CS.
Per-H2{118}. [*Per-5*{095}]. 2H{118}. **ad:** CS/Betzes.
Per-R2{118}. 2RS{118}. **ad:** CS/Imperial; Kharkov/Dakold.

82.2.13.3. PER-3

PER-3 is expressed in embryo {119,816} and scuteller {119} tissues.

Per-A3{119}. 3AL{119}. **v:** CS.
Per-A3a{816}. **v:** CS.
Per-A3b{816}. **v:** Timstein.
Per-A3c{816}. **v:** Hobbit 'S'.
Per-B3{086},{119}. [*Per4*{961}]. 3BL{086,119}. **v:** CS.
Per-B3a{816}. **v:** CS.
Per-B3b{816}. **v:** Hope.
Per-B3c{816}. **v:** *T. macha* IPSR1240005.

Per-B3d{816}. **v:** Timstein.
Per-B3e{816}. **v:** Sears' Synthetic IPSR1190903.
Per-D3{086},{119}. [*Per5*{961}]. 3DL{086,119}. **v:** CS.
Per-D3a{816}. **v:** CS.
Per-D3b{816}. **v:** Hope.
Per-D3c{816}. **v:** Timstein.
Per-D3d{816}. **v:** *T. macha* IPSR 142005.
Per-D3e{816}. **v:** Sava.
Per-D3f{816}. **v:** Cheyenne.
Per-D3g{816}. **v:** Sears' Synthetic IPSR 1190903.
Varietal variation for *Per-3* was reported in {094}.

82.2.13.4. PER-4

PER-4 is expressed in endosperm tissue {086,119}.
Per-A4{695},{119}. [*Per3*{961}]. 7A{695}.7AS{694,086,119}. **v:** CS.
Per-A4a{816}. **v:** CS.
Per-A4b{816}. **v:** Hope.
Per-A4c{816}. **v:** Sicco.
Per-B4{695},{119}. [*Per2*{961}]. 4A{695}.4AL{086,119,694}. **v:** CS.
Per-B4a{816}. **v:** CS.
Per-B4b{816}. **v:** Hope.
Per-B4c{816}. **v:** Thatcher.
Per-D4{695},{119}. [*Per1*{961}]. 7D{695}.7DS{694,086,119}. **v:** CS.
Per-D4a{816}. **v:** CS.
Per-D4b{816}. **v:** Thatcher.
Per-Ag^{e}4. 7Ag^{e}S{694}. **tr:** Certain CS 7D/*Ag^e* lines.
Per-Ag^{i}4. [*Per-Ag^{i}3*{374}]. 7Ag^i{168}. **ad:** Vilmorin 27/*Th. intermedium*.
Cultivar variation for *Per-4* was reported in {094}.

82.2.13.5. PER-5

PER-5 is expressed in roots {816}.
Per-D5{816}. 2DS{816}. **v:** CS.
Per-S^{l}5{816}. 2S^l{816}. **ad:** CS/*Ae. longissima*.

82.2.14. Phosphodiesterase

Pde-A1. [*Pde-A3*{1590}]. 3A{1590}.3AS{1589}. **v:** CS.
Pde-B1. [*Pde-B3*{1590}]. 3B{1590}.3BS{1589}. **v:** CS.
Pde-D1. [*Pde-D3*{1590}]. 3DS{1590}. **v:** CS.
Pde-S^{l}1. 3S^{l}S{172}. **ad:** CS/*Ae. longissima*.
Pde-V1{1518}. 3VS{1518}. **ad:** CS/*D. villosum*.

82.2.15. Phosphogluconate dehydrogenase

Pgd1{282}. [*Pgd3*{282},*Pgd-A3*{963}]. 7A^{m}S{282}. **v:** *T. monococcum*{664}.
PgdR1. 4RL{1191}. **ad:** CS/Imperial; Holdfast/King II.
PgdR2. 6RL{1191}. **ad:** CS/Imperial; Holdfast/King II.

Loci were also identified in 6B {1435}, 1EL {1435}, 1HL {147,1072}, 1H^{ch} {352} and 1RL {779}.

82.2.16. Phosphoglucomutase

Pgm-A1{088}. [*Pgm-B1*{088}]. 4AL{088}. **v:** CS.
Pgm-D1{088}. 4DS{088}. **v:** CS.
Pgm-Ag^{i}1{361},{374}. [*Pgm-X1*{361}]. 4Ag^{i}{361}. **ad:** Vilmorin 27/*Th. intermedium.*
Pgm-H1. [*Pgm-b1*{090}]. 4H{090}. **ad:** CS/ Betzes.
Pgm-H^{ch}1{351}. 4H^{ch}{351}. **ad:** MA/*H. chilense.*
Pgm-R1. 4RS{1561,1253}. **ad:** CS/Imperial 4RS{1253,1561}; Kharkov/Dakold 4R{1253}; Holdfast/King II 4RS{1253,1561}.

82.2.17. Shikimate dehydrogenase

Skdh-A1{706,1065}. 5AS{706,1065}. **v:** CS.
Skdh-B1{706,1065}. 5BS{706,1065}. **v:** CS.
Skdh-D1{706,1065}. 5DS{706,1065}. **v:** CS.
Skdh-H1{085}. 5H{085}. **ad:** CS/Betzes.
Skdh-H^{t}1{1037}. 5H^{t}{1037}. **ad:** CS/*E. trachycaulus.*
Skdh-M^{v}1{985}. [*Skdh-M^{v}1*{985}]. 5M^{v}. **su:** 5M^{v}(5A), 5M^{v}(5D).
Skdh-R1{706}. 5RS{706}.5R{085}. **ad:** CS/King II{085}; CS/Imperial{706}; Kharkov/Dakold{085}. **tr:** CS 4AS-5RL; CS 5BL-5RL.
Skdh-S^{l}1{085}. 5S^{l}S{085}. **ad:** CS/ *Ae. longissima.*
Skdh-S^{s}1{1140}. 5S^{s}{1140}. **ad:** CS/*Ae. searsii.*
Skdh-V1{085}. 5V{085}. **ad:** CS/*D. villosum.*
Skdh-U1. 5U{706}. **ad,su:** CS/*Ae. umbellulata.*

82.2.18. Superoxide dismutase

Sod-A1{1066}. 2AL{1066}. **v:** CS.
Sod-B1{1066}. 2BL{1066}. **v:** CS.
Sod-D1{1066}. 2DL{1066}. **v:** CS.
Sod-E1{808}. VI E{808}. **ad:** CS/*E. elongata.*
Sod-H1{716}. 2H{716}. **ad:** CS/Betzes.
Sod-R1{1066}. [*Sod-3*{586}]. 2R{1066}. **ad:** CS/Imperial.
Sod-S^{s}1{1140}. 2S^{s}{1140}. **ad:** CS/*Ae. searsii.*
Sod-VI{1026}. 7V{1026}. **ad:** CS/*D. villosum.*

82.2.19. Triosephosphate isomerase

Tpi-A1{1139}. 3AS{1139}. **v:** CS.
Tpi-B1{1139}. 3BS{1139}. **v:** CS.
Tpi-D1{1139}. 3DS{1139}. **v:** CS.
Tpi-E1{1139}. 3E{1139}. **ad:** CS/*E. elongata.*
Tpi-H1{1139}. 3H{1139}. **ad:** CS/Betzes.
Tpi-R1{1139}. 3R{1139}. **ad:** CS/Imperial; Kharkov/Dakold.
Tpi-S^{l}1{1139}. 3S^{l}{1139}. **ad:** CS/ *Ae. longissima.*
Tpi-A2{1139}. 5AL{1139}. **v:** CS.
Tpi-B2{1139}. 5BL{1139}. **v:** CS.
Tpi-D2{1139}. 5DL{1139}. **v:** CS.
Tpi-H2{1139}. 5H{1139}. **ad:** CS/Betzes.
Tpi-R2{1139}. 5R{1139}. **ad:** CS/Imperial; Kharkov/Dakold.

Tpi-S^{l}2{1139}. 5S^{l}{1139}. **ad:** CS/*Ae. longissima*.

Tpi-U2{1139}. 5U{1139}. **ad:** CS/*Ae. umbellulata*.

Tpi-Ag^{i}2{374}. 5Ag^{i}{374}. **ad:** Vilmorin 27/*Th. intermedium*.

82.2.20. Aromatic alcohol dehydrogenase

Aadh-A1. [*Adh-A2*{584}]. 5AL{584}. **v:** CS. **ma:** *XksuG44-5A*(proximal) - 6.9 cM - *Aadh-A1* - 24.7 cM - *Xcdo412-5A*(distal){9959}.

Aadh-A1a. **v:** CS; 133 other accessions{584}.

Aadh-A1b. **v:** *T. spelta*; K-24696; other accessions{584}.

Aadh-B1. [*Adh-B2*{584}]. 5BL{584}. **v:** CS.

Aadh-B1a. **v:** CS{1533}.

Aadh-B1b. **v:** Drina {1533}.

Aadh-C1{1278}. C{1278}. **ad:** Alcedo/*Ae. caudata* line C.

Aadh-D1. [*Adh-D2*{584}]. 5DL{584}. **v:** CS.

Aadh-E1. [*Adh-E2*{518}]. 5EL{518}. **ad:** CS/*E. elongata*.

Aadh-R1. 5RL{1280}. **ad:** Holdfast/King II.

Aadh-A2. [*Adh-A3*{508}]. 6A{1279}.6AL{513,587}. **v:** CS{513}; Carola{1279}.

Aadh-B2. [*Adh-B3*{508}]. 6B{1279}.6BL{513}. **v:** CS{513}; Carola{1279}.

Aadh-D2. [*Adh-D3*{508}]. 6D{1279}.6DL{513}. **v:** CS{513}; Carola{1279}.

Aadh-Ag^{e}2{1575}. 6Ag^{e}{1575}. **ad,su:** Rescue/*Th. elongatum*.

Aadh-E2. [*Adh-E3*{518}]. 6EBeta{518}. **ad:** CS/*E. elongata*.

Aadh-R2. 6RL{1280}. **ad:** Holdfast/King II.

Aadh-V2{241}. 6V{241}. **ad:** CS/*D. villosum*.

The *Aadh-1* and *Aadh-2* loci were designated with the synonyms *Adh-2* and *Adh-3*, respectively, in a number of publications in addition to {508,518,584}. These include: {510,509,511,519,517,587,1066,1139}.

82.2.21. Aconitase

Aco-A1{189}. 6AL{189}. **v:** CS.

Aco-A1a. **v:** CS{1533}.

Aco-A1b. **v:** Dubravka{1533}.

Aco-B1{189}. 6BL{189}. **v:** CS.

Aco-B1a. **v:** CS{1533}.

Aco-B1b. **v:** Dubravka{1533}.

Aco-B1c. **v:** Slavonka{1533}.

Aco-D1{189}. 6DL{189}. **v:** CS.

Further alleles at *Aco-A1* and *Aco-B1* are listed in {1127}; these have not been tested against those found in {1533}.

Aco-Ag^{e}1{1575}. 6Ag^{e}{1575}. **ad,su:** Rescue/*Th. elongatum*.

Aco-E1{189}. 6Ebeta{189}. **ad:** CS/*E. elongata*.

Aco-H1{147},{189}. [*Aco-1*{147}]. 6H{147}.6HL{189}. **ad:** CS/Betzes.

Aco-R1{189}. 6RL{189}. **ad:** Sturdy/PI 252003.

Aco-S^{l}1{189}. 6S^{l}{189}. **ad:** CS/*Ae. longissima*.

Aco-S^{s}1{1140}. 6S^{s}{1140}. **ad:** CS/*Ae. searsii*.

Aco-U1{189}. CSU-31{189}. **ad:** CS/*Ae. umbellulata*.

Aco-A2{189}. 5AL{189}. **v:** CS.

Aco-B2{189}. 4BL{1513}. **v:** CS.

Aco-B2a{1513}. **v:** CS.

Aco-B2b{1513}. **v:** PI 278437.

Aco-B2c{1513}. **v:** PI 182575.

Aco-B2d{1513}. **v:** PI 157589.
Aco-D2{189}. 4DL{1513}. **v:** CS.
Aco-E2{189}. 4EL{189}. **ad:** CS/*E. elongata*.
Aco-M^{v}2{1341}. [*Aco-M^{v}2*{985}]. 5M^{v}. **ad:** 5M^{v}(5A),5M^{v}(5D).
Aco-R2{189}. 5RL{189}. **ad:** CS/King II 5R; Holdfast/ King II 5RL.
Aco-S^{s}2{1140}. 4S^{s}{1140}. **ad:** CS/*Ae. searsii*.

82.2.22. NADH dehydrogenase

82.2.22.1. Ndh-1

Ndh-A1{513},{1037}. [*Ndh-B1*{513}]. 4AL{513}. **v:** CS.
Ndh-A1a{1533}. [*Ndh-B1a*{936}]. **v:** CS.
Ndh-A1b{1533}. [*Ndh-B1b*{936}]. **v:** Sutjeska.
Ndh-A1c{1533}. [*Ndh-B1c*{936}]. **v:** Fruskogorka.
Ndh-A1d{1037}. [*Ndh-A1b*{1037}]. **v:** Hope, Timgalen.
Ndh-B1{513}. [*Ndh-A1*{513}]. 4BS{513}. **v:** CS.
Ndh-D1{513}. 4DS{513}. **v:** CS.
Ndh-E1{362}. 4E{362}. **ad:** CS/*E. elongata*.
Ndh-H1{147},{513}. [*Nadhd-1*{147}]. 4H{147}.4HS{813}. **ad:** CS/Betzes.
Ndh-H^{ch}1{813}. 4H^{ch}{813}. **ad:** CS/*H. chilense*.
Ndh-V1{241}. 4V{241}. **ad:** CS/*D. villosum*.
Ndh-R1{813}. 4R{362}.4RS{813}. **ad:** CS/Imperial, CS/King II{813,362}; CS/Dakold{362}.
Ndh-S^{1}1{813}. 4S^{l}{813}. **ad:** CS/*Ae. longissima*.
Ndh-U1{362}. A{362}. **ad:** CS/*Ae. umbellulata*.

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the *Ndh1* (NADH dehydrogenase) and *Dia3* (diaphorase) represent the same locus {0356}.

82.2.22.2. Ndh-2

Ndh-A2{813}. 7A{813}. **v:** Hope.
Ndh-D2{813}. 7DS{813}. **v:** CS.
Ndh-R2{813}. 7RS{813}. **ad:** CS/Imperial, CS/King II, Holdfast/King II (7R).

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that the *Ndh-2* (NADH dehydrogenase) and *Dia2* (diaphorase) represent the same locus {0356}.

82.2.22.3. Ndh-3

Ndh-A3{813}. 3AL{813}. **v:** CS.
Ndh-B3{813}. 3BL{813}. **v:** CS.
Ndh-B3a{813}. **v:** CS.
Ndh-B3b{813}. **v:** Carmen.
Ndh-D3{813}. 3DL{813}. **v:** CS.
A *Ndh* locus, designated *Nadhd2*, was mapped 27 cM from *Est-D10* in an *Ae. taushii* F$_2$ population derived from VIR-1954/VIR-1345 {10046}. This locus may be homologous to *Ndh-D3*
Ndh-H3{813}. 3HL{813}. **ad:** CS/Betzes.
Ndh-R3{813}. 6RL{813}. **ad:** Holdfast/King II, CS/Imperial (6R), CS/King II (6R).
Ndh-S^{l}3{813}. 3S^{l}L{813}. **ad:** CS/*Ae. longissima*; CS/*Ae. sharonesis* (3S^{l}).

Based on the correspondence of the electrophoretic patterns, isoelectric points (pIs) and chromosomal location, it was proposed that *Ndh-3* (NADH dehydrogenase), *Dia1* (diaphorase) and *Mnr1* (menadione reductase) represent the same locus {0356}.

82.2.22.4. Ndh-4

Ndh-A4{813}. 3AS{813}. **v:** CS.

Ndh-B4{813}. 3BS{813}. **v:** CS.

Ndh-E4{813}. 3ES{813}. **ad:** CS/*E. elongata*.

Ndh-H4{813}. 3HS{813}. **ad:** CS/Betzes.

Ndh-R4{813}. 3RS{813}. **ad:** CS/King II, CS/Imperial (3R).

82.2.23. Dipeptidase

Dip-A1{454},{700}. [*Pept-A1*{454}]. 6AL{454,700}. **v:** CS.

Dip-A1a{700}. **v:** CS.

Dip-A1b{700}. **v:** Cheyenne.

Dip-B1{454},{700}. [*Pept-B1*{1533}]. 6BL{454,700}. **v:** CS.

Dip-B1a{700}. **v:** CS.

Dip-B1b{700}. **v:** Cappelle-Desprez.

Dip-D1{700}. 6DL{700}. **v:** CS.

Dip-H1{147},{700}. [*Pept-1*{147},*Dip 1*{145}]. 6H{147,145,700}. **ad:** CS/Betzes.

Dip-J1{700}. 6J{700}. **ad:** CS/*Th. junceum*.

Dip-V1{700}. 6V{700}. **ad:** CS/*D. villosum*.

82.2.24. Malic enzyme

A dimeric enzyme extractable from mature grains.

Mal-A1{809}. 3AL. **v:** CS.

Mal-B1{809}. 3BL. **v:** CS.

Mal-B1a{809}. **v:** CS.

Mal-B1b{809}. **v:** *T. spelta* IPSR line 1.

Mal-B1c{809}. **v:** Sears' Synthetic.

Mal-D1{809}. 3DL. **v:** CS.

Mal-E1{809}. 3E. **ad:** CS/*E. elongata*.

Mal-H1{809}. 3H. **ad:** CS/Betzes.

Mal-R1{809}. 3R. **ad:** CS/Imperial.

82.2.25. Adenylate kinase

Adk-A1{091}. [*Adk-a*{091}]. 7AL{091}. **v:** CS.

Adk-B1{091}. [*Adk-b*{091}]. 7BL{091}. **v:** CS.

Adk-D1{091}. [*Adk-d*{091}]. 7DL{091}. **v:** CS.

Adk-E1{091}. 7E{091}.7E{1435}. **ad:** CS/*E. elongata*.

Adk-H1{091}. 7H{091}.7HS{1435}. **ad:** CS/Betzes.

Adk-M^{v}1{985}. [*Adk-M^{v}1*{985}]. 7M^{v}L. **su:** 7M^{v}(7D).

Adk-R1{091}. 7RL{091}. **ad:** CS/Imperial; Holdfast/King II.

Adk-U1{091}. E{091}. **ad:** CS/*Ae. umbellulata*.

Adk-Ag^{i}1{091}. 7Ag^{i}{091}. **ad:** CS/*Th. intermedium*.

Adk-H2. 6HL{1435}. **ad:** CS/Betzes.

82.2.26. Glutamate-pyruvate transaminase

Gpt-A1{1435}. 1AS{1435}. **v:** CS.
Gpt-B1{1435}. 1BS{1435}. **v:** CS.
Gpt-D1{1435}. 1DS{1435}. **v:** CS.
Gpt-E1{1435}. 1ES{1435}. **ad:** CS/*E. elongata* 1E.
Gpt-H1{1435}. 1H{1435}. **dv:** *H. vulgare* cv. Betzes.

82.2.27. Catalase

Cat-B1{1466}. [*Cat-A1*{1466}]. 4BL{1466}. **v:** CS.

A catalase locus, designated *Cat2,* was mapped 6 cM proximal to *Aco-D2* in an *Ae. tauschii* F_2 population derived from VIR-1954/VIR-1345 cross {10046}. This locus may be orthologous to *Cat-B1* {10046}.

82.2.28. Beta-glucosidase

b-Gls{282}. $2A^mL${282}. **dv:** DV92.
 b-Glsa{282}. **dv:** DV92.
 b-Glsb{282}. Null allele **dv:** G3116.

82.2.29. Starch branching enzyme I

SbeI1{9937}. 1DL{9937}. **v:** CS{9937}.
SbeI2{9937}. 7BL{9937}. **v:** CS{9937}.

82.2.30. Starch branching enzyme II

SbeII.

Suppression of SBEIIb expression alone had no effect on amylose contents, however, suppression of both SBEIIa and SBEIIb expression resulted in wheat starch containing >70% amylose {10534}.

82.2.31. Benzoxinones

The putative role of benzoxinones sets *Bx-1* to *Bx-5* is to catalyze the pathway Indole-3-glycerol phosphate to DIBOA. Primers designated from maize sequences were used to generate RT-PCR products utilised to screen a cDNA library from CS seedlings. Full-length cDNAs were heterologously expressed in yeast and the *Bx* gene products had enzymatic action. The *Bx* genes located by Southern analysis of CS deletion stocks occurred as clustered groups in homoeologous groups 4 (*Bx-1, Bx-2*) and 5 (*Bx-3.1, .2, Bx-4, Bx-5*) {10103}.

82.2.32. Acetohydroxyacid synthase (EC 4.1.3.18)

An orthologous series was mapped as the active target sites of imidazolinone herbicides. See section: Herbicide Response: Imidazolinone resistance.

AhasL-A1{10101}. [*Imi3*{10099}]. 6AL{10101}. **v2:** CDC Teal IMI 15A *Imi3*{10099}.
 dv: *T. monococcum* mutant EM2 (mutant of susceptible line TM23{10102}.
AhasL-B1{10101}. [*Imi2*{10099}]. 6BL{10101}. **v:** CDC Teal IMI 11A=PTA3953{10099}.
AhasL-D1{10101}. [*Imi1*{10099}]. 6DL{10101}. **v:** BW755=Grandin*3/Fidel-Fs-4{10099}.

82.2.33. Phytoene synthase

Phytoene synthase, which condenses two molecules of geranyl geranyl diphosphate to produce phytoene, is the first of the specific enzyme necessary for carotene biosysthesis in plants.

82.2.33.1. Phytoene synthase 1 (EC 2.5.1.32)

Homology with the same gene in rice (*Psy1*) {10230}.

Phytoene synthase is involved in the carotenoid biosynthetic pathway and influences yellow pigment content in grain (See Flour colour and Grain quality parameters: Flour, semolina and pasta colour). The gene *Psy-A1* was cloned and a functional marker developed from the sequence distinguishing Chinese common wheats with high and low pigment contents {10501}. Most hexaploid wheat cultivars have a 676-bp insertion in intron four that is absent in Australian cultivars Dundee, Raven, and Aroona with high yellow pigment. The *Psy-B1b* allele from tetraploid wheat Kofa is the result of a B-A intergenomic conversion event that probably occurred in Cappelli *ph1c* mutant 1 {10530}. An EMS mutation in the *Psy-E1* gene is associated with whiter endosperm in lines carrying the *Th. elongatum* 7EL translocation.

Psy1-A1{10230}. 7AL{10230}. **tv:** Kofa{10230}. **ma:** *Xwmc809-7A* - 5.8 cM - *Yp7A*{10501}.

Psy1-A1a. **tv:** Kofa{10230}. **ma:** *Xwmc809-7A* - 5.8 cM - *Yp7A*{10501}.

Psy1-A1b. **v:** Chinese common wheats with low yellow pigment content{10501}; PH82-2{10501}; Shaan 9314{10501}; Xinong 336{10501}. **c:** GenBank EF600064 {10501}. 37-bp insertion intron 2 (231 bp fragment for marker *Yp7A*) {10501}. 676-bp insertion in intron 4 {10530}.

Psy1-A1c{10530}. **v:** M564{10650}. **c:** GenBank EU650391{10650}; No 37-bp insertion in intron 2 and no 676-bp insertion in intron 4{10530}; High yellow pigment cultivars: Aroona (PI 464647){10530}; Dundee (PI 89424, PI 106125){10530}; Raven (PI 303633, PI 330959){10530}.

Psy1-A1d{10651}. **tv:** Langdon{10651}; *T. dicoccum* DM28{10652}. **c:** GenBank EU263018{10651}; FJ393515{10652}.

Psy1-A1e{10651}. **v:** Sunco{10654}. **tv:** DR8{10651}. **c:** EU649791{10654}; EU263019{10651}.

Psy1-A1f{10652}. **dv:** *T. urartu* PI 428326{10652}. **c:** FJ393516{10652}.

Psy1-A1g{10652}. **dv:** *T. urartu* UR1{10652}. **c:** FJ393517{10652}.

Psy1-A1h{10652}. **dv:** *T. boeoticum* BO1{10652}; *T. monococcum* MO5{10652}. **c:** FJ393518{10652}; FJ393519{10652}.

Psy1-A1i{10652}. **dv:** *T. monococcum* MO1{10652}. **c:** FJ393520{10652}.

Psy1-A1j{10652}. **dv:** *T. monococcum* MO2{10652}. **c:** FJ393521{10652}.

Psy1-A1k{10652}. **v:** Spelt 167{10652}. **tv:** *T. dicoccoides* DS3{10652}; *T. dicoccum* DM37{10652}. **c:** FJ293527{10652}; FJ293522{10652}; FJ293523{10652}.

Psy1-A1l{10652}. **tv:** Kofa{10230,10530}; Strongfield{10653}; *T. dicoccoides* DS6{10652}. **c:** EU096090{10230,10530}; FJ393524{10652}.

Psy1-A1m{10652}. **tv:** *T. dicoccum* DM26{10652}. **c:** FJ393525{10652}.

Psy1-A1n{10652}. **v:** Spelt SP9{10652}. **c:** FJ393526{10652}.

Psy1-A1o{10653}. **tv:** Commander{10653}. **c:** FJ234424{10653}.

Psy1-A1p{10654}. **v:** Tasman{10654}. **c:** EU649792{10654}.

Psy1-A1q{10654}. **v:** Cranbrook{10654}. **c:** EU649793{10654}.

Psy1-A1r{10654}. **v:** Halberd{10654}. **c:** EU649794{10654}.

Psy1-A1s{10654}. **v:** Schomburgk{10654}. **c:** EU649795{10654}.

Psy1-A1t{10920}. **v:** WAWHT2074{10920}. **ma:** *Xwgm344-7A* - 3.9 cM - *Psy1-A1t* - 9.9 cM - *Ccfa2257a-7A*{10920}. **c:** GenBank HM006895{10920}.

Psy1-B1{10230}. 7BL{10230}. **tv:** Kofa{10230}. **ma:** *Xcfa2040-7B* - 12 cM - *Psy-B1* - 5 cM - *Xgwm146-7B*{10230}.

Psy1-B1a{10650}. GenBank EU096093 {10530}. [{10530}]. **v:** Chinese Spring{10530,10650,10654}; Spelt SP9{10652}. **tv:** *T. dicoccoides* DS4{10652}. **c:** FJ393529{10652}; FJ393528{10652}; EU650392{10650}; EU096094{10530}; EU649789{10654}.

Psy1-B1b{10650}. **v:** Neixiang 188{10650}. **c:** EU650393{10650}.

Psy1-B1c{10650}. **v:** CA 9648{10650}. **c:** EU650394{10650}.

Psy1-B1d{10650}. **v:** Ning 98084{10650}. **c:** EU650395{10650}.

Psy1-B1e{10650}. **v:** M484{10650}. **tv:** DR8{10650}; *T. dicoccum* DM28{10652}. **c:** EU263021{10650}; FJ393541{10652}.

Psy1-B1f{10651}. **tv:** Langdon{10651}. **c:** EU263020{10651}.

Psy1-B1g{10651}. **tv:** DR1{10651}; *T. dicoccoides* DS6{10652}. **c:** EU650396{10651}; FJ393530{10652}.

Psy1-B1h{10652}. **tv:** *T. dicoccoides* DS3{10652}. **c:** FJ393531{10652}.

Psy1-B1i{10652}. **tv:** *T. dicoccoides* DS8{10652}. **c:** FJ393532{10652}.

Psy1-B1j{10652}. **tv:** *T. dicoccum* DM26{10652}. **c:** FJ393533{10652}.

Psy1-B1k{10652}. **tv:** *T. dicoccum* DM33{10652}. **c:** FJ393534{10652}.

Psy1-B1l{10652}. **tv:** *T. dicoccum* DM37{10652}. **c:** FJ393535{10652}.

Psy1-B1m{10652}. **v:** Spelt 167{10652}. **tv:** *T. dicoccum* DM47{10652}. **c:** FJ393540{10652}; FJ393539{10652}.

Psy1-B1n{10530}. Previously designated *Psy1-B1b* {10656} **tv:** Kofa. **c:** EU096092{10530}; DQ642439{10230}.

Psy1-B1o{10530}. Previously designated *Psy1-B1a* {10656} **tv:** UC1113{10530}; W9262-260D3{10230}. **c:** EU096093{10530}; DQ642440{10230}.

Psy1-D1{10652}. 7DL{10652}.

Psy1-D1a{10652}. **v:** Chinese Spring{10652}. **c:** EU650397{10652}; EU649790{10654}.

Psy1-D1b{10652}. **dv:** *Ae. tauschii* Ae34{10652}. **c:** FJ393542{10652}.

Psy1-D1c{10652}. **dv:** *Ae. tauschii* Ae46{10652}. **c:** FJ393543{10652}.

Psy1-D1d{10652}. **dv:** *Ae. tauschii* Y99{10652}. **c:** FJ393544{10652}.

Psy1-D1e{10652}. **v:** Spelt SP9{10652}. **c:** FJ393545{10652}.

Psy1-D1f{10652}. **v:** Spelt 217{10652}. **c:** FJ393546{10652}.

Psy1-D1g{10652}. **v:** Zhonliang 88375{10652}. **c:** FJ807498{10652}.

Psy1-D1h{10652}. **dv:** *Ae. tauschii* Ae37{10652}. **c:** FJ807499{10652}.

Psy1-D1i{10652}. **dv:** *Ae. tauschii* Ae38{10652}. **c:** FJ807500{10652}.

Psy1-D1j{10652}. **dv:** *Ae. tauschii* Ae42{10652}. **c:** FJ807501{10652}.

Psy1-D1k{10655}. **v:** Nongda 3291{10655}. **c:** FJ807495{10655}.

Psy1-D1l{10655}. **v:** E 86642{10655}. **c:** FJ807496{10655}.

Psy1-D1m{10655}. **v:** Ning 97-18{10655}. **c:** FJ807497{10655}.

Psy1-E1. [*Psy-E1*].

Psy1-E1a{10530}. GenBank EU096095 {10530}. [*Psy-E1a*{10530}]. **v:** Agatha (7EL translocation){10530}.

Psy1-E1b{10530}. = EU096095 with P to L mutation at amino acid 422 {10530}. [*Psy-E1b*{10530}]. **v:** EMS mutant Agatha-28-4{10530}; Wheatear{10530}.

Psy1-S1{10652}. **al:** *Ae. speltoides* Ae48{10652}.

Psy1-S1a{10652}. **al:** *Ae. speltoides* Ae48{10652}. **c:** FJ393536{10652}.

Psy1-S1b{10652}. **al:** *Ae. speltoides* Ae49{10652}. **c:** FJ393537{10652}.

Psy1-S1c{10652}. **al:** *Ae. speltoides* Y162{10652}. **c:** FJ393538{10652}.

82.2.33.2. Phytoene synthase 2 (EC 2.5.1.32)

Homology with the same gene in rice (*Psy2*) {10230}.

Psy2-A1{10230}. 5A{10230}. **tv:** Kofa{10230}.

Psy2-B1{10230}. 5B{10230}. **tv:** Kofa{10230}. **ma:** *Xgwm191-5B* - 17 cM - *Psy-B2*{10230}.

82.2.34. Polyphenol oxidase

High PPO activity in kernels and flour leads to a time-dependent discolouration of end products such as noodles, pasta and breads.

Primers different from those in {10386} were developed in {10504}, but their ability to distinguish phenotypic groupings (alleles) were similar. A null allele of *Ppo-D1* was identified for this locus using primer pair WP3-2 {10504}.

Ppo-A1{10386}. *PPO-2A* {10385}. 2AL{10385}. **ma:** Detected with STS markers PPO18{10385}; and PPO33{10386}; *Xgwm321-2A* - 1.4 cM - *Ppo-A1* - 5.8 cM - *Xgwm294-2A*{10385}.

Ppo-A1a{10386}. *PPO-2Aa* {10385}. **v:** Nongda 139{10386}; Zhongyou 9507{10385,10386,10504}; others{10386,10504}. **c:** EF070147{10386}.

Wheats with this allele tend to have lower PPO activity {10385,10386}.

Ppo-A1b{10386}. *PPO-2Ab* {10385}. **v:** Chinese Spring{10386}; CA 9632{10385,10386}; Nongda 183{10504}; others{10386,10504}. **tv:** *T. dicoccoides* DS4{10386}. **c:** EF070148 {10386}.

Wheats with this allele tend to have lower PPO activity {10385,10386}.

Ppo-A1c{10657}. **dv:** *T. urartu* UR1{10657}. **c:** EU371651{10657}.

Ppo-A1d{10657}. **dv:** *T. boeoticum* BO1{10657}. **c:** EU371652{10657}.

Ppo-A1e{10657}. **tv:** DR8{10657}. **dv:** *T. monococcum* MO1{10657}. **c:** EU371653{10657}.

Ppo-A1f{10657}. **tv:** *T. dicoccoides* DS3{10657}. **c:** EU371654{10657}.

Ppo-A1g{10657}. **tv:** Langdon{10657}. **c:** EU371655{10657}.

Ppo-B1{10658}. **v:** Chinese Spring{10658}.

Ppo-B1a{10658}. **v:** Chinese Spring{10658}. **c:** GQ303713{10658}.

Ppo-D1{10386}. **ma:** Detected with primers PPO16 and PPO29. *Xwmc41-2D* - 2.0 cM - *Ppo-D1*{10386}.

Ppo-D1a{10386}. **v:** Chinese Spring{10386}; Zhonghou 9507{10386,10504}; others{10386,10504}. **c:** EF070149{10386}.

Wheats with this allele tend to have lower PPO activity {10386}.

Ppo-D1b{10386}. EF070150 {10386}. **v:** CA 9632{10386}; CA 9719{10386}; Nongda 183{10504}; others{10386,10504}. **c:** EF070150{10386}.

Wheats with this allele tend to have higher PPO activity {10386}.

Ppo-D1c{10657}. **dv:** *Ae. tauschii* Ae38{10657}. **c:** EU371656{10657}.

Ppo-D1d{10657}. **dv:** *Ae. tauschii* Y59{10657}. **c:** EU371657{10657}.

Ppo-D1e{10504}. [*Ppo-D1null*{10504},*Ppo-D1c*{10656}]. **v:** Gaiyuerui{10504}; Zm2851{10504}; XM2855{10504}; 9114{10504}.

Wheats with this allele tend to have lower PPO activity {10504}.

82.2.35. Protein disulfide isomerase (EC 5.3.4.1)

Pdi-A1{10422}. 4AL{10422}. **v:** {10422}.

Pdi-B1{10422}. 4DS{10422}. **v:** {10422}.

Pdi-D1{10422}. 4BS{10422}. **v:** {10422}.

The genes for PDI and their promoters were sequenced in {10423}. A related sequence on 1BS was shown to be a partial, non-expressed copy in {10424}, but not detected in {10409}. PCR-RFLP markers for [*TaPDI-4A*] and [*TaPDI-4B*] were designated [*Xvut(PDI)-4A*] and [*Xvut(PDI)-4B*] in {10409}. These were also closely associated with Germin (oxalate oxidase {10441}) genes {10409}.

82.2.36. Isoamylase 1

Iso-1{10295}. [*ISA-1*{10295}]. **dv:** *Ae. tauschii*{10295}.

82.2.37. Polygalacturonase-inhibiting proteins

PGIPs are leucine-rich repeat (LRR) proteins involved in plant defence.

Pgip1{10390}. 7BS{10390}. **v:** CS ditelo 7BL{10390}. **v2:** Chinese Spring *Pgip2*{10390}. **tv:** Langdon{10390}.

Pgip-A1{10608}. *Tapgip3*, AM180658 {10608}. **dv:** *T. monococcum* PI 538722{10608}. Not expressed in *T. urartu* PI 428315 (AM884191) {10608} or in polyploid wheat because of inactivation by an inserted copia transposon in the fourth LRR {10608}.

Pgip2{10390}. 7DS{10390}. **v:** CS ditelo 7DL{10390}. **v2:** Chinese Spring *Pgip1*{10390}.

Pgip-B1{10608}. [*Tapgip1*{10610}]. 7BS{10610,10608}. **ma:** *XS13M50-7B* - 5 cM - *Pgip-B1* - 11.7 cM - *Xmgb105s-7B*{10608}.

Pgip-B1a{10608}. *Tapgip1a* {10608}. **tv:** Messapia{10608}.

Pgip-B1b{10608}. *Tapgip1b*, AM884195 {10608}. **tv:** *T. turgidum* ssp. *dicoccoides* MG4343{10608}.

This non-expressed allele produces a large amplicon in southern blots using the Pgip sequence as probe, due to an insertion of a Vacuna mutator element {10608}.

Pgip-D1{10608}. [*Tapgip2*{10610}]. 7DS{10610}. **tv:** Langdon 7D(7A){10610}; Langdon 7D(7B){10610}.

82.2.38. Flavone 3-hydroxylase (EC 1.14.11.9)

F3h-A1{10823}. 2AL{10823}. **v:** CS{10823}. **ma:** *Xgwm1067-2A* - 2.1 cM - *F3h-A1* - 11.4 cM - *Xgwm1070-2A*{10823}.

F3h-B1{10823}. 2BL{10823}. **v:** CS{10823}. **ma:** *F3H-B1/Xgwm1067-2B* - 11.4 cM - *Xgwm1070-2B*{10823}.

F3h-D1{10823}. 2DL{10823}. **v:** CS{10823}. **ma:** *Xgwm877-2D* - 1.8 cM - *F3h-D1/Xgwm1264-2D* - 22.7 cM - *Xgwm301-2D*{10823}.

F3h-B2{10823}. 2BL{10823}. **v:** CS{10823}. **ma:** *Xgwm1070-2B* - 30.1 cM - *F3h-B2*{10823}; Located in the terminal region near *Xgwm1027-2B*{10823}.

82.2.39. Zeta-carotene desaturase

Zds-A1{10905}. 2A{10905}. **tv:** Langdon{10905}.

Zds-B1{10905}. 2B{10905}. **tv:** Langdon{10905}.

Zds-D1{10906}. 2DL{10906}. **v:** CS{10906}.

Zds-D1a{10906}. [*TaZDS-D1a*{10906}]. **v:** CA9632{10906}; Many Chinese weat and 80 CIMMYT lines{10906}.

Zds-D1b{10906}. [*TaZDS-D1b*{10906}]. **v:** Ning 99415-8{10906}; Zhengzhou 9023{10906}; Zhongyou 9507{10906}; Zhoumai 13{10906}.

Cv. Zhongyou 9507 has lower yellow flour pigment content, preferred for Chinese steamed bread and dry Chinese noodles. A QTL in the *Zds-D1a* region explained 18.4 % of the variation in yellow pigment content in Zhongyou 9507/CA 9632 {10906}.

82.2.40. Carotenoid beta-hydroxylase (non-heme di-iron type)

HYD are non-heme di-iron b-hydroxilases that act primarily on b-carotene.

Hyd-A1{10913}. 2AL{10913}. **tv:** Kronos{10913}. **v:** UC1041{10913}.
Hyd-B1{10913}. 2BL{10913}. **tv:** Kronos{10913}. **v:** UC1041{10913}.
Hyd-D1{10913}. 2DL{10913}. **tv:** Kronos{10913}. **v:** UC1041{10913}.
Hyd-A2{10913}. 5AL{10913}. **tv:** Kronos{10913}. **v:** UC1041{10913}.
Hyd-B2{10913}. 4BL{10913}. **tv:** Kronos{10913}. **v:** UC1041{10913}.
Hyd-D2{10913}. 4DL{10913}. **tv:** Kronos{10913}. **v:** UC1041{10913}.

82.3. Endosperm storage proteins

82.3.1. Glutenins

These are heterogeneous mixtures of proteins comprising subunits linked by disulfide bonds. 'A' are high-molecular-weight (HMW) and 'B', 'C' and 'D' are low-molecular-weight (LMW) subunits.

Using proteomic analysis of 2D gels of seed storage proteins in 39 ditelocentric lines of cv. CS, 105 protein spots were resolved {03129}. Locations of structural genes controlling 26 spots were identified in 10 chromosomal arms (4 on 1BL, 5 on 1BS, 4 on 1DL, 4 on 1DS, 2 on 6AS, 3 on 6BS, 1 on 6DL, 1 on 6DS, 1 on 3BS and 1 on 3BL). Multiple regulators of the same protein located on various chromosome arms were observed. Two novel subunits, named 1Bz and 1Dz, were found to have very similar structures to HMW glutenin subunit 12 (encoded by *Glu-D1-2a* - see the relevant list below) and were located to chromosome arms 1BL and 1DL, respectively.

82.3.1.1. Glu-1

The *Glu-1* loci, all of which are compound, encode HMW glutenin subunits.
Each *Glu-1* locus in hexaploid wheat contains two genes, the products of which were described as 'x-type' and 'y-type' based on differences in molecular weight and isoelectric point {1118}.

Other evidence has shown that these gene products differ in electrophoretic fingerprint pattern {1124} and cysteine content {1028}, and the genes themselves differ in nucleotide sequence {1470,1433,373}.

Although early evidence suggested up to 6 genes in total at each locus {1471,373], it appears likely that only a single copy of each gene is present at the 1AL, 1BL, and 1DL loci {495}.

No 'y-type' protein from the *Glu-A1* locus has been demonstrated in hexaploid wheat {1118}, although they are found in diploid wheats {1535,798}, and sequencing experiments have shown the presence of two stop codons in the transcribed portion of the gene {10088}. Definitive evidence that subunit 21^* {602}, which has a mobility close to that of subunit 21, is a 'x-type' protein rather than a 'y-type' protein has not been obtained. The gene coding for 'x-type' proteins within *Glu-A1* is also often silent {1118,420}.

The symbols for the genes within the *Glu-1* loci coding for 'x-type' and 'y-type' proteins will be *Glu-1-1* and *Glu-1-2*, respectively, rather than *Glu-1x* and *Glu-1y* {1470}. The genes are closely linked but recombination has been observed between *Glu-B1-1* and *Glu-B1-2* with a frequency of 3 in 3,450 {1117}. The gene order, relative to the centromere, has not been

ascertained.
The subunit nomenclature used is that devised in {1116}; however, an alternative system based upon molecular weight was proposed in {1068}. A system of naming the *Glu-A1-1, Glu-A1-2*, *Glu-B1-1* and *Glu-B1-2* alleles in *T. turgidum* var. *dicoccoides* is given in {796}.

In {00116}, a comparison between spelt wheats (*T. spelta*) and bread wheat was carried out for the glutenins using a nomenclature system described in {00117}.
The *Glu-1* loci may be recognised by the DNA probe pTag1290 {1471} and probe pwhe1(Dy10) {030}. Individual *Glu-1-1* loci on 1A, 1B and 1D and the *Glu-1-2* loci may be recognised by specific primers {263}.
In {00105}, the evolution of the high molecular weight glutenin loci of the A, B, D and G genomes of wheat was explored; 30 partial allele sequences were compared, designated by Greek letters (alpha, beta, gamma, etc.) (5 of which were cited as Schlumbaum, pers. comm.; the remaining 25 were deposited as GenBank, accession nos. X98583-X98592, X98711-X98715 and Y12401-Y12410). These partial alleles derive from all six *Glu-1-1* and *Glu-1-2* loci in current-day samples taken from seven species of wheat, as well as from DNA extracted from charred grain of two samples from archaeological excavations, dated 3000 and 5000 years old, respectively.

Following the first listing which considers the *Glu-1* set for hexaploid wheat as a single locus, there is a provisional listing based on x- and y- type glutenins. These are not referenced.

The importance of the HMW glutenin subunits for bread-making quality was first noted from observations in wheat cultivars of related pedigree on the effects of the presence of subunit 1 encoded by *Glu-A1a* {0197}, effects that have repeatedly been confirmed since (for example {0198,0199,01100}).

A nomenclature system for prolamin banding patterns of triticale was proposed in {03139}.
Extensive allelic variation in triticale at *Glu-A1, Glu-B1, Glu-R1* and *Gli-R2* loci was reported in {03121}.

Glu-A1{780,1125}. [*Glt-A1*{420},*Glt-A2*{420},*Glu 1A*{1415}]. 1A{780}.1AL{781,1125}. **s:** CS*/Hope 1A{1125}. **v:** CS{780,781}; various{420}.
Primers were designated that enabled Ax2* to be distinguished from Ax1 or Ax-null {10641}.
Glu-A1a{1116}. 1{1116}. **v:** Hope.
Glu-A1b{1116}. 2*{1116}. **v:** Bezostaya 1.
Glu-A1c{1116}. Null allele{1116}. **v:** CS.
Glu-A1d{1535}. **v:** V74, Spain{1115}.
Glu-A1e{1535}. **v:** 132c, Poland{1115}.
Glu-A1f{1535}. **v:** 112-29, Sudan{1115}.
Glu-A1g{1535}. **v:** Landrace 1600.
Glu-A1h{1527}. [*GLU-A1-I*{1527}]. **tv:** PI 94683, USSR, *T. dicoccum*.
Glu-A1i{1527}. [*GLU-A1-II*{1527}]. **tv:** CI 12213, India, *T. dicoccum*; Lambro{1523}.
Glu-A1j{1527}. [*GLU-A1-III*{1527}]. 1'{125}. **tv:** PI 352359, Germany, *T. dicoccum*.
Glu-A1k{478}. 26{478}. **v:** BT-2288{478}.
Glu-A1l{847}. **tv:** Chinook, Canada.
Glu-A1m{1069}. **tv:** Nugget Biotype 1, Canada, *T. durum*.
Glu-A1n{1526}. [*Glu A1-IV*{1526},*Glu-A1m*{959}]. 1'{125}. **tv:** Corado, Portugal{1526}.
Glu-A1o{1526,125}. [*Glu A1-V*{1526,125},*Glu-A1n*{959}]. 2**{125}. **tv:** Aric 581/1{125}; PI 61189{1525}; USSR.
Glu-A1p{1146}. 3*{1146}. **v:** David 1.
Glu-A1q{125}. [*Glu A1VI*{125}]. 2***{125}. **tv:** Melianopus 1528.

Glu-A1r{1232}. 39+40{1232}. **i:** *T. thaoudar* IPSR 1020006/6*Sicco.

Glu-A1s{1231}. 41+42{1231}. **i:** *T. thaoudar* G3152/6*Sicco.

Glu-A1t{602}. 21*{602}. **v:** W29323, W3879, W31169.

Glu-A1u{02106}. 2^{*B}{02106}. **v:** Bankuti 1201.

The allele designated *Glu-A1u* and *Glu-A1-1u* in the appropriate list below encodes a high molecular weight glutenin subunit (denominated 2^{*B}) that is identical to subunit 2* apart from one amino acid difference involving the exchange of serine for cysteine (which itself is due to a C to G point mutation at the 1181 bp point of the coding region of 2*). The authors of {02106} suggest that the additional cysteine residue facilitates the formation of further disulphide bonds (cf. the 1Dx5 subunit) which might lead to an improvement in gluten quality characters.

Glu-A1v{10327}. 2.1* {10327} **v:** Grado{10327}; KU-1026{10327}; KU-1086{10327}; KU-1094{10327}; KU-1139{10327}.

Glu-A1w{10327}. 2' {10327} **v:** TRI14165/91{10327}.

Glu-A1x{10327}. 2'{10327}. **v:** TRI14165/91{10327}.

Glu-A1y{10535}. [*2″*{10535}]. **v:** 211.12014{10535}.

There is a possibility that *Glu-A1* alleles *i, j* {1527} and *k* {478} correspond to alleles *d, e, f* or *g* {1535} that were published shortly earlier. *Glu-A1m* [{1526}] was changed to *n*, because the *m* allele in {1069} has precedence. Allele *n* [{1526}] was changed to *o*. An earlier reference to an allele designated *Glu-A1d* {1411} was withdrawn {1114}. There appears to be a minor band associated with subunit 2 encoded by *Glu-A1b* {1516}; this may be the same as a band named A5 in {420}.

Six combinations involving 5 HMW subunits [1A (u-z)] are listed in {420}, from a study of 109 genotypes including representatives of botanical varieties. A number of alleles in *T. turgidum* var. *dicoccoides* populations, 12 at *Glu-A1-1* and 3 at *Glu-A1-2*, were described in {798}. In a further study using different germplasm of this species {205}, 14 alleles at *Glu-A1* were observed, including 12 not previously found; the 15 alleles included up to 15 alleles at *Glu-A1-1* (with up to 10 not previously observed), and 5 alleles at *Glu-A1-2* (with 4 not previously observed) (numbers take the null allele into account). The uncertainty in numbers is due to the very similar electrophoretic mobilities of some of the subunits compared with others observed either in this study or previously. In a study including emmers (*T. dicoccum*) {00115}, new subunits named 1$^+$ and 2$^-$ were found in accessions MG4378/1 and MG5380/1, respectively, and provisionally assigned to *Glu-A1*. Until confirmed, they are not included in the *Glu-A1* list.

Glu-A1z{10805}. [*Glu-A1*^{m}*a*{10805}]. **dv:** PI 191146, *T. monococcum* ssp. *monococcum*{10805}.

Glu-A1aa{10805}. [*Glu-A1*^{m}*b*{10805}]. **dv:** PI 190946, *T. monococcum* L. ssp. *monococcum*{10805}.

Glu-A1ab{10805}. [*Glu-A1*^{m}*c* {10805}]. **dv:** PI 191098, *T. monococcum* ssp. *monococcum*{10805}.

Glu-A1ac{10806}. [*Glu-A*^{u}*1-I* {10806}]. **dv:** PI 428319{10806}.

Glu-A1ad{10806}. [*Glu-A*^{u}*1-II*{10806}]. **dv:** PI 428232{10806}.

Glu-A1ae{10806}. [*Glu-A*^{u}*1-III*{10806}]. **dv:** PI 428240{10806}.

Glu-A1af{10806}. [*Glu-A*^{u}*1-IV*{10806}]. **dv:** PI 428335{10806}.

Glu-A1ag{10806}. [*Glu-A*^{u}*1-V*{10806}]. **dv:** PI 538741{10806}.

Glu-A1ah{10806}. [*Glu-A*^{u}*1-VI*{10806}]. **dv:** PI 428230{10806}.

Glu-A1ai{10806}. [*Glu-A*^{u}*1-VII*{10806}]. **dv:** PI 428253{10806}.

Glu-A1aj{10806}. [*Glu-A*^{u}*1-VIII*{10806}]. **dv:** PI 427328{10806}.

Glu-A1ak{10806}. [*Glu-A*^{u}*1-IX*{10806}]. **dv:** PI 428327{10806}.

Glu-A1al{10806}. [*Glu-A*^{u}*1-X*{10806}]. **dv:** PI 428256{10806}.

Glu-A1am{10806}. [*Glu-A*^{u}*1-XI*{10806}]. **dv:** PI 428224{10806}.

Glu-A1an{10806}. [*Glu-A*^{u}*1-XII*{10806}]. **dv:** PI 428228{10806}.

Glu-A1ao{10806}. [*Glu-A*^{u}*1-XIII*{10806}]. **dv:** PI 538724{10806}.

Glu-A1ap{10806}. [*Glu-A*^{u}*1-XIV*{10806}]. **dv:** TRI 6734{10806}.

Glu-A1aq{10806}. [*Glu-A*^{u}*1-XV*{10806}]. **dv:** TRI 11494{10806}.

Glu-A1ar{10806}. [*Glu-A*^{u}*1-XVI*{10806}]. **dv:** TRI 11495{10806}.

Glu-A1as{10806}. [*Glu-A*^{u}*1-XVII*{10806}]. **dv:** PI 428217{10806}.

Glu-A1at{10806}. [*Glu-A*^{u}*3-XVIII* {10806}]. **dv:** PI 428225{10806}.

Glu-A1au{10806}. [*Glu-A*^{u}*3-XIX*{10806}]. **dv:** PI 538733{10806}.

Glu-A1av{10806}. [*Glu-A*^{u}*3-XX*{10806}]. **dv:** PI 428196{10806}.

Glu-A1aw{10806}. [*Glu-A*^{u}*3-XXI*{10806}]. **dv:** PI 538724{10806}.

Glu-A1ax{10806}. [*Glu-A*^{u}*3-XXII*{10806}]. **dv:** PI 428191{10806}.

Glu-A1ay{10806}. [*Glu-A*^{u}*3-XXIII* {10806}]. **dv:** TRI 6734{10806}.

Glu-A1az{10806}. [*Glu-A*^{u}*3-XXIV* {10806}]. **dv:** TRI 11496{10806}.

Glu-B1{107},{1125}. [*Glt-B1*{420},*Glt-B2*{420},*Glt-B3*{420},*Glu 1B*{1415}]. 1BL{107,780,1125}. **v:** CS.

Glu-B1a{1116}. 7{1116}. **v:** Flinor.

Glu-B1b{1116}. 7+8{1116}. **v:** CS.

Glu-B1c{1116}. 7+9{1116}. **v:** Bezostaya 1.

Glu-B1d{1116}. 6+8{1116}. **v:** Hope.

Glu-B1e{1116}. 20{1116}.20x+20y{03133}. **v:** Federation.

Glu-B1f{1116}. 13+16{1116}. **v:** Lancota (rare).

Glu-B1g{1116}. 13+19{1116}. **v:** NS 335 (rare).

Glu-B1h{1116}. 14+15{1116}. **v:** Sappo (rare).

Glu-B1i{1116}. 17+18{1116}. **v:** Gabo.

Glu-B1j{1116}. 21{1116}.21x+21y{03116}. **v:** Dunav (rare); Foison{03116}.

Glu-B1k{1116}. 22{1116}. **v:** Serbian (rare).

Glu-B1l{778}. 23+24{778}. **v:** Spica D.

Glu-B1m{1527}. [*GLU-B1-I*{1527}]. **tv:** PI 94640, Iran, *T. dicoccum.*

Glu-B1n{1527}. [*GLU-B1-II*{1527}]. **tv:** PI 355505, Germany, *T. dicoccum.*

Glu-B1o{1527}. [*GLU-B1-III*{1527}]. **tv:** PI 352354, Ethiopia, *T. dicoccum.*

Glu-B1p{1527}. [*GLU-B1-IV*{1527}]. 23+18{125}. **tv:** Dritto{1523}; Ethiopia, PI 94655, *T. dicoccum*{1527}.

Glu-B1q{1527}. [*GLU-B1-V*{1527}]. **tv:** PI 94633, Morocco, *T. dicoccum.*

Glu-B1r{1527}. [*GLU-B1-VI*{1527}]. 19{125}. **tv:** PI 946669, Bulgaria, *T. dicoccum*{1527}; Lambro{1523}.

Glu-B1s{478}. 7+11{478}. **v:** BT-2288.

Glu-B1t{847}. **v:** Supreza, Canada.

Glu-B1u{1069}. 7*+8{1146}. **v:** Owens{1069}; Fiorello{1146}.

Glu-B1v{1069}. **v:** Mondor.

Glu-B1w{1069}. 6*+8*{1146}. **v:** Dawbull{1069}; Sieve{1146}.

Glu-B1x{1526}. [*Glu-B1-VII*{1526},*Glu-B1t*{959}]. **tv:** Canoco de Grao Escuro, Portugal, *T. turgidum.*

Glu-B1y{1526}. [*Glu-B1-VIII*{1526},*Glu-B1u*{959}]. **tv:** Tremez Mollez, Portugal, *T. durum.*

Glu-B1z{1524}. [*Glu-B1-IX*{1524},*Glu-B1v*{959}]. 7+15{125}. **tv:** Roccia, Italy, *T. durum* {1523,125}.

Glu-B1aa{1524}. [*Glu-B1-X*{1524},*Glu-B1w*{959}]. **tv:** Quaduro, Italy, *T. durum.*

Glu-B1ab{1523}. [*Glu-B1-XI*{1523},*Glu-B1x*{959}]. **tv:** Athena, Italy, *T. durum.*

Glu-B1ac{125}. [*Glu B1XIII*{125}]. 6+16{125}. **tv:** Espa l8914, *T. durum.*

Glu-B1ad{125}. [*Glu B1XIV*{125}]. 23+22{125}. **tv:** Greece 20, *T. durum.*

Glu-B1ae{1146}. 18*{1146}. **v:** David.

Glu-B1af{1146}. 26+27{1146}. **v:** Cologna 1.

Glu-B1ag{1146}. 28+29{1146}. **v:** Forlani.

Glu-B1ah{782}. null allele{782}. **v:** Olympic mutant.

Glu-B1ai{714}. 7'{714}. **v:** Adonis.

Glu-B1aj{759}. 8{759}. **v:** AUS 14444, Afghanistan.

Glu-B1ak{899}. $7^{*}+8^{*}${899}. **v:** Norstar.

Glu-B1al{899}. $7^{OE}+7^{OE}+8^{*}${899}. **v:** Benkuti 1201{10196, 10197}; Glenlea{899}; Klein Universal II{10196}; Tezanos Pintos Precoz {10196}; Tobari 66{10196}.

Other genotypes are listed in {10196}.

Many of the cultivars carrying the over-expressed subunit 7 encoded by *Glu-B1al* show %UPP values that transcend the normal range observed for cultivars that lack this subunit {10089}, which presumably is associated in some way with its unusually high amount in the grain. The underlying cause of the increased amount may be due to an increased transcriptional rate compared to other alleles, for which a known difference in promoter sequence compared to other alleles expressing normal levels of this subunit {10090} may be responsible.

However, there is evidence that over-expression is due to duplication of subunit 7 {10196}. In regard to subunit 8^{*}, evidence was presented to indicate that in Glenlea, one of the standard cultivars for the allele, this subunit is the same as subunit 8 {10808}.

Glu-B1am{1229}. 18{1229}. **v:** Royo.

Glu-B1an{1229}. 6{1229}. **v:** BG-2013.

Glu-B1ao{1229}. 7+16{1229}. **v:** BG-3545.

Glu-B1ap{1229}. 30+31{1229}. **v:** Marinar.

Glu-B1aq{1229}. 32+33{1229}. **v:** BG-1943.

Glu-B1ar{1229}. 34+35{1229}. **v:** Jeja Almendros.

Glu-B1as{1229}. 13{1229}. **v:** PI 348435.

Glu-B1at{1229}. 13+18{1229}. **v:** PI 348449.

Glu-B1au{1032}. 37{1032}. **v:** Shedraya Polesja.

Glu-B1av{03116}. [*Glu-B1r*{03116}]. 7-18{03116}. **v:** Triticor hexaploid *triticale*{03116}.

Glu-B1aw{03116}. [*Glu-B1s*{03116}]. 6.8-20y{03116}. **v:** Carnac hexaploid *triticale*{03116}.

Glu-B1ax{03137}. [*Glu-B1-XV*{03137}]. XV{03137}. **tv:** PI-190922, BG-012302 emmers{03137}.

Glu-B1ay{03137}. [*Glu-B1-XVI*{03137}]. XVI{03137}. **tv:** PI 277681 emmer{03137}.

Glu-B1az{03137}. [*Glu-B1-XVII*{03137}]. XVII{03137}. **tv:** PI 348620 emmer{03137}.

Glu-B1ba{03122}. [*Glu-B1-XVIII*{03122}]. $13^{*}+16${03122}. **v:** PI 348767 spelt {03122}.

Glu-B1bb{03122}. [*Glu-B1-XLX*{03122}]. 6+18'{03122}. **v:** PI 348631 spelt{03122}.

Glu-B1bc{03138}. 6+17{03138}. **v:** ICDW 20975{03138}.

Glu-B1bd{03140}. 20+8{03140}. **v:** Abadja{03140}.

Glu-B1be{10186}. **tv:** *T. dicoccoides* Israel-A{10186}.

Glu-B1bf{10186}. **tv:** *T. dicoccoides* PI 481521{10186}.

Glu-B1bg{10186}. **tv:** *T. dicoccoides* PI 478742{10186}.

Glu-B1bh{10327}. 13+22{10327}. **v:** Grado{10327}; KU-1026{10327}; KU-1086{10327}; KU-1094{10327}; KU-1139{10327}.

Glu-B1bi{10327}. 13+22.1{10327}. **v:** KU-1135{10327}.

Glu-B1bj{10327}. 14*+15*{10327}. **v:** TRI11553/92{10327}.

Glu-B1bk{10327}. [*Glu-B1be*{10327}]. 6.1+22.1{10327}. **v:** Hercule{10327}; Rouguin{10327}; Schwabenkorn{10327}; SP3{10327}; Steiners Roter Tiroler{10327}.

Glu-B1bl{10327}. [*Glu-B1bf*{10327}]. 6.1{10327}. **v:** KU-3418{10327}; KU-3446{10327}; TRI4613/75{10327}.

Glu-B1bm{10327}. [*Glu-B1bg*{10327}]. 13*+19*{10327}. **v:** KU-3410{10327}; Renval{10327}; Rechenbergs Fruher Dinkel{10327}; Schlegel{10327}; SP1{10327}; TRI9885/74{10327}; Zeiners WeiSer{10327}.

Glu-B1bn{10425}. 7+19{10425}. **v:** Triticales: Lasko, Dagno, Tewo, Vision, Dato{10425}.

Glu-B1bo{10425}. 7+26{10425}. **v:** Triticales: Presto, Modus{10425}.
The number 26 was also used to designate a subunit encoded by *Glu-A1k* and *Glu-A1-1k*.

The alleles formerly designated *t* to *x* in {959} were renamed *x* to *ab* because allele *t* in {847} and alleles *u, v* and *w* in {1069} had precedence. Subunit 8 of *Glu-B1b* (7+8) is more acidic in isoelectric focusing than subunit 8 of *Glu-B1d* (6+8) {555}. Variation in the mobility of subunits designated 7 has been observed {1118}, which accords with more recent observations {714,1069}. The subunit encoded by *Glu-B1v* {1069} has the same mobility as subunit 7 of *Glu-B1c* (7+9); it could be the same subunit as 7' encoded by *Glu-B1ai* [{714}].

Variation in the staining intensity of subunit 7 in different lines was observed {1069}; a duplication of the gene encoding subunit 7 probably occurred in cultivar 'Red River 68', as evidenced by increased intensity of the subunit in SDS-PAGE and by approximately doubled intensity of restriction fragments carrying the gene in Southern blotting {9989}. Possible low gene expression at *Glu-B1* was noted for *Glu-B1w*, where subunits 6^{*}+8^{*} stain very faintly {1146}.

One of the *Glu-B1af* subunits was numbered 26 in {1146}; 26 was previously used to number the subunit encoded by *Glu-A1k* {478}. Subunit 28 of *Glu-B1ag* (28+29) {1146} is referred to as subunit 19^{*} in {1068}. Subunit 23 of *Glu-B1p* {23+18} and *Glu-B1ad* (23+22) {125} may not be the same subunit as that numbered 23 of *Glu-B1l* {23+24} {778}. *Glu-Blz* carried by Roccia was numbered (7+15) and named *Glu-B1-XII* in {125}; however, the earlier name, *Glu-B1-IX* {1523}, has precedence; also, {1523} states that the *Glu-B1-IX* subunit of faster mobility is slightly slower than subunit 15. Subunit 11 of *Glu-B1s* {7+11} was so numbered in {478} because its mobility is the same as one of the subunits encoded by a *Glu-D1* allele (2+11) described in {755}.

Eight alleles at *Glu-B1-1* and 10 alleles at *Glu-B1-2* in *T. turgidum* var. *dicoccoides* populations were described in {798}. In a further study using different germplasm of this species {205}, 19 alleles at *Glu-B1* were observed, including 15 not previously observed; the 19 alleles included 11 alleles at *Glu-B1-1* and 14 alleles (including the null allele) at *Glu-B1-2*, although, as the authors pointed out, it was not conclusively clear how many of these alleles were distinct from each other, or from others previously observed.

In a study including emmer wheats (*T. dicoccon*) {00115}, new subunits named 7^{+} (in accessions MG5400/5 and MG30835/1), 8^{-} (in accessions MG5400/5, MG30835/1, MG5333/1 and MG5507) and 13^{-} (in accession MG5282/2) were found and provisionally assigned to *Glu-B1*. Until confirmed, they are not included in the *Glu-B1* list.

Although alleles *Glu-B1i* enconding subunits 17+18, and *Glu-B1bc* encoding subunit 6+17, apparently share a common subunit (Ax17 and By17, respectively) it is not clear that this is in fact true.

Primers were designed to distinguish subunit By8 from By8*, for distinguishing subunit By9-containing alleles from non-By9 alleles, and for diagnosing the presence of *Glu-B1f*.

Glu-B1bp{10643}. 7^{**}+8 {10643}. **v:** XM1368-2{10643}; XM1404-2{10643}.

Glu-B1bq{10643}. 7+8^{**} {10643}.

Glu-B1br{10807}. 7.1+7.2+8^{*}{10807}. **v:** H45{10807}.

Glu-B1bs{10807}. 7.3+7^{OE}+8^{*}{10807}. **v:** VQ0437{10807}.

Glu-B1bt{10809}. 17'+18'{10809}. **tv:** TGR-214{10809}.

Glu-B1bu{10809}. 17'+18^{*}{10809}. **tv:** TGR-2246{10809}.

Glu-B1bv{10809}. 13^{**}+8^{*}{10809}. **tv:** TGR-003{10809}.

Glu-B1bw{10809}. 8'{10809}. **tv:** TGR-244{10809}.

Glu-B1bx{10810}. 7+17{10810}. **v:** CWI-59797, *T. aestivum* var. *ferrugineum*{10810}.

Glu-B1by{10808}. 7b*+8{10808}. **v:** Eshimashinriki{10808}.

Glu-B1bz{10808}. 7^{OE}{10808}. **v:** Attila{10808}; Darius{10808}; Cappelle-Desprez{10808}; Festin{10808}; Petrel{10808}.

Glu-B1ca{10808}. 6+8b*{10808}. **v:** Appolo{10808}; Brimstone{10808}; Clement{10808}; Nidera Baguette 10{10808}; Ruso{10808}; Pepital{10808}; Thesee{10808}.

Glu-B1cb{10808}. 7^{OE}+8{10808}. **v:** ACA 303{10808}; Courtot{10808}; Demai 3{10808}; Shinchunaga{10808}.

Glu-B1cc{10808}. 7^{OE}+8a*{10808}. **v:** Klein Jabal 1{10808}; Pioneer{10808}; ProINTA{10808}; Redemon{10808}.

Glu-B1cd{10808}. 7^{OE}+8b*{10808}. **v:** ACA 601{10808}.

Glu-B1ce{10808}. 7+8a*{10808}. **v:** Jing 411{10808}; Tasman{10808}.

Glu-D1{1100,1125}. [*Glt-D1*{420},*Glt-D2*{420},*Glu 1D*{1415}].

1DL{107,150,780,1100,1125}. **v:** CS.

Primers were designated that enabled Dx2 to be distinguished from Dx5 and Dy10 from Dy12 {10641}.

Glu-D1a{1116}. 2+12{1116}. **v:** CS.

Glu-D1b{1116}. 3+12{1116}. **v:** Hobbit.

Glu-D1c{1116}. 4+12{1116}. **v:** Champlein.

Glu-D1d{1116}. 5+10{1116}. **v:** Hope.

Glu-D1e{1116}. 2+10{1116}. **v:** Flinor (rare).

Glu-D1f{1116}. 2.2+12{1116}. **v:** Danchi (rare).

Glu-D1f is present at high frequencies in wheats of southern Japan. Its presence may be associated with white salted noodle (Udon) quality {10573}.

Glu-D1g{478}. 5+9{478}. **v:** BT-2288.

Glu-D1h{1145}. 5+12{1145}. **v:** Fiorello, Italy.

Note that the cultivar Fiorello is given as a standard for *Glu-D1h* encoding subunits 5+12 and for *Glu-D1w* encoding subunits 5*+10. An attempt to resolve this apparent conflict will be made in a future update.

Glu-D1i{107}. null{107}. **v:** Nap Hal, Nepal.

Glu-D1j{1146}. 2+12*{1146}. **v:** Tudest.

Glu-D1k{421}. 2{421}. **s:** CS/Timstein 1D.

Glu-D1l{759}. 12{759}. **v:** AUS 10037, Afghanistan.

Glu-D1m{759}. 10{759}. **v:** AUS 13673, Afghanistan.

Glu-D1n{759}. 2.1+10{759}. **v:** AUS 14653, Afghanistan.

Glu-D1o{755}. 2.1+13{755}. **v:** AUS 14519, *T. macha*.

Glu-D1p{1233}. 36{1233}. **i:** Iranian landrace accession 3048/5* Sicco.

Glu-D1q{124}. 2+11{124}. **v:** Flinor.

Glu-D1r{1229}. 2.3+12{1229}. **v:** PI 348465.

Glu-D1s{1032}. 38{1032}. **v:** Leningradka.

Glu-D1t{668}. 43+44{668}. **i:** *Ae. tauschii* accession TA2450/2*.

Glu-D1u{836}. 2+10'{836}. **v:** Coker 68-15.

Glu-D1v{755}. 2.1+10.1{755}. **dv:** *Ae. tauschii.*

Glu-D1w{03124}. 5*+10{03124}. **v:** Fiorello{03124}.

Note that the cultivar Fiorello is given as a standard for *Glu-D1h* encoding subunits 5+12 and for *Glu-D1w* encoding subunits 5*+10. An attempt to resolve this apparent conflict will be made in a future update.

Glu-D1x{755}. 2+T2{755}.2^t+12.2^t{03124}. **dv:** *Ae. tauschii.*

Glu-D1y{755}. 3+T2{755}.3^t+12.2^t{03124}. **dv:** *Ae. tauschii.*

Glu-D1z{755}. 3+10{755}. **dv:** *Ae. tauschii.*

Glu-D1aa{755}. 3+10.3{755}. **dv:** *Ae. tauschii.*

Glu-D1ab{755}. 4.1+10{755}. **dv:** *Ae. tauschii.*

Glu-D1ac{755}. 4+10{755}. **dv:** *Ae. tauschii.*

Glu-D1ad{755}. 5.1+10.2{755}. **dv:** *Ae. tauschii.*

Glu-D1ae{1578}. 2.1+T2{1578}.2.1^{t}+12.2^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1ag{1578}. 1.5+T2{1578}.1.5^{t}+12.2^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1ah{1578}. 1.5+10{1578}. **dv:** *Ae. tauschii.*

Glu-D1ai{1578}. 2.1+10.5{1578}. **dv:** *Ae. tauschii.*

Glu-D1aj{1578}. 1.5+12{1578}. **dv:** *Ae. tauschii.*

Glu-D1ak{1578}. 3+10.5{1578}. **dv:** *Ae. tauschii.*

Glu-D1al{02107}. 2.2^{*}{02107}. **v:** MG315.

Glu-D1am{03122}. [*Glu-D1-I*{03122}]. 2+12'{03122}. **v:** PI 348495 spelt {03122}.

Glu-D1an{03122}. [*Glu-D1-II*{03122}]. 2+12^{*}{03122}. **v:** PI 348672 spelt {03122}.

Glu-D1ao{03122}. [*Glu-D1-III*{03122}]. 2.4+12{03122}. **v:** PI 348473 spelt {03122}.

Glu-D1ap{03122}. [*Glu-D1-IV*{03122}]. 2.5+12{03122}. **v:** PI 348572 spelt {03122}.

Glu-D1aq{03124}. 1.5^{t}+10.1^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1ar{03124}. 2^{t}+10.1^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1as{03124}. 1.5^{t}+10.2^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1at{03124}. 3^{t}+10.1^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1au{03124}. 2.1^{t}+10.2^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1av{03124}. 2^{t}+12.3^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1aw{03124}. 1^{t}+10^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1ax{03124}. 1^{t}+12^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1ay{03124}. 1^{t}+10.1^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1az{03124}. 4^{t}+12.2^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1ba{03124}. 1^{t}+12.3^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bb{03124}. 1.5^{t}+11^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bc{03124}. 1.5^{t}+10.3^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bd{03124}. 1^{t}+11^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1be{03124}. 2.1^{t}+12.4^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bf{03124}. 2^{t}+12.1^{t}{03124}. **dv:** *Ae. tauschii*{03124}.

Glu-D1bg{03124}. 3^{t}+10.2^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bh{03124}. 4^{t}+10.1^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bi{03124}. 4^{t}+10.2^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bj{03124}. 5^{t}+11^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bk{03124}. 5^{t}+10.1^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bl{03124}. 5^{t}+12.2^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1bm{03124}. 5^{*t}+null{03124}. **dv:** *Ae. tauschii.*

Glu-D1bn{03124}. 5^{*t}+12{03124}. **dv:** *Ae. tauschii.*

Glu-D1bo{10091}. 5'+12{10091}. **v:** W958{10091}.

This putative new allele encodes two subunits that have very similar electrophoretic mobilities compared to subunits 5+12 encoded by *Glu-D1h*, but analysis using the specific PCR primers for Dx5 described in {10092} and {10093} shows that the x-type subunit of *Glu-D1bo*, provisionally denominated 5' {10091}, does not appear to be the same protein as subunit 5 {10091}. Definitive evidence awaits sequencing information (See note to allele *Glu-D1-1s*).

Glu-D1k {421} appears to have arisen as the result of a deficiency of subunit 12 from *Glu-D1a* (2+12); subunits 2 and 12 are referred to as D1 and D5 in {421}. One of the *Glu-D1o* subunits has been numbered 13 in {755}; 13 was previously used to number a subunit encoded by *Glu-B1f* (13+16) and *Glu-B1g* (13+19) {1116}. Subunit 9 of *Glu-D1g* (5+9) was so numbered in {478} because its mobility is the same as one of the subunits encoded by *Glu-B1c* (7+9).

Glu-D1bp{10327}. 2.1'+12{10327}. **v:** KU-1034{10327}.

Glu-D1bq{10304}. [*Glu-D1bp(t)*{10304}]. 2.6+12{10304}. **v:** Baidongmai{10304}; Hongdongmai{10304}; Hongkedongmai{10304}; Jinbaojin{10304}.

The complete sequence of this subunit was determined {10319}.

Glu-D1br{10426}. 5*t+10.1t{10426}. **tv:** *Ae. tauschii* TD81{10426}.

Subunit 10.1t possesses a mobility slightly lower than subunit 10 in SDS-PAGE and its deduced amino acid sequence is similar to subunit 12 (8 amino acid differences) {10426}; the authors used the complete coding sequence to make phylogenetic comparisons with 19 other subunits including both x-type and y-type subunits and concluded that *Glu-1* gene duplication event probably occurred about 16.83 million years ago.

Five combinations involving 6 HMW subunits [1D (p-t)] are listed in {420}. Eleven additional *Glu-D1* alleles in *T. tauschii* were described {755}.

Seven transfers of *Glu-D1a* and 10 of *Glu-D1d* (5+10) from chromosome 1D to chromosome 1A in triticale were described {846}.

The subunit 2.2* encoded by *Glu-D1al* and *Glu-D1-1m* in the appropriate list below has an unusually high Mr. Comparison of its N-terminal sequence and amino acid composition with those of subunit 2 (encoded by *Glu-D1-1a*) indicated that its greater Mr could be due to the presence of a larger central repetitive domain, although further evidence suggested that this does not affect the conformational properties of the subunit {02107}. The alleles originally designated *Glu-D1w* (encoding 'subunits' 2 (or 2^t denoting its origin in the *Ae. tauschii* genome) +T1+T2), *Glu-D1af* (encoding 3 (or 3^t)+T1+T2) and *Glu-D1ag* (encoding 1.5 (or1.5^t)+T1+T2) share the component T1 that was originally classified as a HMW glutenin. However, it has since been shown {02108} that this protein is soluble in aqueous ethanol, casting doubt upon this classification. More recently, it was shown {02109}, from one and two dimensional gel electrophoresis based upon SDS-PAGE and A-PAGE, and from N-terminal sequencing, that this protein is an omega-gliadin of unusually low electrophoretic mobility in SDS-PAGE, encoded by a locus located on the short arm of chromosome 1D, though distant (13.18 cM) from the principle gliadin-encoding locus on 1D, *Gli-D1*, and 40.20 cM from the high molecular weight encoding locus, *Glu-D1*. The authors named the locus *Gli-DT1* (see Gliadins). Reference to T1 was consequently removed from the *Glu-D1* list. As a consequence of this finding, allele *Glu-D1w* was reused for a distinct allele, and *Glu-D1af* was omitted and will be reused for a future allele, since the combinations of subunits that these alleles originally represented are no longer unique.

In {03124}, null alleles were observed for both *Glu-D1-1* and *Glu-D1-2*,which, naturally, are not necessarily the same as those previously reported for this locus, meaning that composite alleles involving them in this study and corresponding to combinations apparently already listed in the Catalogue, may, in fact, represent novel alleles. It is also found that certain subunits of apparently identical relative mobility in SDS-PAGE showed different surface hydrophobocities in RP-HPLC; and the reverse situation was also observed (the same hydrophobicity, but different electrophoretic mobilities).

It was shown {03126} that the relatively small size of a y-type HMW glutenin subunit, named 12.4^t (encoded by *Glu-D1-1t* {03124} - see below) and carried by accession CPI110750 of *Ae. tauschii*, is due to the deletion of blocks of repetitive motifs, amounting to approximately 200 amino acids, probably caused by unequal crossing-over.

<u>Alleles and subunits at *Glu-A1-1* and *Glu-A1-2*: </u>*Glu-A1-1* encodes X-type glutenins and *Glu-A1-2* encodes y-type glutenins.

Glu-D1bs{10642}. 1.6^t+12.3^t {10642}. **dv:** *Ae. tauschii* TD16{10642}.

Glu-D1bt{10568}. 2.1^t+12^t {10568}. **v:** Syn 396{10568}.

Glu-D1bu{10810}. 2'+12{10810}. **v:** CWI-64806, *T. aestivum* var. *aestivum*{10810}.

Glu-D1bv{10810}. 2"+10{10810}. **v:** CWI-65297, *T. aestivum* var. *erythroleucon*{10810}.

Glu-D1bw{10810}. 2"+12{10810}. **v:** CWI-60509, *T. aestivum* var. *graecum*{10810}.

Glu-A1-1.

Glu-A1-1a. Null. **v:** CS.

Glu-A1-1b. 1. **v:** Hope.

Glu-A1-1c. 2^{*}. **v:** Bezostaya 1.

A PCR marker specific for the *Glu-A1-1c* (Ax2^{*}) allele was developed in {0147}.

Glu-A1-1d. **v:** V74, Spain.

Glu-A1-1e. **v:** 132c, Poland.

Glu-A1-1f. **v:** 112-29, Sudan.

Glu-A1-1g. **v:** Landrace 1600.

Glu-A1-1h. **tv:** PI 94683, USSR, *T. dicoccum*.

Glu-A1-1i. **tv:** CI 12213, India, *T. dicoccum*.

Glu-A1-1j. 1'. **tv:** PI 352359, Germany, *T. dicoccum*; Lambro.

Glu-A1-1k. 26. **v:** BT-2288.

Glu-A1-1l. **tv:** Chinook, Canada.

Glu-A1-1m. **tv:** Nugget Biotype 1, Canada.

Glu-A1-1n. 1". **tv:** Corado, Portugal.

Glu-A1-1o. 2^{**}. **tv:** PI 61189, USSR, Aric 581/1.

Glu-A1-1p. 3^{*}. **v:** David 1.

Glu-A1-1q. 2^{***}. **tv:** Melianopus 1528.

Glu-A1-1r. 39. **i:** *T. thaoudar* IPSR 1020006/6^{*} Sicco.

Glu-A1-1s. 41. **i:** *T. thaoudar* G3152/6^{*}Sicco.

Glu-A1-1t{602}. 21^{*}{602}. **v:** W29323, W 3879, W 31169.

Glu-A1-1t is a provisional designation; definitive evidence that subunit 21^{*}, which has a mobility similar to that of subunit 21, is a 'x-type' and not a 'y-type' protein has not been obtained.

Glu-A1-1u{02106}. 2^{*B}{02106}. **v:** Bankuti 1201.

Glu-A1-1v{10327}. 2.1*{10327}. **v:** Grado{10327}; KU-1026{10327}; KU-1086{10327}; KU-1094{10327}; KU-1139{10327}.

Glu-A1-1w{10327}. 2'{10327}. **v:** TRI14165/91{10327}.

Glu-A1-1x{10535}. 2"{10535}. **v:** 211.12014{10535}.

Glu-A1-2.

Glu-A1-2a. Null. **v:** CS.

Glu-A1-2b. 40. **i:** *T. thaoudar* IPSR1020006/6^{*} Sicco.

Glu-A1-2c. 42. **i:** *T. thaoudar* G3152/6^{*}Sicco.

Glu-B1-1.

Glu-B1-1a. 7. **v:** CS.

A PCR marker (2373 bp) for the *Glu-B1-1a* (Bx7) allele was developed in {0145}.

Glu-B1-1b. 7,7^{*}. **v:** Flinor, Bezostaya 1, Owens, Norstar.

Glu-B1-1c. 7'. **v:** Adonis.

Glu-B1-1d. 6. **v:** Hope.

Glu-B1-1e. 20. **v:** Federation.

Glu-B1-1f. 13. **v:** Lancota.

Glu-B1-1g. 14. **v:** Sappo.

Glu-B1-1h. 17. **v:** Gabo.

Glu-B1-1i. 21.21x{03116}. **v:** Dunav; Foison{03116}.

Glu-B1-1j. 23. **v:** Spica D.

Glu-B1-1k. **tv:** PI 94640, Iran, *T. dicoccum*.

Glu-B1-1l. **tv:** PI 355505, Germany, *T. diccocum*.

Glu-B1-1m. **tv:** PI 352354, Ethiopia, *T. dicoccum*.
Glu-B1-1n. **tv:** PI 94633, Morocco, *T. dicoccum*.
Glu-B1-1o. **v:** Supreza, Canada.
Glu-B1-1p. **v:** Mondor.
Glu-B1-1q. **tv:** Canoco de Grao Escuro, Portugal.
Glu-B1-1r. **tv:** Tremez Mollez, Portugal.
Glu-B1-1s. **tv:** Quaduro, Italy.
Glu-B1-1t. **tv:** Athena, Italy.
Glu-B1-1u. 26. **v:** Cologna 1.
Glu-B1-1v. 28. **v:** Forlani.
Glu-B1-1w. Null. **v:** Olympic mutant.
Glu-B1-1x. 30. **v:** Marinar.
Glu-B1-1y. 32. **v:** BG-1943.
Glu-B1-1z. 34. **v:** Jeja Almendros.
Glu-B1-1aa. 37. **v:** Shedraya Polesja.
Glu-B1-1ab. 6^{*}. **v:** Dawbill.
Glu-B1-1ac{03116}. 6.8{03116}. **v:** Carnac hexaploid triticale{03116}.
Glu-B1-1ad{03122}. 13^{*}{03122}. **v:** PI 348767 spelt {03122}.
Glu-B1-1ae{10327}. 14*{10327}. **v:** TRI11553/92{10327}.
Glu-B1-1af{10327}. 6.1{10327}. **v:** Hercule{10327}; KU-3418{10327}; KU-3446{10327}; Rouguin{10327}; Schwabenkorn{10327}; SP3{10327}; Steiners Roter Tiroler{10327}; TRI4613/75{10327}.
Glu-B1-1ag{10643}. 7^{**} {10643}. **v:** XM1368-2{10643}.
Glu-B1-1ah{899}. 7^{OE}{899}. **v:** Benkuti 1201{10196,10197}; Glenlea{899}; Klein Universal II{10196}; Tezanos Pintos Precoz{10196}; Tobari{10196}.
Glu-B1-1ai{10807}. 7.1{10807}. **v:** H45{10807}.
Glu-B1-1aj{10807}. 7.2{10807}. **v:** H45{10807}.
Glu-B1-1ak{10807}. 7.3{10807}. **v:** VQ0437{10807}.
Glu-B1-1al{10809}. 17'{10809}. **tv:** TGR-214{10809}; TGR-2246{10809}.
Glu-B1-1am{10809}. 13^{**}{10809}. **tv:** TGR-003{10809}.
Glu-B1-1an{10808}. $7b^{*}${10808}. **v:** Eshimashinriki{10808}.

Glu-B1-2.

Glu-B1-2a. 8. **v:** CS.
Glu-B1-2b. 9. **v:** Bezostaya 1.
Glu-B1-2c. 16. **v:** Lancota.
Glu-B1-2d. 19. **v:** NS 335.
Glu-B1-2e. 15. **v:** Sappo.
Glu-B1-2f. 18. **v:** Gabo.
Glu-B1-2g. 22. **v:** Serbian.
Glu-B1-2h. 24. **v:** Spica D.
Glu-B1-2i. **tv:** PI 355505, Germany, *T. dicoccum*.
Glu-B1-2j. **tv:** PI 352354, Ethiopia, *T. dicoccum*.
Glu-B1-2k. **tv:** PI 94633, Morocco, *T. dicoccum*.
Glu-B1-2l. 11. **v:** BT-2288.
Glu-B1-2m. **v:** Supreza, Canada.
Glu-B1-2n. **v:** Mondor.
Glu-B1-2o. 8^{*}. **v:** Dawbull.
Glu-B1-2p. **tv:** Canoco de Grao Escuro, Portugal.
Glu-B1-2q. **tv:** Tremez Mollez, Portugal, *T. durum*.
Glu-B1-2r. **tv:** Quaduro, Italy, *T. durum*.
Glu-B1-2s. 18^{*}. **v:** David.
Glu-B1-2t. 27. **v:** Cologna 1.

Glu-B1-2u. 29. **v:** Forlani.

Glu-B1-2v. Null. **v:** Olympic mutant.

Glu-B1-2w. 31. **v:** Marinar.

Glu-B1-2x. 33. **v:** BG-1943.

Glu-B1-2y. 35. **v:** Jeja Almendros.

Glu-B1-2z{03116}. 20y{03116}. **v:** Carnac hexaploid triticale{03116}.

Glu-B1-2aa{03122}. 18'{03122}. **v:** PI 348631 spelt {03122}.

Glu-B1-2ab{03116}. 21y{03116}. **v:** Foison{03116}.

Glu-B1-2ac{10327}. 22*{10327}. **v:** Grado{10327}; KU-1026{10327}; KU-1086{10327}; KU-1094{10327}; KU-1139{10327}.

Glu-B1-2ad{10327}. 22.1{10327}. **v:** Hercule{10327}; KU-1135{10327}; Rouguin{10327}; Schwabenkorn{10327}; SP3{10327}; Steiners Roter Tiroler{10327}.

Glu-B1-2ae{10327}. 15*{10327}. **v:** TRI11553/92{10327}.

Glu-B1-2af{10327}. 19*{10327}. **v:** KU-3410{10327}; Rechenbergs Fruher Dinkel{10327}; Renval{10327}; SP1{10327}; TRI9885/74{10327}; Zeiners Weiser Schlegel{10327}.

Glu-B1-2ag{10643}. [*8***{10643}]. **v:** XM1404-2{10643}.

Glu-B1-2ai{10809}. 8'{10809}. **tv:** TGR-244{10809}.

Glu-B1-2aj{10808}. 8a*{10808}. **v:** Jing 411{10808}; Pioneer{10808}; Tasman{10808}.

Glu-B1-2ak{10808}. 8b*{10808}. **v:** ACA 601{10808}; Nidera Baguette 10{10808}.

Glu-D1-1.

Glu-D1-1a. 2. **v:** CS.

Glu-D1-1b. 3. **v:** Hobbit.

Glu-D1-1c. 4. **v:** Champlein.

Glu-D1-1d. 5. **v:** Hope.

PCR markers specific for the *Glu-D1-1d* (Dx5) allele were developed in {0145} and {0147}.

Glu-D1-1e. 2.2. **v:** Danchi.

Glu-D1-1f. Null. **v:** Nap Hal, Nepal.

Glu-D1-1g. 2.1. **v:** AUS 14653, Afghanistan.

Glu-D1-1h. 2.3. **v:** PI 348465.

Glu-D1-1i. 38. **v:** Leningradka.

Glu-D1-1j{668}. 43{668}. **i:** *Ae. tauschii* accession TA2450/2*.

Glu-D1-1k{755}. 4.1{755}. **dv:** *Ae. tauschii.*

Glu-D1-1l{1578}. 1.5{1578}.D^{t}x1.5{10306}. **dv:** *Ae. tauschii* accession SQ-214{10306}.

A restriction enzyme based method named the 'restricted deletion method' was used to characterize the ORF of this subunit {10306} (as in the case of subunit D^{t}y10 encoded by *Glu-D1-2u* {10306}. Allele-specific PCR markers were developed based upon SNPs located at the non-repetitive N-terminal {10320}.

Glu-D1-1m{02107}. 2.2*{02107}. **v:** MG315.

Glu-D1-1n{03122}. 2.4{03122}. **v:** PI 348473 spelt{03122}.

Glu-D1-1o{03122}. 2.5{03122}. **v:** PI 3484572 spelt{03122}.

Glu-D1-1p{03124}. 1^{t}{03124}. **dv:** *Ae. tauschii*{03124}.

Glu-D1-1q{03124}. 5^{*t}{03124}. **dv:** *Ae. tauschii*{03124}.

Glu-D1-1r{755}. 5.1{755}. **dv:** *Ae. tauschii.*

This allele was designated *Glu-D1-1j* in the 1998 Catalogue edition.

Glu-D1-1s{10091}. 5'{10091}. **v:** W958{10091}.

This putative allele encodes a subunit, provisionally denominated 5' {10091}, that has a very similar electrophoretic mobility compared to subunit 5 encoded by *Glu-D1-1d*, but analysis using the specific PCR primers for Dx5 described in {10092} and {10093} shows that it does not appear to be the same protein as subunit 5 {10091}. Definitive evidence awaits sequencing information (See note to allele *Glu-D1bo*).

Glu-D1-1t{10304}. 2.6{10304}. **v:** Baidongmai{10305}; Jinbaojin{10305}; Hongdongmai{10305}; Hongkedongmai{10305}.

Glu-D1-1u{10327}. 2.1'{10327}. **v:** KU-1034{10327}.

Glu-D1-1v{10642}. [*1.6*^{t}{10642}]. **dv:** *Ae. tauschii* TD16{10642}.

Glu-D1-2.

Glu-D1-2a. 12. **v:** CS.

A PCR marker (612 bp) for the *Glu-D1-2a* (Dy12) allele was developed in {0145}.

Glu-D1-2b. 10. **v:** Hope.

PCR markers (576 bp and 2176bp) for the *Glu-D1-2b* (Dy10) allele were developed in {0145} and {0147}, respectively.

Glu-D1-2c. 9. **v:** BT-2288.

Glu-D1-2d. Null. **v:** Nap Hal, Nepal.

Glu-D1-2e. 12*. **v:** Tudest.

Glu-D1-2f. 13. **v:** AUS 14519, *T. macha*.

Glu-D1-2g. 36. **i:** Iranian landrace 3048/5* Sicco.

Glu-D1-2h. 11. **v:** Flinor.

Glu-D1-2i{668}. 44{668}. **i:** *Ae. tauschii* TA2450/2*.

Glu-D1-2j{836}. 10'{836}. **v:** Coker 68-15.

Glu-D1-2k{755}. T1{755}. **dv:** *Ae. tauschii.*

Glu-D1-2l{755}. T2{755}. **dv:** *Ae. tauschii.*

Glu-D1-2m{755}. 10.1{755}. **dv:** *Ae. tauschii.*

Glu-D1-2n{755}. 10.2{755}. **dv:** *Ae. tauschii.*

Glu-D1-2o{755}. 10.3{755}. **dv:** *Ae. tauschii.*

Glu-D1-2p{1578}. 10.5{1578}. **dv:** *Ae. tauschii.*

Glu-D1-2q{03122}. 12'{03122}. **v:** PI-348495 spelt wheat accession{03122}.

Glu-D1-2r{03124}. 12.1^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1-2s{03124}. 12.3^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1-2t{03124}. 12.4^{t}{03124}. **dv:** *Ae. tauschii.*

Glu-D1-2u{10306}. D^{t}y10{10306}. **v:** *Ae. tauschii* accession SQ-214{10306}.

A restriction enzyme based method named the 'restricted deletion method' was used to characterize the ORF of this subunit {10306} (as in the case of subunit 1.5 (or D^{t}x1.5 {10306}) encoded by *Glu-D1-1l* {10306}. This subunit was first recognized as being different from subunit 1- encoded by *Glu-D1-2b* in hexaploid wheat in {10307}.

Glu-Ag^{i}1{374}. 1Ag^{i}{374}. **ad:** Vilmorin 27/*Th. intermedium*.

Glu-E1{781}. 1ES{781}. **ad:** CS/*E. elongata*.

HMW glutenin y-type subunit Ee1.5 encoded by this locus was sequenced {10439} and compared with other y-type subunits, particularly subunit 1Dy10. It has major deletions in its middle region and is one of the smallest known HMW glutenin subunits. It has an additional Cys residue in the middle of the repetitive domain, but lacks one Cys residue commonly found towards the end of this domain. These changes may influence inter- or intra-molecular disulphide bond formation.

Four {10660, 10661} and 11 {10662} alleles were observed in *Agropyron elongatum* (E^{e} genome, 2n = 10X = 70) and named *Aex1* to *Aex5* (producing x-type subunits) and *Aey1* to *Aey10* (producing y-type subunits). *Aex4, Aey7* and *Aey9* were very similar to three alleles in the diploid progenitor *Lophopyrum elongatum* {10439, 10663}. The C-terminal regions of three of the y-type subunits (products of *Aey8, Aey9* and *Aey10*) were more similar to x-type subunits than to other y-type subunits {10662}. The subunit from *Aex4* contained an additional cysteine residue, which may be associated with good processing quality in wheat introgression lines {10662}. Allele *Aey-4* was a chimeric gene formed by recombination of two other genes {10662}.

Glu-E1a{781}. **ad:** CS/*L. elongatum* W0622{781}.

Glu-E1b{10644}. **ad:** Langdon/*L. elongatum* DGE-1{10644}. **al:** *L. elongatum* PI 531719{10644}.

Glu-H1{781}. [*Hor 3*{1337}]. 1H{781}.1HL{1337}. **ad:** CS/Betzes{781}. **al:** Various barley cultivars{1337}.

Glu-H^{ch}***1***. 1H^{ch}{1123}. **ad:** CS/*H. chilense*.

38 accessions (natural populations) of *Hordeum chilense* carrying the following 10 subunits were used as the maternal parents of 121 lines of primary tritordeum, and evaluations for associations with bread-making quality initiated {03114}. Subunits 1^{Hch}, 2^{Hch} and 3^{Hch} were previously referred to as H^{ch}a, H^{ch}b and H^{ch}c {03112}.

Glu-H^{ch}***1a***{03114}. 1^{Hch}{03114}. **al:** *H. chilense* Accession H1{03114}.
Glu-H^{ch}***1b***{03114}. 2^{Hch}{03114}. **al:** *H. chilense* Accession H11{03114}.
Glu-H^{ch}***1c***{03114}. 3^{Hch}{03114}. **al:** *H. chilense* Accession H7{03114}.
Glu-H^{ch}***1d***{03114}. 4^{Hch}{03114}. **al:** *H. chilense* Accesion H16{03114}.
Glu-H^{ch}***1e***{03114}. 5^{Hch}{03114}. **al:** *H. chilense* Accession H47{03114}.
Glu-H^{ch}***1f***{03114}. 6^{Hch}{03114}. **al:** *H. chilense* Accession H220{03114}.
Glu-H^{ch}***1g***{03114}. 7^{Hch}{03114}. **al:** *H. chilense* Accession H293{03114}.
Glu-H^{ch}***1h***{03114}. 8^{Hch}{03114}. **al:** *H. chilense* Accession H297{03114}.
Glu-H^{ch}***1i***{03114}. 9^{Hch}{03114}. **al:** *H. chilense* Accession H252{03114}.
Glu-H^{ch}***1j***{03114}. 10^{Hch}{03114}. **al:** *H. chilense* Accession H210{03114}.

Glu-H^{t}***1***{1037}. 1H^{t}L{1037}. **ad:** CS/*E. trachycaulum*.

Glu-R1{781,1356}. [*Sec 3*{1336}]. 1R{781,1336}.1RL{1356,1340}. **ad:** CS/Imperial; Holdfast/ King II{1340}. **tr:** CS Imperial 1DS.1RL{1356}.

Glu-R1a{03116}. 1^{r}-4^{r}{03116}. **v:** Indiana hexaploid triticale{03116}.
Glu-R1b{03116}. 2^{r}-6.5^{r}{03116}. **v:** Graal hexaploid triticale{03116}.
Glu-R1c{03116}. 6^{r}-13^{r}{03116}. **v:** Almao hexaploid triticale{03116}.
Glu-R1d{03116}. 2^{r}-9^{r}{03116}. **v:** Olympus hexaploid triticale{03116}.
Glu-R1e{03116}. 6.5^{r}{03116}. **v:** Clercal hexaploid triticale{03116}.
Glu-R1f{03115}. 0.8^{r}-6^{r}{03115}. **v:** Carmara hexaploid triticale{03115}.
Glu-R1g{03115}. 5.8^{r}{03115}. **v:** Arrayan hexaploid triticale{03115}.

There is a difficulty in the assignment of subunit 6^{r} in the *Glu-R1-1* and *Glu-R1-2* lists, since it appears as an x-type subunit in allele *Glu-R1c* and as a y-type subunit in allele *Glu-R1f.* It is currently provisionally assigned to the *Glu-R1-1* list since, based upon its relative electrophoretic mobility, it is considered more likely to be an x-type subunit. Some of the remaining designations should also be considered as provisional since they too are not free of ambiguity.

From study of chromosome substitutions in bread wheat {03117}, it was found that a chromosome 1R carrying HMW secalin subunit 6.5^{r} (*Glu-R1e*), originally derived from the 'Petkus' rye population, was associated with bread making quality (i) intermediate between chromosome 1A carrying the null allele *Glu-A1c* and chromosome 1A carrying HMW glutenin subunit 2* encoded by *Glu-A1b*; (ii) equivalent to a chromosome carrying HMW glutenin subunit 7 encoded by *Glu-B1a*; and (iii) inferior to chromosomes 1D with distinct alleles.

Five new x-type subunits (plus the null allele) and four y-type subunits were reported in {10094}. They vary principally through duplications and deletions of the tri-, hexa- and nona-peptide motifs found in the central repetitive region of the subunits. Orthologous genes were found to be more closely related than paralogous genes, supporting the hypothesis that gene duplication occurred before Triticeae speciation {10095, 10094}.

Glu-R1-1.

Glu-R1-1a{03116}. 1^{r}{03116}. **v:** Indiana hexaploid triticale{03116}.
Glu-R1-1b{03116}. 2^{r}{03116}. **v:** Graal hexaploid triticale{03116}.

Glu-R1-1c{03116}. 6^r{03116}. **v:** Alamo hexaploid triticale{03116}.

Glu-R1-1d{03115}. 0.8^r{03115}. **v:** Carmara hexaploid triticale{03115}.

Glu-R1-1e{03115}. 5.8^r{03115}. **v:** Arrayan hexaploid triticale{03115}.

Glu-R1-2. 1R, 1RL.

Glu-R1-2a{03116}. 4^r{03116}. **v:** Indiana hexaploid triticale{03116}.

Glu-R1-2b{03116}. 6.5^r{03116}. **v:** Graal hexaploid triticale{03116}.

Glu-R1-2c{03116}. 13^r{03116}. **v:** Alamo hexaploid triticale{03116}.

Glu-R1-2d{03116}. 9^r{03116}. **v:** Olympus hexaploid triticale{03116}.

Glu-R^{m}1{1339}. $1R^mL${1339,1340}. **ad:** CS/*S. montanum*{1339,1340}.

Glu-S^{l}1{1228}. $1S^lL${1228}. **ma:** In *Ae. longissima 2 /Ae. longissima 10,Glu-S^{l}1, Glu-S^{l}3,* one glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one and other {1228} as follows: *Glu-S^{l}1* - 15.9 cM - *Gpi-S^{l}1* - 38 cM - *Gli-S^{l}4* - 7.1 cM - *Glu-S^{l}3* - 0.9 cM - *Gli-S^{l}1* - 5.6 cM - *Gli-S^{l}5*. *Glu-S^{l}1* is located in $1S^lL$ and the other loci are in $1S^lS$.

Glu-U1{150}. 1U{150,781}. **ad:** CS/*Ae. umbellulata* {150,781}.

Glu-V1{111,242,1026}. 1V{1026,111}. **ad:** CS/*D. villosum*; Creso/*D. villosum*.

Glu-V1a{1651}. 71{1651}. **al:** *D. villosum*.

Glu-V1b{1651}. 72{1651}. **al:** *D. villosum*.

Glu-V1c{1651}. 73{1651}. **al:** *D. villosum*.

Glu-V1d{1651}. 74{1651}. **al:** *D. villosum*.

Glu-V1e{1651}. 75{1651}. **al:** *D. villosum*.

Glu-V1f{1651}. 76{1651}. **al:** *D. villosum*.

Glu-V1g{1651}. 77{1651}. **al:** *D. villosum*.

Glu-V1h{1651}. 78{1651}. **al:** *D. villosum*.

Glu-V1i{1651}. 79{1651}. **al:** *D. villosum*.

Glu-V1j{1651}. 80{1651}. **al:** *D. villosum*.

Glu-V1k{1651}. null{1651}. **al:** *D. villosum*.

Glu-V1l{1651}. 81+82{1651}. **al:** *D. villosum*.

Glu-V1m{1651}. 83+84{1651}. **al:** *D. villosum*.

Glu-V1n{1651}. 85+86{1651}. **al:** *D. villosum*.

Alleles and subunits at *Glu-V1-1* and *GLU-V1-2* : The following is analogous to the *Glu-1-1* and *Glu-1-2* lists given earlier to identify x-type and y-type subunits in wheat. It was assumed that where an allele at *Glu-V1* produces only a single subunit, it is an x-type subunit and so encoded by *Glu-V1-1* rather than by *Glu-V1-2*; the electrophoretic mobilities of the subunits are all greater, though some only marginally so, than subunit 7 encoded by *Glu-B1-1a* (an x-type subunit), and extend beyond the mobility of subunit 12 encoded by *Glu-D1-2a* (a y-type subunit) {1651}; therefore, it is quite possible that any one of the subunits designated as encoded by *Glu-V1-1* is, in fact, encoded by *Glu-V1-2*. The designation given here is intended to be the most practically useful until the identities of the genes encoding the alleles are directly established.

Glu-V1-1.

Glu-V1-1a{1651}. 71{1651}. **al:** *D. villosum*.

Glu-V1-1b{1651}. 72{1651}. **al:** *D. villosum*.

Glu-V1-1c{1651}. 73{1651}. **al:** *D. villosum*.

Glu-V1-1d{1651}. 74{1651}. **al:** *D. villosum*.

Glu-V1-1e{1651}. 75{1651}. **al:** *D. villosum*.

Glu-V1-1f{1651}. 76{1651}. **al:** *D. villosum*.

Glu-V1-1g{1651}. 77{1651}. **al:** *D. villosum*.

Glu-V1-1h{1651}. 78{1651}. **al:** *D. villosum*.

Glu-V1-1i{1651}. 79{1651}. **al:** *D. villosum*.

Glu-V1-1j{1651}. 80{1651}. **al:** *D. villosum*.

Glu-V1-1k{1651}. null{1651}. **al:** *D. villosum*.

Glu-V1-1l{1651}. 81{1651}. **al:** *D. villosum*.

Glu-V1-1m{1651}. 83{1651}. **al:** *D. villosum*.

Glu-V1-1n{1651}. 85{1651}. **al:** *D. villosum*.

Glu-V1-2.

Glu-V1-2a{1651}. null{1651}. **al:** *D. villosum*.

Glu-V1-2b{1651}. 82{1651}. **al:** *D. villosum*.

Glu-V1-2c{1651}. 84{1651}. **al:** *D. villosum*.

Glu-V1-2d{1651}. 86{1651}. **al:** *D. villosum*.

A Chinese cultivar of *T. aestivum*, Xiaoyanmai 7, carries a subunit with electrophoretic mobility in 10% SDS-PAGE well beyond that of subunits so far observed in *T. aestivum*. It may derive from *Agropyron elongatum*, which was used in the breeding programme that led to the variety {1538}. It has not been given a subunit number or allelic designation, because its genetic control has not been elucidated.

Glu-Ta1{10449}. **al:** *Taenitherum crinitum* PI 204577{10449}.

Glu-Ta1a{10449}. **al:** *Ta. crinitum* PI 204577{10449}.

Glu-Ta1b{10449}. **al:** *Ta. crinitum* PI 205590{10449}.

Glu-Ta1c{10449}. **al:** *Ta. crinitum* PI 561094{10449}; *Ta. asperum* PI 561091{10449}; PI 561092{10449}.

Glu-Ta1d{10449}. **al:** *Ta. caput-medusae* PI 598389{10449}.

Glu-Ta1e{10449}. **al:** *Ta. caput-medusae* PI 577708{10449}.

Glu-Ta1f{10449}. **al:** *Ta. caput-medusae* PI 577710{10449}.

Each allele identified to date encodes two subunits, an x-type and a y-type. The x-type subunits are slower or equal in mobility to subunit Dx2 of wheat, whereas the y-type subunits are faster than subunit Dx12 {10449}. Phylogenetic analysis based upon the sequence of two genes designated *Tax* and *Tay* isolated from *Ta. crinitum* PI 204577 suggest that the *Tax* subunit was most closely related to Ax1, Cx (*Ae. caudata*), Ux (*Ae. umbellulata*) and Dx5, and the *Tay* subunit to Ay, Cy and Ry (*Secale cereale*) {10449}.

82.3.1.2. Glu-2

Glu-B2{819,277}. [*XGlu-B2*{277}]. 1BS. **s:** CS*/Cheyenne 1B{277}. **stv:** Langdon*/*T. turgidum* var. *dicoccoides* 1B{277}.

Glu-B2a{00114}. 12{00114}. **tv:** Mexicali.

Glu-B2b{00114}. Null{00114}. **tv:** Langdon.

Gli-B3 was designated *Glu-B2* {589} until the name of the locus was changed in {1119}.

Glu-B2c{10215}. 12*{10215}. **tv:** Alcala la Real{10215}.

82.3.1.3. Glu-3

The *Glu-3* loci are defined as the cluster of LMW glutenin genes previously considered a component of the compound *Gli-1* loci.

More than 30 LMW glutenin complete genes, partial genes or pseudogenes have been sequenced from *Triticum* species (reviewed in {0245}).

In *T. aestivum*, only *Glu-B3* was shown to recombine with the gliadin genes (1.7 +/- 0.8) {1355,1358}. However, in *T. durum*, recombination was observed for both *Glu-A3* and *Glu-B3* with their respective *Gli-1* loci: the map distance between *Glu-A3* and *Gli-A1* has been estimated as 1.3 +/- 0.4 cM {1242}, and that between *Glu-B3* and *Gli-B1* as 2.0 +/- 0.8 in {1144} and as 2.0 +/- 0.4 in {1242}. It appears that *Glu-B3* is proximal to *Gli-B1*, and there is some evidence that *Glu-A3* is proximal to *Gli-A1* {1242}.

Whereas hitherto it was widely thought that all LMW glutenin subunits were encoded by genes located on the chromosomes of homoeologous group 1, it has been demonstrated that, although the majority of the subunits are indeed controlled by genes on this group, some of

the C subunits must be controlled by loci elsewhere in the genome {482}.
A novel type of polymeric protein (M_r approx. 71,000) was reported in the Australian advanced breeding line DD118 {03125}. It participates in the polymeric structure of glutenin (possibly as a chain terminator), and has an M_r of approximately 71,000, could be considered as a D-subunit of LMW glutenin. However, N-terminal sequencing suggests it to be a *Gli-B1* type omega-gliadin that has acquired a cysteine residue through mutation.

In an electrophoretic survey of 51 primary tritordeums {03113}, 20 distinct whole banding patterns (a-t), each consisting of between one and three bands, were observed for D-zone prolamins exhibiting glutenin-like solubility characteristics.

In 85 Japanese common wheat cultivars and 61 elite F_6 breeding lines, 3 alleles were observed at each of *Glu-A3* and *Glu-B3*, and 2 alleles at *Glu-D3* were named according to their parental origins in three doubled haploid mapping populations {03135}.

C-type LMW glutenin subunits in CS were assigned to chromosome groups 1 and 6, and shown to have sequences very similar to those of alpha- and gamma-gliadins {03134}. The authors suggest that they may be encoded by novel genes at loci tightly linked or present within the *Gli-1* and *Gli-2* loci, unlike other LMW glutenin subunits encoded by the *Glu-3* loci.

The HMW and LMW glutenin subunits carried by chromosome $1A^m$ of *T. monococcum* accession G1777 were characterised electrophoretically and evaluated for quality characteristics using recombinant chromosome substitution lines with chromosome 1A of CS {03142}. The HMW subunits from G1777 are promising for bread-making quality, whereas its LMW subunits are promising for biscuit-making quality.

The bread wheat cv. Salmone was shown to carry two DNA fragments designated as SF720 and SF750 located on the chromosome 1B satellite and associated with the presence of two LMW glutenin subunits {03143}. However, the authors suggest that they occur at a locus other than *Glu-B3* due to their relatively high frequency of recombination with *Gli-B3*.

A naming system in which Roman numerals are assigned to whole banding patterns for the LMW glutenin subunit is given in {03131} as an alternative to the LMW-1/-2 system described in {03136}. A further system naming whole banding patterns from LMW-1 to LMW-23 in emmer wheat is described in {03137}.
In {00111}, in a study of common and durum wheats from Portugal, the authors used the nomenclature system described in {00113} for the LMW subunits in common wheat, and that described in {00114} for the LMW subunits in durum wheat. The latter system was updated according to {02110}, but has been changed herein to new alleles with the earlier durum designation {00114} given as synonyms.In {03116}, it was suggested that *Glu-B3d* (common wheat standard genetic stock) is equivalent to *Glu-B3r* (durum wheat standard genetic stock), and that (referring to article {03127}) LMWsubunits observed in some Portugese triticales could be of the durum type.

A novel storage protein gene with chimeric structure was isolated from the old Hungarian cultivar Bankuti 1201, containing gamma-gliadin sequences in the 5' region, LMW-glutenin sequences in the 3' region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated *Ch1* to *Ch8*, seem to derive from four gamma-gliadin and three LMW-glutenin sequences and are probably the result of crossing over between the loci *Gli-1* and *Glu-3*. However, the precise recombinational mechanism that gave rise to them has yet to be elucidated {10307}.

Glu-A3{1358}. 1AS{1358}. **v:** CS.

The first 7 alleles were distinguished using 5 allele-specific primer sets {10185}. Further mainly Australian genotypes with alleles *a* to *f* are listed in {10185}.

Glu-A3a{481}. **v:** CS.
Glu-A3b{481}. **v:** Gabo.
Glu-A3c{481}. **v:** Cheyenne.
Glu-A3d{481}. **v:** Cappelle Desprez, Orca; Suneca{10185}.
Glu-A3e{481}. **v:** Halberd{10185}; Hope, Insignia.
Glu-A3f{481}. **v:** Rescue.
Glu-A3g{00113}. **v:** Glenlea{10185}.
Glu-A3h{00114,03116}. [*Glu-A3d'*{03116}]. Null{00114}. **v:** Magistral hexaploid triticale{03116}.
Glu-A3i{02110}. 8^*+11{02110}. **tv:** Mourisco Fino.

In 112 common wheat cultivars from Argentina, 11 microsatellite alleles plus a null allele were found at the *Glu-A3* locus {03123}.

Glu-A3j{00114}. [*Glu-A3a*{00114}]. 6{00114}. **tv:** Mexicali.
Glu-A3k{00114}. [*Glu-A3b*{00114}]. 5{00114}. **tv:** Langdon.
Glu-A3l{00114}. [*Glu-A3c*{00114}]. 6+10{00114}. **tv:** Cocorit.
Glu-A3m{00114}. [*Glu-A3d*{00114}]. 6+11{00114}. **tv:** Alaga.
Glu-A3n{00114}. [*Glu-A3e*{00114}]. 11{00114}. **tv:** Blatfort.
Glu-A3o{00114}. [*Glu-A3f*{00114}]. 6+11+20{00114}. **tv:** Clarofino.
Glu-A3p{00114}. [*Glu-A3h*{00114}]. Null{00114}. **tv:** Jiloca.
Glu-A3q{10215}. [*Glu-A3i*{10215}]. 5+20{10215}. **tv:** Fanfarron{10215}.
Glu-A3r{03116}. [*Glu-A3d'*{03116}]. **v:** Magistral hexaploid triticale{03116}.
Glu-A3s{00114}. [*Glu-A3g*{00114}]. 6+10+20{00114}. **tv:** Claro de Balazote{00114}.
Glu-A3t{10805}. [*Glu-A3^{m}a*{10805}]. **dv:** PI 190947, *T. monococcum* ssp. *monococcum*{10805}.
Glu-A3u{10805}. [*Glu-A3^{m}b*{10805}]. **dv:** PI 190946, *T. monococcum* ssp. *monococcum*{10805}.
Glu-A3v{10805}. [*Glu-A3^{m}c*{10805}]. **dv:** BGE-020466, *T. monococcum* ssp. *monococcum*{10805}.
Glu-A3w{10805}. [*Glu-A3^{m}d*{10805}]. **dv:** PI 191097, *T. monococcum* ssp. *monococcum*{10805}.
Glu-A3x{10805}. [*Glu-A3^{m}e*{10805}]. **dv:** BGE-013624, *T. monococcum* ssp. *monococcum*{10805}.
Gllu-A3y{10805}. [*Glu-A3^{m}f*{10805}]. **dv:** PI 191094, *T. monococcum* ssp. *monococcum*{10805}.
Glu-A3z{10806}. [*Glu-A^{u}3-I*{10806}]. **dv:** PI 428139, *T. urartu*{10806}.
Glu-A3aa{10806}. [*Glu-A^{u}3-II*{10806}]. **dv:** PI 428327, *T. urartu*{10806}.
Glu-A3ab{10806}. [*Glu-A^{u}3-III*{10806}]. **dv:** PI 428340, *T. urartu*{10806}.
Glu-A3ac{10806}. [*Glu-A^{u}3-IV*{10806}]. **dv:** PI 428322, *T. urartu*{10806}.
Glu-A3ad{10806}. [*Glu-A^{u}3-V*{10806}]. **dv:** PI 428188, *T. urartu*{10806}.
Glu-A3ae{10806}. [*Glu-A^{u}3-VI*{10806}]. **dv:** PI 428203, *T. urartu*{10806}.
Glu-A3af{10806}. [*Glu-A^{u}3-VII*{10806}]. **dv:** PI 428255, *T. urartu*{10806}.
Glu-A3ag{10806}. [*Glu-A^{u}3-VIII*{10806}]. **dv:** PI 428328, *T. urartu*{10806}.
Glu-A3ah{10806}. [*Glu-A^{u}3-IX*{10806}]. **dv:** PI 428256, *T. urartu*{10806}.
Glu-A3ai{10806}. [*Glu-A^{u}3-X*{10806}]. **dv:** PI 428217, *T. urartu*{10806}.
Glu-A3aj{10806}. [*Glu-A^{u}3-XI*{10806}]. **dv:** PI 428335, *T. urartu*{10806}.
Glu-A3ak{10806}. [*Glu-A^{u}3-XII*{10806}]. **dv:** PI 428186, *T. urartu*{10806}.
Glu-A3al{10806}. [*Glu-A^{u}3-XIII*{10806}]. **dv:** PI 428183, *T. urartu*{10806}.

Glu-A3am{10806}. [*Glu-A*^{u}*3-XIV*{10806}]. **dv:** TRI 11563, *T. urartu*{10806}.

Glu-A3an{10806}. [*Glu-A*^{u}*3-XV*{10806}]. **dv:** PI 427328, *T. urartu*{10806}.

Glu-A3ao{10806}. [*Glu-A*^{u}*3-XVI*{10806}]. **dv:** PI 428253, *T. urartu*{10806}.

Glu-A3ap{10806}. [*Glu-A*^{u}*3-XVII*{10806}]. **dv:** PI 538735, *T. urartu*{10806}.

Glu-A3aq{10806}. [*Glu-A*^{u}*3-XVIII*{10806}]. **dv:** PI 428225, *T. urartu*{10806}.

Glu-A3ar{10806}. [*Glu-A*^{u}*3-XIX*{10806}]. **dv:** PI 538733, *T. urartu*{10806}.

Glu-A3as{10806}. [*Glu-A*^{u}*3-XX*{10806}]. **dv:** PI 428196, *T. urartu*{10806}.

Glu-A3at{10806}. [*Glu-A*^{u}*3-XXI*{10806}]. **dv:** PI 538724, *T. urartu*{10806}.

Glu-A3au{10806}. [*Glu-A*^{u}*3-XXII*{10806}]. **dv:** PI 428191, *T. urartu*{10806}.

Glu-A3av{10806}. [*Glu-A*^{u}*3-XXIII*{10806}]. **dv:** TRI 6734, *T. urartu*{10806}.

Glu-A3aw{10806}. [*Glu-A*^{u}*3-XXIV*{10806}]. **dv:** TRI 11496, *T. urartu*{10806}.

Glu-A3ax{10116}. 6.1{10116}. **tv:** Buck Cristal{10116}.

The designation of this protein (subunit 6.1) as an allele of *Glu-A3* was deduced from its electrophoretic mobility and awaits confirmation through mapping studies.

Glu-B3{1358}. 1BS{1358}. **v:** CS.

Glu-B3a{481,}. **v:** CS.

Glu-B3b{481}. **v:** Gabo, Timstein, Hope.

Glu-B3c{481}. **v:** Insignia, Halberd.

Glu-B3d{481}. **v:** Orca.

Glu-B3e{481}. **v:** Cheyenne.

Glu-B3f{481}. **v:** Radja.

Glu-B3g{481}. **v:** Kharkov, Bungulla.

Glu-B3h{481}. **v:** Thatcher, Rescue.

Glu-B3i{481}. **v:** Norin-61.

Glu-B3j{476,02110}. 4+6*+15+19{02110}. **tv:** Duramba-B, Duramba-D, Langdon; Mourisco Fino.

Glu-B3k{476,02110}. 8+9+13+16+19{02110}. **tv:** ALP-153, Dural, Durati, Edmore; Faisca.

Glu-B3l{476}. **tv:** Gionp-1954.

Glu-B3m{03120}. [*Glu-B3b'*{03120}]. **v:** Soissons{03120}.

Glu-B3n{03120}. [*Glu-B3c'*{03120}]. **v:** Courtot{03120}.

Glu-B3o{03116}. [*Glu-B3i'*{03116}]. **v:** Olympus hexaploid triticale{03116}.

Glu-B3p{03116}. [*Glu-B3k*{03116}]. **v:** Alamo hexaploid triticale{03116}.

Glu-B3q{03115}. [*Glu-B3h'*{03115}]. **v:** Torote hexaploid triticale{03115}.

Glu-B3r{00114}. [*Glu-B3a*{00114}]. 2+4+15+19{00114}. **tv:** Mexicali.

Glu-B3s{00114}. [*Glu-B3b*{00114}]. 8+9+13+16{00114}. **tv:** Langdon.

Glu-B3t{00114}. [*Glu-B3c*{00114}]. 2+4+14+15+19{00114}. **tv:** Jiloca.

Glu-B3u{00114}. [*Glu-B3d*{00114}]. 2+4+15+17+19{00114}. **tv:** Mundial.

Glu-B3w{00114}. [*Glu-B3f*{00114}]. 2+4+15+17{00114}. **tv:** Ardente.

Glu-B3v {00114}. [*Glu-B3e*{00114}]. 2+4+15+16+18{00114}. **tv:** Granja Badajoz.

Glu-B3x{00114}. [*Glu-B3g*{00114}]. 2+4+15+16{00114}. **tv:** Claro de Balazote.

Glu-B3y{00114}. [*Glu-B3h*{00114}]. 1+3+14+18{00114}. **tv:** Alaga.

Glu-B3aa{10215}. [*Glu-B3l*{10215}]. 1+3+13*+16{10215}. **tv:** Blancal de Nules{10215}.

Glu-B3ab{10804}. **v:** Hope{10804}; Nanbukomugi{10804}.

Glu-B3ac{10804}. **v:** ACA 801{10804}; Klein Proteo{10804}; Thesee{10804}.

Glu-B3ad{10804}. **v:** AC Vista{10804}; Heilo{10804}; Opata85{10804}; Ruso{10804}.

Glu-D3{1358,707}. 1DS{707,1358}. **v:** CS.

Three different approaches were emplyed to identify putative SNPs used to design gene-specific primers for LMW-GS genes, and six functional STS markers, three for *Glu-B3* and three for *Glu-D3* {10664}. These markers distiguished cultivars with different haplotypes at the *Glu-B3* and *Glu-D3* loci, but there was no clear correlation between the alleles of cultivars defined by protein electrophoretic mobility and the separation patterns of the DNA markers, since all three *Glu-3* loci were multiple gene loci and each protein electrophoretic mobility allele was controlled by 3-6 coding genes {10665}.

Glu-D3a{481}. **v:** CS.
Glu-D3b{481}. **v:** Gabo.
Glu-D3c{481}. **v:** Insignia, Cappelle Desprez.
Glu-D3d{481}. **v:** Jufy-1{10813}; Norin-61A.
Glu-D3e{481}. **v:** Orca, Thatcher.
Glu-D3f{10548}. **v:** Cheyenne{10548}.
Glu-D3g{10558}. **v:** Hira-1{10558}.
Glu-D3h{10558}. **v:** India 115{10558}.
Glu-D3i{10558}. **v:** Bolac{10558}.
Glu-D3j{10558}. **v:** Hira-2{10558}.
Glu-D3k{10558}. **v:** Lincoln{10558}.
Glu-D3l{10804}. **v:** Heilo{10804}; Jing411{10804}; Pepital{10804}; Thesee{10804}.
Glu-D3m{10804}. **v:** Darius{10804}.

Glu-E3{480}. 1ES{480}. **su:** CS/*E. elongata*.

Glu-S^{l}***3***{480,1228}. 1S^{l}{480}.1S ^{1}S{1228}. **su:** CS/*Ae. longissima*{480,1228}. **ma:** In *Ae. longissima 2 /Ae.longissima 10* glucose phosphate isomerase locus, and three gliadin loci were mapped relative to one another in {1228} as follows: *Glu-S*^{l}*1* - 15.9 cM - *Gpi-S*^{l}*1* - 38 cM- *Gli-S*^{l}*4* - 7.1 cM - *Glu-S*^{l}*3* - 0.9 cM - *Gli-S*^{l}*1* - 5.6 cM - *Gli-S*^{l}*5*. *Glu-S*^{l}*1* is located in 1S^{l}L and the other loci are in 1S^{1}S.

Glu-U3{480}. 1U{480}. **su:** CS/*Ae. umbellulata*.

A series of papers {00106, 00107, 00108 and 00109} describe considerable variation in primitive wheats not present in bread wheat (A genome species *T. boeoticum, T. urartu, T. thaoudar, T. aegilopoides, T. monococcum*, and D-genome species *T. tauschii*) for the low molecular weight subunits, sufficient to use them as a source for potentially changing flour properties in bread wheat.

In {00110}, variants for LMW glutenin subunits were reported from study of twenty-four accessions of einkorn wheat (*T. monococcum* ssp. *monococcum*). Nine of these showed two electrophoretic bands for LMW subunits, arbitrarily designated 'a' and 'b', that appeared to be associated with good bread-making quality.The isolation of a new low-molecular-weight glutenin subunit gene, located on chromosome 1D, was reported in {0350}.

82.3.1.4. Glu-4

The following loci, *Glu-D4* and *Glu-D5*, encoding low molecular weight subunits of glutenin (30-32 kDa) were described in {02111}; the proteins encoded by them were first observed earlier {02114, 02115}, and the former was later tentatively assigned the symbol *Glu-4* {02116}, before its chromosomal location was established and the locus definitively named as *Glu-D4* in {02111}. While this locus is located on chromosome 1D (in accordance with the position on the group 1 chromosomes of the remaining glutenin encoding loci found to date), the locus *Glu-D5* is located on chromosome 7D. In SDS-PAGE, the proteins from both loci are detected only in the presence of 4-vinylpyridine added to the sample extract. Their amino acid compositions do not match those of the major prolamin groups; nonetheless, they classify as glutenins based upon solubility, immunological behaviour and N-terminal amino acid sequence (the latter suggesting an evolutionary link with the major (B and C) low molecular weight glutenin subunits).

Glu-D4{02111}. 1D{02111}. **su:** CS/Langdon 1D(1A); CS/Langdon 1D(1B){02111}.
Glu-D4a{02111}. **v:** J 24.
Glu-D4b{02111}. **v:** PBW 154.

Glu-D4c{02111}. Null allele. **v:** NI 4.

82.3.1.5. Glu-5

Glu-D5{02111}. 7D{02111}. **su:** CS/Langdon 7D(7A); CS/Langdon 7D(7B){02111}.

Glu-D5a{02111}. **v:** PBW 154.

Glu-D5b{02111}. Null allele. **v:** K 68.

A collection of 173 *Ae. tauschii* accessions were analysed for low molecular weight glutenin subunits by SDS-PAGE {02112}. Thirty three different patterns for B-subunits and 43 for C-subunits were identified, some of which were of identical electrophoretic mobility to those observed in common wheat. Also observed were subunits with the same mobilities as the D-subunits and as the subunits encoded by the *Glu-D4* and *Glu-D5* loci. This variation represents a source of novel germplasm of potential value for breeding programmes aimed at improving the D-genome of common wheat in the context of bread-making quality.

PCR amplification of genomic DNA was used to isolate three LMW glutenin genes in cultivar Chinese Spring, named LMWG-MB1, LMWG-MB2 and LMWG-MB3 {01101}. The deduced amino-acid sequences showed a high similarity between these ORFs and with those of other LMW glutenin genes. The authors state that the study provided direct evidence that insertions and/or deletions provide a mechanistic explanation for the allelic variation, and hence the resultant evolution, of prolamin genes, and comment on relationships with gamma-secalins and beta-hordein families. Single-base substitutions at identical sites generate premature stop codons in both LMWG-MB2 and LMWG-MB3, indicating that these clones are pseudogenes.

82.3.2. Gliadins

These are heterogeneous mixtures of alcohol-soluble polypeptides without quaternary structure. The *Gli-1* loci are compound and are now considered to comprise the omega-gliadin and gamma gliadin {982,1415} multigene families {494}, which in some circumstances may be divided into *Gli-1-1* and *Gli-1-2*, respectively. The LMW glutenin multigene families, which are closely linked to the *Gli-1* loci {588}, are listed separately as the *Glu-3* set {1358}; information on map distance and gene order in relation to *Glu-3* and the centromere is given in the preamble for the *Glu-3* loci. There is evidence that a few of the omega-gliadin genes are separated from the main omega-gliadin gene cluster {993}. Variation at the *Gli-1* loci was described earlier {634,996,1126} and applied in mapping experiments {1243,1125,196,422,1120}. A rational system of naming the alleles was produced by Dr. E.V. Metakovsky{988}. This nomenclature is reproduced below. A considerable number of alleles were added to the original list given in {988}, and referenced here accordingly. A few alleles have been deleted, because, following much detailed comparison, there is now doubt that they can be reliably distinguished from existing alleles {9981}. The allelic letter in these cases has not been reused. To facilitate practical use of the list, the aim was to give at least three standard cultivars from a range of countries for each allele {9981}. This was achieved for the vast majority of entries and is a change from the original list compiled from {988}, where up to two standards were given. While the three or more standards described almost always include the original standards, some have been replaced for various reasons, such as international awareness of the cultivar, availability of seed, or the ease with which an allele can be identified in a particular genetic background {9981}. In the original list, where two cultivars were given as prototypes for an allele, the first named was from the USSR and the second from elsewhere; this is no longer the case, although care was taken to include a Russian cultivar where possible, to maintain a wide base of germplasm in which the alleles are available, as well as to acknowledge the research

groups in the country where much of the pioneering work was carried out.
For discussion of null alleles at the *Gli-1* and *Gli-2* loci, see {9984}.
Recombination was observed within the gliadin multigene family at *XGli-A1* {277}. These closely linked genes may correspond to *Gli-A1* and *Gli-A5*, but they were temporarily designated *XGli-A1.1* and *XGli-A1.2* until orthology with *Gli-A1* and/or *Gli-A5* is established.

Note: The catalogue entries reproduced here only refer to alleles in *T. aestivum*; there is, however, enormous variation in the gliadins in the close relatives of wheat; see, for example, {989} for studies in *T. monococcum* (more than 80 gliadin electrophoretic patterns observed in 109 accessions), {990} for studies in *T. boeoticum* (more than 50 electrophoretic patterns in 60 accessions), and {1076} studies in *T. durum* (19 electrophoretic patterns, referring only to variation in the omego-gliadins, in 243 accessions).
In {00110}, variants for omega-gliadins were reported from study of twenty-four accessions of einkorn wheat (*T. monococcum* ssp. *monococcum*). In {00111}, in a study of common wheat and durum from Portugal, the authors used the nomenclature system described in {00112} for the omega-gliadins. In {00116}, a comparison between spelt and common wheat was carried out for the gliadins using a nomenclature system described in {00118}.
The *Gli-1*loci may be recognised by probes pcP387 {372} and pTag1436 {065}, and by specific microsatellites primers {252}. Furthermore, it was shown that probe pTag1436 differentiates gliadin alleles rather well; using this probe, families of gliadin alleles and some of their relationships were described {9988}.

Twenty eight gamma-gliadin gene sequences from GenBank were grouped into nine subgroups in {10063}. Primers were developed against some of the subgroups and the chromosomal locations of the gamma-gliadin genes were determined {10063}.

Based upon morphological observation and RFLP analysis, it was proposed that the cultivar 'Chinese Spring' is a strain of the landrace 'Chengdu-guangtou' from the Chengdu Plain, Sichuan Province; this proposal is supported by the observation that CS and the landrace share the same alleles at all nine *Gli-1*, *Gli-2* and *Glu-1* loci {see 01102}.
PCR primers GAG5 and GAG6 were applied to 35 cultivars of closely related spelt and hexaploid wheat, and to eight cultivars of durum, to yield products originating from two gamma-gliadin genes mapped to chromosomes 1B (termed GAG56B) and 1D (termed GAG56D) {01103}. Two alleles for GAG56D (differing in a 9 bp deletion/duplication and single nucleotide polymorphism) were found, one a new allele and the other previously published {01104}. Meanwhile two alleles found for GAG56B among the durum wheats correlated with the presence of gluten quality markers, gamma-gliadins 42 or 45.

1B and 1D sulphur-poor omega-gliadins in cultivar Butte 86 were characterised by RP-HPLC, SDS-PAGE, two-dimensional PAGE, amino acid composition determination and sequencing, matrix assisted laser desorption ionisation-time of flight mass spectrometry and circular dichroism spectroscopy to reveal the detailed nature of the peptides belonging to the two groups, and showing that the complexity of mixtures of the peptides of the 1B group was greater than that of the 1D group {01105}. Although circular dichroism spectra were similar for the two groups of peptides, and suggested a mainly flexible random structure, there was evidence for a significant amount of left-handed polyproline II helical conformation in the case of the 1D components. The authors placed some of the results in the context of the possible ancestor of the B-genome and relationships with the barley C-hordeins and rye omega-secalins.
Eleven new gliadin alleles were found in a collection of 52 Spanish landraces of common wheat {03141}.

A new family of low-molecular-weight gliadin genes located on groups 4 and 7 were reported in {10117}. They appear to influence rheological properties and seem to be closely related to the 17kDa epsilon hordein, important in beer foam stability.

A novel storage protein gene with chimeric structure was isolated from the old Hungarian cultivar Bankuti 1201, containing gamma-gliadin sequences in the 5' region, LMW-glutenin sequences in the 3' region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated *Ch1* to *Ch8*, seem to derive from four gamma-gliadin and three LMW-glutenin sequences and are probably the result of crossing over between the loci *Gli-1* and *Glu-3*. However, the precise recombinational mechanism that gave rise to them has yet to be elucidated {10307}.

Transcriptome analysis showed the presence of proteins called avenin-like a and b. The former contained a duplicated sequence of about 120 residues and corresponded to the LMW-gliadins. The latter was not previously characterized, but may form part of the glutenin fraction and hence influence quality. These avenin-like proteins showed higher expression levels in three *Aegilops* species (*Ae. caudata*, *Ae. cylindrica* and *Ae. tauschii*) than in common wheat {10321}.

82.3.2.1. Gli-1

Gli-A1{1334,1125}. [*Gld 1A*{1415}]. 1AS{150,634,1334,1607}. **s:** CS*/Cheyenne{634}. **v:** CS{150,1334,1607}.

Gli-A1a{988}. **v:** Castan{991}; CS{988}; Mara{9986}; Mentana{9986}; Millewa{00119}.
Gli-A1b{988}. **v:** Bezostaya 1, Mercia{988}; Tracy{991}.
Gli-A1c{988}. **v:** Ukrainka{998}; Gazul{9985}; Sava{994}; Hopps{00119}.
Gli-A1d{988}. **v:** Dankowska{988}; Cabezorro{9985}.
Gli-A1e{988}. **v:** Falchetto{988}; Open{991}; Touzelle{991}.
Gli-A1f{988}. **v:** Mironovskaya 808, Maris Freeman{988}; Arminda{991}.
Note: An allele *Gli-A1f** is mentioned in {03130}.
Gli-A1g{988}. **v:** Gabo{988}; Adalid{9985}.
Gli-A1h{988}. **v:** Sadovo I{988}; Predela{9981}; Krajinka{9981}.
Gli-A1i{988}. **v:** Saratovskaya 36{988}.
Gli-A1j{988}. **v:** Lutescens 62{988}.
Gli-A1k{988}. **v:** Courtot{991}; Skala (heterogeneous){988}; Soissons{991}; Spada{9986}.
Gli-A1l{988}. **v:** Lesostepka 75{988}; David{9986}; Salmone{9986}; Mura{9981}.
Gli-A1m{988}. **v:** Marquis{988}; Dneprovskaya 521{988}; Carat{991}; Liocorno{9986}.
Gli-A1n{988}. **v:** Intensivnaya{988}.
Gli-A1o{988}. **v:** Odesskaya 16 (heterogeneous){988}; Oderzo{9986}; Cappelle-Desprez{991}; Capitole{991}.
Gli-A1p{988}. **v:** Pyrotrix 28{988}; Zagore{9981}.
Gli-A1q{988}. **v:** Akmolinka 1{988}.
Gli-A1r{988}. **v:** Ranniaya 73{988}; Barbilla{9985}.
Gli-A1s.
Although reported {9986}, this gene is omitted because it requires further confirmation {9981}.
Gli-A1t{9985}. **v:** Jeja del Pais{9985}; Milturum 553{9981}; Strela{9981}.
Gli-A1u{9985}. **v:** Candeal Alcala{9985}.
Gli-A1v{9981}. **v:** Japhet{9981}; Rouge de Bordeaux{9981}.
Gli-A1w{9984,9987}. null allele **v:** Saratovskaya 29 (mutant){9987}; E. Mottin{9981}.

Gli-A1x{10805}. [*Gli-A1*^{m}*a*{10805}]. **dv:** PI 191146, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A1y{10805}. [*Gli-A1*^{m}*b*{10805}]. **dv:** PI 190947 *T. monococcum* ssp. *monococcum*{10805}.

Gli-A1z{10805}. [*Gli-A1*^{m}*c*{10805}]. **dv:** PI 190946, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A1aa{10805}. [*Gli-A1*^{m}*d*{10805}]. **dv:** PI 191097, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A1ab{10805}. [*Gli-A1*^{m}*e*{10805}]. **dv:** BGE-020466, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A1ac{10805}. [*Gli-A1*^{m}*f*{10805}]. **dv:** BGE-013626, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A1ad{10805}. [*Gli-A1*^{m}*g*{10805}]. **dv:** BGE-013628, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A1ae{10811}. [*Gli-A*^{u}*1-I*{10811}]. **dv:** PI-428333, *T. urartu*{10811}.

Gli-A1af{10811}. [*Gli-A*^{u}*1-II*{10811}]. **dv:** PI-428319, *T. urartu*{10811}.

Gli-A1ag{10811}. [*Gli-A*^{u}*1-III*{10811}]. **dv:** PI-428335, *T. urartu*{10811}.

Gli-A1ah{10811}. [*Gli-A*^{u}*1-IV*{10811}]. **dv:** PI-428323, *T. urartu*{10811}.

Gli-A1ai{10811}. [*Gli-A*^{u}*1-V*{10811}]. **dv:** PI-428231, *T. urartu*{10811}.

Gli-A1aj{10811}. [*Gli-A*^{u}*1-VI*{10811}]. **dv:** PI-428194, *T. urartu*{10811}.

Gli-A1ak{10811}. [*Gli-A*^{u}*1-VII*{10811}]. **dv:** PI-428256, *T. urartu*{10811}.

Gli-A1al{10811}. [*Gli-A*^{u}*1-VIII*{10811}]. **dv:** PI-428234, *T. urartu*{10811}.

Gli-A1am{10811}. [*Gli-A*^{u}*1-IX* {10811}]. **dv:** PI-428320, *T. urartu*{10811}.

Gli-A1an{10811}. [*Gli-A*^{u}*1-X*{10811}]. **dv:** PI-428255, *T. urartu*{10811}.

Gli-A1ao{10811}. [*Gli-A*^{u}*1-XI*{10811}]. **dv:** PI-428241, *T. urartu*{10811}.

Gli-A1ap{10811}. [*Gli-A*^{u}*1-XII*{10811}]. **dv:** PI-428235, *T. urartu*{10811}.

Gli-A1aq{10811}. [*Gli-A*^{u}*1-XIII*{10811}]. **dv:** PI-428183, *T. urartu*{10811}.

Gli-A1ar{10811}. [*Gli-A*^{u}*1-XIV*{10811}]. **dv:** PI-428317, *T. urartu*{10811}.

Gli-A1as{10811}. [*Gli-A*^{u}*1-XV*{10811}]. **dv:** PI-427328, *T. urartu*{10811}.

Gli-A1at{10811}. [*Gli-A*^{u}*1-XVI*{10811}]. **dv:** PI-428327, *T. urartu*{10811}.

Gli-A1au{10811}. [*Gli-A*^{u}*1-XVII*{10811}]. **dv:** PI-428253, *T. urartu*{10811}.

Gli-A1av{10811}. [*Gli-A*^{u}*1-XVIII*{10811}]. **dv:** PI-428224, *T. urartu*{10811}.

Gli-A1aw{10811}. [*Gli-A*^{u}*1-XIX*{10811}]. **dv:** PI-538727, *T. urartu*{10811}.

Gli-A1ax{10811}. [*Gli-A*^{u}*1-XX*{10811}]. **dv:** PI-428211, *T. urartu*{10811}.

Gli-A1ay{10811}. [*Gli-A*^{u}*1-XXI*{10811}]. **dv:** PI-538724, *T. urartu*{10811}.

Gli-A1az{10811}. [*Gli-A*^{u}*1-XXII*{10811}]. **dv:** PI-428191, *T. urartu*{10811}.

Gli-A1ba{10811}. [*Gli-A*^{u}*1-XXIII*{10811}]. **dv:** TRI-6735, *T. urartu*{10811}.

Gli-A1bb{10811}. [*Gli-A*^{u}*1-XXIV*{10811}]. **dv:** TRI-11494, *T. urartu*{10811}.

Gli-A1bc{10811}. [*Gli-A*^{u}*1-XXV*{10811}]. **dv:** TRI-6734, *T. urartu*{10811}.

Gli-A1bd{10811}. [*Gli-A*^{u}*1-XXVI*{10811}]. **dv:** TRI-11496, *T. urartu*{10811}.

Gli-B1{1607,1125}. [*Gld 1B*{1243,1415},*Gld-B1*{420},*Gld-B2*{420},*Gld-B3*{420},*Gld-B4*{420},*Gld-B5*{420},*Gld-B6*{420}]. 1B{1607}.1BS{150,634}. **s:** CS*/Cheyenne{634}. **v:** CS{1607,150}.

Gli-B1a{988}. **v:** CS{988}.

Gli-B1b{988}. **v:** Bezostaya 1{988}; Carat{991}; Marquis{988}; Liocorno{9986}; Soissons{991}.

Gli-B1c{988}. **v:** Siete Cerros 66{988}; Prinqual{991}; Loreto{9986}.

Gli-B1d{988}. **v:** Dneprovskaya 521{988}; Chopin{991}; Petrel{991}; Tiberio{9986}; Yecora{9985}; Neepawa{995}; Suneca{00119}.

Gli-B1e{988}. **v:** Apexal{991}; Fournil{991}; Lutescens 62{988}; Oderzo{9986}.

Gli-B1f{988}. **v:** Capitole{991}; Cappelle-Desprez{991}; Dankowska{988}; Maris Freeman{988}; Mercia{998}.

Gli-B1g{988}. **v:** Champtal{991}; Galahad{988}; Mara{9986}; Sadovo 1{988}; Tracy{991}.

Gli-B1h{988}. **v:** Cabezorro{9985}; Krasnodonka{988}; Pepital{991}; Rudi{991}Tincurrin{00119}.

Gli-B1i{988}. **v:** Ghurka{988}; Insignia{988}.

Gli-B1j{988}. **v:** Cluj 650{988}.

Gli-B1k{988}. **v:** Crverkapa{994}; De Carolis{9986}; Kremena{988}; Mentana{9986}.

Gli-B1l{988}. **v:** Avrova{9981}; Clement{991}; Damier{991}; Fiocco{9986}; Kavkaz{9981}.

Gli-B1l encodes secalins ssociated with the 1BL.1RS translocation.

Gli-B1m{988}. **v:** Costantino{9986}; Et.d'Choisy{991}; Pyrotrix 28{988}.

Gli-B1n{988}. **v:** Intensivnaya{988}.

Gli-B1o{988}. **v:** Aragon 03{9985}; Levent{988}; Pippo{9986}; San Rafael{9985}.

Gli-B1p{988}. **v:** Inia 66{9985}; New Pusa 834{988}.

Gli-B1q{9986}. **v:** Gallo{9986}; Goelent{991}; Goya{991}.

Gli-B1r{995}. **v:** Chinook{995}; Gazul{9985}; Sevillano{9985}.

Gli-B1s{9986}. **v:** Salmone{9986}; Resistente{9986}; E.Mottin{9981}.

Gli-B1t{9985}. **v:** Jeja del Pais{9985}.

Gli-B1u{9985}. **v:** Negrillo{9985}.

Gli-B1v{9985}. **v:** Montjuich{9985}.

Gli-B1w{9981}. **v:** Ardica{9981}; Barbilla (MCB-1017){9981}.

Gli-B1x{9984,9987,991}. Null allele **v:** Touzelle{991}; Florence Aurora{9985}.

In 112 bread wheat cultivars from Argentina, 12 microsatellite alleles plus a null allele were found at the *Gli-B1* locus tightly linked to *Glu-B3* {03123}.

Gli-D1{121,1125}. [*Gld 1D*{1415},*Gld-D1*{420},*Gld-D2*{420},*Gld-D3*{420}]. 1DS{121,150,634,1334,1607}. **s:** CS*/Cheyenne{634}. **v:** CS{121,150,1334,1607}.

Gli-D1a{988}. **v:** CS{988}; Marquis{988}; Mentana{9986}; Prinqual{991}; Saratovskaya 36{988}.

Gli-D1b{988}. **v:** Bezostaya 1{988}; Cappelle-Desprez{991}; Etoile d'Choisy{991}; Galahad{988}.

Gli-D1c{988}. **v:** Skorospelka Uluchshennaya (biotype){988,9982}.

Gli-D1d{988}. **v:** De Carolis{9986}; Solo{988}.

Gli-D1e{988}. **v:** Gerek 79{988}.

Gli-D1f{988}. **v:** Carlos{991}; Gabo{988}; Maris Freeman{988}; Orso{9986}.

Gli-D1g{988}. **v:** Fournil{991}; Ghurka{988}; Mironovskaya 808{988}; Open{991}.

Gli-D1h{988}. **v:** Sadovo I{988}; Zlatostrui{9981}.

Gli-D1i{988}. **v:** Insignia{988}; Napayo (biotype){995}; San Rafael{9985}; Tselinogradka{988}.

Gli-D1j{988}. **v:** Aubain{991]; Chinook{995}; Inia 66{9985}; Petrel{991}; Promin{988}.

Gli-D1k{988}. **v:** Cargimarec{991}; Kremena{988}; Mara{9986}; Pippo{9986}.

Gli-D1l{988}. **v:** Artaban{991}; Corin{991}; Longbow{988}.

Gli-D1m{991}. **v:** Heurtebise{991}.

Gli-D1n{981}. **v:** Blanquillo de Toledo (MCB-0950){9981}.

Gli-D1o{9984,9987,991}. Null allele **v:** Darius{991}; Touzelle{991}; Saratovskaya 29 (mutant){9987}.

Gli-Ag^{i}1. 1Ag^i{168}. **ad:** Vilmorin 27/*Th. intermedium*.

Gli-DT1{02109}. 1DS{02109}. **v:** L/18913 (synthetic). **dv:** *Ae. tauschii* AUS18913.

A locus designated *Gli-DT1* controlling an omega-gliadin of *Ae. tauschii* was mapped on the short arm of chromosome 1D between loci *Gli-D1* (strictly *Gli-D^{t}1*) and *Glu-D1* (strictly *Glu-D^{t}1*), 13.18 cM proximal to the former and 40.20 cM from the latter {02109}. The only omega-gliadin to date identified as being encoded by this locus, namely T1, is of unusually low electrophoretic mobility in SDS-PAGE gels and was formally thought to be a high molecular weight glutenin encoded by the *Glu-D^{t}1* locus of *Ae. tauschii* (see note following the *Glu-D1* list in section 'Glutenins'). The authors speculate that, due to their similar relative map positions, the loci *Gli-A4, Gli-D4, Gli-R3, Gli-S^{l}4* and this locus, *Gli-DT1,* form a series of '*Gli-4*' orthologous loci. However, this should be interpreted in the light of the above discussion on *Gli-A3* and *Gli-A4*.

A 1,200 bp Dra I RFLP was identified as a gene-specific probe for the T1 omega-gliadin {10645}.

Gli-DT1a{02109}. T1. **v:** L/18913 (synthetic). **dv:** *Ae. tauschii* AUS18913.

Gli-E1{781}. 1ES{781}. **ad:** CS/*E. elongata*.

Gli-H^{t}1{1037}. 1H^{t}p{1037}. **ad:** CS/*E. trachycaulum*.

Gli-R1{1334}. [*SecR1*{1356},*Sec1*{1336}]. 1RS{781,1334,1336,1340}. **ad:** CS/Imperial{781,1334,1336,1340}; Holdfast/King II{1334,1340}. **tr:** CS 1DS. Imperial 1RL{1356}.

Sec-12 and *Sec13* are given as allelic alternatives in 1BL.1RS translocation lines by {03132}.

Gli-R^{m}1{1340}. 1R^{m}S{1340}. **ad:** CS/*S. montanum*.

Gli-S^{l}1{573}. 1S^{l}{573}. **ad:** CS/*Ae. longissima*.

Gli-U1{1335}. 1U{1335,150}. **ad:** CS/*Ae. umbellulata*.

Gli-V1{1026,111}. 1V{1026,111}. **ad:** CS/*D. villosum*{1026}; Creso/*D. villosum*{111}.

In barley, the B and C hordeins are controlled by the *Hor2* and *Hor1* loci, respectively, which are linked {1341} on chromosome 1HS {1063,1153}. The map distances and homology of the proteins indicate that *Hor1,* the locus closest to the centromere, is equivalent to the omega-gliadins (*Gli-1-1*) in *Gli-1* {1338}.

Three alleles at each of the *Gli-1-1* (omega gliadin) loci were noted {1358}. The complexity of the *Gli-1* compound loci is further emphasized by a report of individual genes being separable by recombination, where *G1d-1A* (a block of gamma and omega genes) is separable by 0.3% from *Gld4-1A* (omega gliadins) which is in turn, separable by 1.5% from *Gld3-1A* (omega gliadins) {1103}.

Elsewhere, variation was described {634,996,1126} and applied in mapping experiments {107,196,422,1120,1125,1243}. Sixteen combinations of *Gli-B1* and 4 combinations of *Gli-D1* subunits are listed in {420}. Multiple alleles described in {996}, number 15 at *Gli-A1,* 18 at *Gli-B1,* and 8 at *Gli-D1.*

The *Gli-1* alleles present in 57 Yugoslav wheat varieties were reported in {994}.

82.3.2.2. Gli-2

Gli-A2{1334,1125}. [*Gld 6A*{1415}]. 6A{1334}.6AS{1122}. **v:** CS.

Gli-A2a{988}. **v:** Cabezorro{9985}; CS{988}; Insignia{988}; Rieti DIV{9986}.

Gli-A2b{988}. **v:** Aradi{9985}; Bezostaya 1{988}; Rivoli{991}; Tiberio{9986}.

Gli-A2c{988}. **v:** Eagle{00119}; Escualo{9985}; Loreto{9986}; Prinqual{991}; Siete Cerros 66{988}.

Gli-A2d{988}. **v:** Dneprovskaya 521{988}; Kenyon (biobype){995}; Mocho Sobarriba{9985}.

Gli-A2e{988}. **v:** Cobra{991}; Mentana{9986}; Resistente{9986}; Sadovo 1{988}; Sevillano{9985}.

Gli-A2f{988}. **v:** Adalid{9985}; Gala{991}; Maris Freeman{988}; Sistar{9986}.

Gli-A2g{988}. **v:** Cappelle-Desprez{991}; Ducat{988}; Mahissa 1{9985}; Mara{9986}.

Gli-A2h{988}. **v:** Apollo{991}; Basalt{9981}; Hereward{988}; Montjuich{9985}; N. Strampelli{9986}.

Gli-A2i{988}. **v:** Krasnodonka{988}; Lesostepka 75{988}.

Gli-A2j{988}. **v:** Avalon{9981}; Camp Remy{991}; E. Mottin{9981}; Recital{991}.

Gli-A2k{988}. **v:** Akmolinka 1{988}; Estica{991}; Pyrotrix 28{988}; Renan{991}; Zena{9986}.

Gli-A2l{988}. **v:** Chamorro{9985}; Champlein{991}; Longbow{988}.

Gli-A2m{988}. **v:** Marquis{988}; Rex{991}; Suneca{00119}.

Gli-A2n{988}. **v:** Mironovskaya 808{988}.

Gli-A2o{988}. **v:** Calatrava{9985}; Castan{991}; Glenwari{9981}; Lontra{9986}; Touzelle{991}.

Gli-A2p{988}. **v:** Cajeme 71{9985}; Capitole{991}; Clement{991}; Pliska{988}; S. Lorenzo{9986}; Yecora 70{9985}.

Gli-A2q{988}. **v:** Candeal Alcala{9985}; Montcada{9985}; Saratovskaya 39{988}.

Gli-A2r{988}. **v:** Genial{991}; Open{991}; Riband{988}.

Gli-A2s{988}. **v:** Saratovskaya 36{998}.

Gli-A2t{988}. **v:** Courtot{991}; Prostor{9981}; Rinconada{9985}; Soissons{991}.

Gli-A2u{988}. **v:** Aragon 03{9985}; Kirgizskaya Yubileinaya{988}; Saunders{995}; Titien{991}.

Gli-A2v{988}. **v:** Kzyl-Bas{988}.

Gli-A2w{988}. **v:** Bezenchukskaya 98 (biotype){988}.

Gli-A2x{988}. **v:** Solo{988}.

Gli-A2y{9981}. **v:** Gentil Rosso 202{9981}; PI 191245{9981}.

Gli-A2z{9986}. **v:** Gallo{9986}; Giuliana{9986}.

Gli-A2aa{9985}. **v:** Navarro 122{9985}.

Gli-A2ab{9985}. **v:** Navarro 150{9985}.

Gli-A2ac{9981}. **v:** Blanquillo de Barcarrota (MCB-0893){9981}.

Gli-A2ad{9981}. **v:** Hembrilla Soria (MCB-1298){9981}.

Gli-A2ae{9981}. **v:** Candeal de S.Lorenzo Parrilla (MCB-0932){9981}.

Gli-A2af{9981}. **v:** Barbilla de Leon (MCB-1292){9981}.

Gli-A2ag{9981}. **v:** Gluclub{9981}; Tincurrin{9981}.

Gli-A2ah{9981}. **v:** Candeal de Nava del Rey (MCB-0892){9981}.

Gli-A2ai{9981}. **v:** Blanquillo (MCB-0908){9981}.

Gli-A2aj{9984,9987}. null allele **v:** Saratovskaya 29 (mutant){9987}.

Gli-A2ak{10805}. [*Gli-A2*^{m}*a*{10805}]. **dv:** BGE-013630, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2al{10805}. [*Gli-A2*^{m}*b*{10805}]. **dv:** PI 094740, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2am{10805}. [*Gli-A2*^{m}*c*{10805}]. **dv:** PI 190942, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2an{10805}. [*Gli-A2*^{m}*d*{10805}]. **dv:** PI 190947, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2ao{10805}. [*Gli-A2*^{m}*e*{10805}]. **dv:** PI 190946, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2ap{10805}. [*Gli-A2*^{m}*f*{10805}]. **dv:** BGE-013626, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2aq{10805}. [*Gli-A2*^{m}*g*{10805}]. **dv:** PI 191095, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2ar{10805}. [*Gli-A2*^{m}*h*{10805}]. **dv:** BGE-001937, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2as{10805}. [*Gli-A2*^{m}*i*{10805}]. **dv:** PI 191096, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2at{10805}. [*Gli-A2*^{m}*j*{10805}]. **dv:** BGE-020466, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2au{10805}. [*Gli-A2*^{m}*k*{10805}]. **dv:** BGE-001937, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2av{10805}. [*Gli-A2*^{m}*l*{10805}]. **dv:** BGE-029108, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2aw{10805}. [*Gli-A2*^{m}*m*{10805}]. **dv:** BGE-013627, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2ax{10805}. [*Gli-A2*^{m}*n*{10805}]. **dv:** BGE-001937, *T. monococcum* ssp. *monococcum*{10805}.

Gli-A2ay{10811}. [*Gli-A*^{u}*2-I*{10811}]. **dv:** PI-428333, *T. urartu*{10811}.

Gli-A2az{10811}. [*Gli-A*^{u}*2-II*{10811}]. **dv:** PI-428320, *T. urartu*{10811}.

Gli-A2ba{10811}. [*Gli-A*^{u}*2-II*{10811}]. **dv:** PI-428230, *T. urartu*{10811}.

Gli-A2bb{10811}. [*Gli-A*^{u}*2-IV*{10811}]. **dv:** PI-428319, *T. urartu*{10811}.

Gli-A2bc{10811}. [*Gli-A*^{u}*2-V*{10811}]. **dv:** PI-428239, *T. urartu*{10811}.

Gli-A2bd{10811}. [*Gli-A*^{u}*2-VI*{10811}]. **dv:** PI-428336, *T. urartu*{10811}.

Gli-A2be{10811}. [*Gli-A*^{u}*2-VII*{10811}]. **dv:** PI-428235, *T. urartu*{10811}.

Gli-A2bf{10811}. [*Gli-A*^{u}*2-VIII*{10811}]. **dv:** PI-428234, *T. urartu*{10811}.

Gli-A2bg{10811}. [*Gli-A*^{u}*2-IX*{10811}]. **dv:** PI-428183, *T. urartu*{10811}.

Gli-A2bh{10811}. [*Gli-A*^{u}*2-X*{10811}]. **dv:** PI-428256, *T. urartu*{10811}.

Gli-A2bi{10811}. [*Gli-A*^{u}*2-XI*{10811}]. **dv:** PI-428255, *T. urartu*{10811}.

Gli-A2bj{10811}. [*Gli-A*^{u}*2-XII*{10811}]. **dv:** PI-428224, *T. urartu*{10811}.

Gli-A2bk{10811}. [*Gli-A*^{u}*2-XIII*{10811}]. **dv:** PI-428208, *T. urartu*{10811}.

Gli-A2bl{10811}. [*Gli-A*^{u}*2-XIV*{10811}]. **dv:** PI-428202, *T. urartu*{10811}.

Gli-A2bm{10811}. [*Gli-A*^{u}*2-XV*{10811}]. **dv:** PI-428217, *T. urartu*{10811}.

Gli-A2bn{10811}. [*Gli-A*^{u}*2-XVI*{10811}]. **dv:** PI-427328, *T. urartu*{10811}.

Gli-A2bo{10811}. [*Gli-A*^{u}*2-XVII*{10811}]. **dv:** PI-428317, *T. urartu*{10811}.

Gli-A2bp{10811}. [*Gli-A*^{u}*2-XVIII*{10811}]. **dv:** PI-428253, *T. urartu*{10811}.

Gli-A2bq{10811}. [*Gli-A*^{u}*2-XIX*{10811}]. **dv:** PI-538742, *T. urartu*{10811}.

Gli-A2br{10811}. [*Gli-A*^{u}*2-XX*{10811}]. **dv:** PI-428232, *T. urartu*{10811}.

Gli-A2bs{10811}. [*Gli-A*^{u}*2-XXI*{10811}]. **dv:** PI-428188, *T. urartu*{10811}.

Gli-A2bt{10811}. [*Gli-A*^{u}*2-XXII*{10811}]. **dv:** PI-428244, *T. urartu*{10811}.

Gli-A2bu{10811}. [*Gli-A*^{u}*2-XXIII*{10811}]. **dv:** PI-538733, *T. urartu*{10811}.

Gli-A2bv{10811}. [*Gli-A*^{u}*2-XXIV*{10811}]. **dv:** PI-428212, *T. urartu*{10811}.

Gli-A2bw{10811}. [*Gli-A*^{u}*2-XXV*{10811}]. **dv:** TRI-6734, *T. urartu*{10811}.

Gli-A2bx{10811}. [*Gli-A*^{u}*2-XXVI*{10811}]. **dv:** PI-428254, *T. urartu*{10811}.

Gli-B2{1607,1125}. [*Gld 6B*{1415}]. 6B{1607}.6BS{1122}. **v:** CS.

Gli-B2a{988}. **v:** CS{988}.

Gli-B2b{988}. **v:** Bezostaya 1{988}; Cobra{991}; Gladio{9986}; Sideral{991}.

Gli-B2c{988}. **v:** Courtot{991}; Escuala{9985}; Gabo{988}; Loreto{9986}; Manital{9986}; Prinqual{991}; Siete Cerros 66{988}; Sinton{995}; Yecora 70{9985}.

Gli-B2d{988}. **v:** Akmolinka 1{988}; Cesar{9981}; Friedland{991}; Tselinnaya 20{988}.

Gli-B2e{988}. **v:** Arsenal{991}; Veronese{9986}; Zlatna Dolina{994}.

Gli-B2f{988}. **v:** Basalt{9981}; Maris Freeman{988}; Master{991}.

Gli-B2g{988}. **v:** Capitole{991}; Capelle-Desprez{991}; Galahad{988}; Forlani{9986}.

Gli-B2h{988}. **v:** Castan{991}; Mentana{9986}; Pane 247{9985}; Partizanka{994}; Sadovo 1{988}; Sistar{9986}.

Gli-B2i{988}. **v:** Insignia{988}; Robin{9981}.

Gli-B2j{988}. **v:** Farnese{9986}; Funo R250{9986}; Novosadska Rana 1{994}.

Gli-B2k{988}. **v:** Skala{988}.

Gli-B2l{988}. **v:** Clement{991}; Longbow{988}; Tracy{991}.

Gli-B2m{988}. **v:** Mironovskaya 808{988}; Open{991}; Renan{991}.

Gli-B2n{988}. **v:** Japhet{9981}; Rouge de Bordeau{9981}; Solo{988}.

Gli-B2o{988}. **v:** Hardi{9981}; Mara{9986}; Odesskaya 16{988}; Pippo{9986}; Rivoli{991}; Slavjanka{9981}.

Gli-B2p{988}. **v:** Pliska{983}; Champtal{991}; Oderzo{9986}; Recital{991}; Gazul{9985}.

Gli-B2q{988}. **v:** Saratovskaya 39{988}.

Gli-B2r{991}. **v:** Arminda{991}; Estica{991}; Genial{991}.
Gli-B2s{988}. **v:** Aquila{9981}; Saratovskaya 36{988}.
Gli-B2t{988}. **v:** Tselinogradka{988}.
Gli-B2u{988}. **v:** Kirgizskaya Yubileinaya{988}.
Gli-B2v{988}. **v:** Declic{991}; Garant{991}; Libellula{9986}; Mahissa 1{9985}; Poljarka{988}.
Gli-B2w{995,9986}. **v:** Palata{9986}; Pembina{995}; Rieti DIV{9986}.
Gli-B2x{994}. **v:** Super Zlatna (biotype){994}; Prostor{9981}; 251/83{9981}.
Gli-B2y{9986}. **v:** Centauro{9986}; E. Morandi{9986}.
Gli-B2z{9985}. **v:** Maestro{9985}.
Gli-B2aa{9986}. **v:** Salmone{9986}; E. Mottin{9981}.
Gli-B2ab{991}. **v:** Bordier{9981}; Orepi{991}.
Gli-B2ac{991}. **v:** Scipion{991}; Artaban{991}; Riol{991}; Lontra{9981}.
Gli-B2ad{991}. **v:** Champion{991}; Chopin{991}.
Gli-B2ae{991}. **v:** Priam{991}; Etoile d'Choisy{991}; Campeador{9985}; Krajinka (biotype){994}.
Gli-B2af{9985}. **v:** Montjuich{9985}; Mocho Sobarriba{9985}.
Gli-B2ag{9981}. **v:** Jeja del Pais{9985}; Barbilla de Leon (MCB-1292){9981}.
Gli-B2ah{9981}. **v:** Rojo de Humanes (MCB-1262){9981}; Grano de Miracolo{9981}.
Gli-B2ai{9981}. **v:** Blanquillo (MCB-0908){9981}.
Gli-B2aj{9981}. **v:** Negrete de Malaga (MCB-1754){9981}.
Gli-B2ak{9981}. **v:** HY320{9981}; Leader{9981}.
Gli-B2al{9981}. **v:** Dankowska{991}.
Gli-B2am{9981}. **v:** TM-275{9981}; Uralochka{9981}.
Gli-B2an{9981}. **v:** Eagle{9981}; Glenwari{9981}.
Gli-B2ao{9981}. **v:** Olympic{9981}; Mokoan{9981}.
Gli-B2ap{9981}. **v:** Veda{9981}; Magnif 27{9981}.
Gli-B2aq{9981}. **v:** Winglen{9981}; Isis{9981}.
Gli-B2ar{9981}. **v:** Arbon{9981}; Roazon{9981}.
Gli-B2as{9981}. **v:** Strela{9981}; Sredneuralskaya{9981}.
Gli-B2at{9981}. **v:** Ranee{9981}; Javelin 48{9981}.
Gli-B2au{9984,9987}. Null allele **v:** Saratovskaya 29{9987}.

Gli-D2{1334,1125}. [*Gld 6D*{1415}]. 6D{1334}.6DS{1122}. **v:** CS.
Gli-D2a{988}. **v:** CS{988}; Maris Freeman{988}; Sistar{9986}; Tracy{991}.
Gli-D2b{988}. **v:** Bezostaya 1{988}; Cobra{991}; Farnese{9986}; Partizanka{994}.
Gli-D2c{988}. **v:** Escualo{9985}; Eridano{9986}; Rieti DIV{9986}; Siete Cerros 66{988}.
Gli-D2d{988}. **v:** Dneprovskaya 521{988}.
Gli-D2e{988}. **v:** Dollar{9985}; Lada{9981}; Mironovskaya 808{988}; Open{991}.
Gli-D2f{988}. **v:** Creneau{991}; Kirgizskaya Yubileinaya{988}; Rempart{991}.
Gli-D2g{988}. **v:** Capelle-Desprez{991}; Futur{991}; Galahad{988}; Ghurka{988}; Mec{9986}.
Gli-D2h{988}. **v:** Capitole{991}; Chinook{995}; Eagle{00119}; Garant{991}; Sadovo 1{988}; Thatcher{995}.
Gli-D2i{988}. **v:** Insignia 49{00119}; Lario{9986}.
Gli-D2j{988}. **v:** Arcane{991}; Gallo{9986}; Gazul{9985}; Inia 66{9985}; Mentana{9986}.
Gli-D2k{988}. **v:** Crvencapa{944}; Kzyl-Bas{988}; Skala{988}.
Gli-D2l.
Omitted. No reliable differences compared to existing alleles {9981}.
Gli-D2m{988}. **v:** Marquis{988}; Rex{991}; Rinconada{9985}; Suneca{00119}; Veronese{9986}; Yecora 70{9985}.

Gli-D2n{988}. **v:** Castan{991}; Champlein{991}; Mahissa 1{9985}; Mercia{988}; Pippo{9986}.

Gli-D2o{988}. **v:** Omskaya 12{988}.

Note: cultivars Salmone and Resistente, which carry *Gli-D2aa* {9981}, were erroneously given as standards for allele *Gli-D2o* in {9986}.

Gli-D2p{988}. **v:** New Pusa {988}.

Gli-D2q{988}. **v:** Cook{9981}; E. Mottin{9981}; Fournil{991}; Volshebnitsa (biotype){988}; Winglen{9981}; Soissons{991}.

Gli-D2r{988}. **v:** Kremena{988}; Mara{9986}; Montcada{9985}.

Gli-D2s{988}. **v:** Akmolinka 1{988}; Bezenchukskaya 98{988}; Selkirk (biotype){995}.

Gli-D2t{9986}. **v:** Golia{9986}; Gabo{9981}; Manital{9986}; Bokal{9981}.

Gli-D2u{9986}. **v:** Loreto{9986}; Martial{991}; Cibalka{9981}.

Gli-D2v{991}. **v:** Epiroux{991}; Arbon{991}.

Gli-D2w{9985}. **v:** Navarro 150{9985}; Javelin{9981}; Hopps{9981}; Canaleja{9985}.

Gli-D2x{9985}. **v:** Montjuich{9985}; Blanquillo{9985}.

Gli-D2y{9985}. **v:** Candeal Alcala{9985}.

Gli-D2z{9985}. **v:** Aragon 03{9985}.

Gli-D2aa{9981}. **v:** Salmone{9981}; Resistente{9981}.

Gli-D2ab{9981}. **v:** Rojo de Boadilla de Campos (MCB-1031){9981}.

Gli-D2ac{9981}. **v:** Albatros{9981}.

Gli-D2ad{9981}. **v:** Hembrilla Soria (MCB-1298){9981}.

Gli-D2ae{9984,9987}. null allele **v:** Saratovskaya 29 (mutant){9987}.

Gli-Ag^{i}***2***{374}. 6Ag^{i}{374}. **ad:** Vilmorin 27/ *Th. intermedium*.

Gli-R2{781}. [*Sec 2*{1336}]. 2R{781,1336}.2RS{1340}. **ad:** CS/Imperial{781,1336,1340}; Holdfast/King II{1340}.

Gli-R2a{03116}. d1{03116}. **v:** Carnac hexaploid triticale{03116}.

Gli-R2b{03116}. d2{03116}. **v:** Mostral hexaploid triticale{03116}.

Gli-R2c{03116}. t1{03116}. **v:** Alamo hexaploid triticale{03116}.

Gli-R2d{03116}. Null{03116}. **v:** Triticor hexaploid triticale{03116}.

Gli-R2e{03115}. t2{03115}. **v:** Tornado hexaploid triticale{03115}.

Gli-R^{m}***2***{1339}. 6R^{m}{1339,1340}. **ad:** CS/*S. montanum*.

The location of *Gli-R2* in *S. cereale* is thought to have evolved from *S. montanum* {1339} via a translocation between 2R and 6R {1530}.

Gli-S^{l}***2***{573}. 6S^{l}{573}. **ad,su:** CS/*Ae. longissima*.

Gli-U2{1335}. 6U{1335}. **ad:** CS/*Ae. umbellulata*.

Gli-V2{111}. 6VS{111}. **ad:** Creso/*D. villosum*.

Prior to the publication of {988}, allelic variation was demonstrated at all of the wheat *Gli-2* loci, including 13 alleles at *Gli-A2*, 11 at *Gli-B2*, and 10 at *Gli-D2*, in a study of 39 cultivars {996}.

The *Gli-2* alleles present in *57* Yugoslav wheat varieties were determined {994}.

82.3.2.3. Gli-3

A *Gli-3* set of loci coding for omega-type gliadins are located 22 to 31 cM proximal to *Gli-1* on the short arms of group 1 chromosomes {422,1403,589}.

Gli-A3{1403,1119}. [*Gld-2-1A*{1416}]. 1AS{1403}. **v:** Bezostaya 1.

Each of the following *Gli-A3* alleles, apart from *Gli-A3d*, which is a null, controls one minor omega-gliadin with molecular mass about 41k that occurs in the middle of the omega-region of APAGE fractionation. Gliadins controlled by these alleles differ in their electrophoretic mobility in APAGE in that the fastest of three known *Gli-A3*-gliadins is controlled by *Gli-A3a* and the slowest by *Gli-A3c* {9983}.

Gli-A3a{9983}. **v:** CS, Prinqual, Courtot, Tselinogradka, Bezenchukskaya 98.

Gli-A3b{9983}. **v:** Bezostaya 1.

Gli-A3c{9983}. **v:** Anda.

Gli-A3d{9983}. Null{9983}. **v:** Saratovskaya 210, Kharkovskaya 6, Richelle.

Gli-B3{422,1119}. [*Gld-B6*{422},*Glu-B2*{589}]. 1BS{422,589}. **s:** CS*/Thatcher1B{422}. **v:** Sicco{589}.

Gli-B3a{422,589,1119}. **v:** CS.

Gli-B3b{589}. **v:** Sicco.

Gli-B3c{422,1119}. **s:** CS*/Thatcher1B.

Gli-R3{164}. 1RS{164}. **al:** Four inbred lines (R2, J14, 8t, E2666).

Gli-S^{l}***3***{1228}. 1S^{l}S{1228}. **ad,su:** CS/*Ae. longissima*. **ma:** In *Ae. longissima 2/Ae. longissima 10*, three gliadin loci, one glucose phosphate isomerase, and two glutenin loci were mapped relative to one another {1228} as follows: *Glu-S*^{l}*1* 15.9 cM - *Gpi-S*^{l}*1* - 38 cM - *Gli-S*^{l}*4* - 7.1 cM - *Glu-S*^{l}*3* - 0.9 cM - *Gli-S*^{l}*1* - 5.6 cM - *Gli-S*^{l}*5*. *Glu-S*^{l}*1* is located in 1S^{l}L and the other loci are in 1S^{l}S.

Gli-V3{111}. 4VL{111}. **ad:** Creso/*D. villosum*.

82.3.2.4. Gli-4

It is not clear how *Gli-S*^{l}*4* and *Gli-S*^{l}*5* relate to the *Gli-4* and *Gli-5* sets described below.

A locus designated *Gli-A4* controlling omega-gliadins in cv. Perzivan biotype 2 was mapped at 10 cM proximal to *Gli-A1* on the short arm of chromosome 1A {1205}.

However, Metakovsky *et al.* {9983} have since shown that this locus and *Gli-A3* are, in fact, the same locus. Furthermore, Dubcovsky *et al.* {277} did not find evidence for the simultaneous presence of both *Gli-A3* and *Gli-A4* in five 1A or 1A^{m} mapping populations and concluded that *Gli-A4* should be considered to be *Gli-A3* until conclusive evidence for the former is obtained. For these reasons, the locus *Gli-A4* is deleted from the catalogue.

82.3.2.5. Gli-5

A locus designated *Gli-5* controlling omega-gliadins was mapped to the short arms of chromosomes 1A and 1B, distal to *Gli-1* {1147}. The map distance between *Gli-B5* and *Gli-B1* was estimated as 1.4 cM (recombination value of 1.4 +/- 0.4%), although there was significant variation in recombination values over crosses, ranging from 0 % to 5.9 % over the six crosses analysed. This variation was attributed to genotypic influence on the frequency of recombination.

Gli-A5{1147}. 1AS{1147}. **v:** Salmone.

Gli-A5a{9983}. Null{9983}. **v:** CS.

Gli-A5b{9983}. **v:** Marquis.

Allele *Gli-A5b* controls two slow-moving, easily-recognizable omega-gliadins. It is present in all common wheat cultivars having alleles *Gli-A1m* and *Gli-A1r* (and, probably, in those having *Gli-A1e*, *Gli-A1l* and *Gli-A1q*), because earlier (for example, in {988}) two minor omega-gliadins encoded by *Gli-A5b* were considered to be controlled by these *Gli-A1* alleles {9983}.

Gli-B5{1147}. 1BS{1147}. **v:** Salmone.

Gli-B5a{1147}. **v:** CS.

Gli-B5b{1147}. **v:** Salmone.

In {988}, omega-gliadins controlled by *Gli-B5* (allele *Gli-B5b*) were attributed to alleles at the *Gli-B1* locus (alleles *Gli-B1c, i, k, m, n* and *o*).

82.3.2.6. Gli-6

Gli-A6{9983,993}. 1AS{9983}.

Gli-A6 was first explicitly described in {9983}, but it was first observed without designation in {993}. There is strong evidence that it is distinct from *Gli-A3* and *Gli-A5*, mapping distally to *Gli-A1*, with which it recombines at a frequency of 2-5%. Currently three alleles are known, of which *Gli-A6c* is particularly well-described in {9983}: the molecular mass of the omega-gliadin controlled by this allele is slightly lower than those of the omega-gliadins controlled by *Gli-A3* alleles. In {988}, the omega-gliadin controlled by *Gli-A6c* was attributed to *Gli-A1f*. *Gli-A6c* is rather frequent in common wheat and may relate to dough quality (preliminary data {9983}). *Gli-A6a* is null {9983}.

Gli-A6a{9983}. Null{9983}. **v:** CS, Bezostaya 1.
Gli-A6b{9983}. **v:** Bezenchukskaya 98.
Gli-A6c{9983}. **v:** Courtot, Anda, Mironovskaya 808.

82.3.2.7. Gli-7

Gli-A7{10547}. 1DS{10547}. **dv:** AUS18913{10547}.

The gamma-gliadin encoded by this locus co-segregated with the T1 omega-gliadin encoded by the *Gli-D^{t}T1* locus (currently included in the Catalogue as locus (*Gli-DT1*). *Gli-A7* was located 0.69 cM from *Gli-D^{t}1* {10547}.

Four new classes of low molecular weight proteins related to gliadins, though not sufficiently similar to be classified as such, were reported in {02113}. One of the classes has no close association to previously described wheat endosperm proteins.

82.3.3. Other endosperm storage proteins

Tri-A1{1357, 1358}. 1AS{1357}. **v:** CS.
  Tri-A1a. [*cs*{1358}]. **v:** CS.
  Tri-A1b. [*h*{1358}]. **v:** Hope.
Tri-D1{1357,707,1358}. 1DS{1357}. **v:** CS.
  Tri-D1a. [*cs*{1358}]. **v:** CS.
  Tri-D1b. [*i*{1358}]. **v:** India 115.

82.3.3.1. Triticin proteins

The triticin proteins {1360} or [Triplet proteins {1357}] are storage globulins with homology to pea legumins and related proteins in oats, rice and several dicotyledonous species {1360}. Triticin gene segments including its hypervariable region were PCR-amplified, with preferential amplification of *Tri-D1* for the only pair of primers giving consistent results {10322}.

82.4. Enzyme Inhibitors

82.4.1. Inhibitors of alpha-amylase and subtilisin

Isa-A1{908}. 2AL{908}. **v:** CS.
  Isa-A1a{908}. **v:** CS.
  Isa-A1b{908}. Null allele. **v:** Cajeme 71.
Isa-B1{908}. 2BL{908}. **v:** CS.
  Isa-B1a{908}. **v:** CS.

Isa-B1b{908}. **v:** Bihar.
Isa-D1{908}. 2DL{908}. **v:** CS.

Orthologous genes were identified in *Ae. speltoides* and *T. timopheevii* {908}. All durum wheats investigated had the genotype *Isa-A1b, Isa-B1b*.

82.4.2. Inhibitors (dimeric) of heterologous alpha-amylases

Chromosome 3BS has duplicated loci controlling two dimeric inhibitors of exogenous a-amylases, one known as 0.53 or Inh I {1260}, and the other as WDA I-3 {1260}. Chromosome 3DS has a homoeologous locus controlling a dimeric inhibitor of exogenous a-amylases, known as 0.19 or Inh III {1260,0124}, that is closely related to 0.53/Inh I. Intervarietal polymorphism for the WDA-3 protein was identified by isoelectric focussing of water-soluble endosperm proteins {0124}. This was interchromosomely mapped on 3BS using both a DH population of Cranbrook/Halberd, and a set of RILs of Opata 85/W-7984 (ITMI population) {0125}.

Three genome allele specific primer sets were designed for the 3BS and 3DS alpha-amylase inhibitors in cv. Chinese Spring, based upon SNPs. Their validity was confirmed in 15 accessions of *Triticum urartu, Triticum monococcum, Aegilops tauschii* and *Triticum dicoccoides*. The results offered support that the 24kDa dimeric alpha-amylase inhibitors in cultivated wheat are encoded by a multigene family {10323}, previously proposed in {10324}, as the result of phylogenetic analysis of sequences characterized by cSNPs.
Iha-B1.1{1260}. 3BS{1260}. **v:** CS{1260}.
Iha-B1.2{0124}. 3BS{0124}. **v:** CS{0124}.
Iha-B1.2a{0124}. **v:** CS{0124,0125}.
Iha-B1.2b{0125}. Null allele. **v:** Cadoux{0125}; Cranbrook{0125}; Tasman{0125}.
Iha-D1{1260}. 3DS{1260}. **v:** CS{1260}.

82.4.3. Subtilisin inhibition

Si-R1{529}. 2R{529}.2RS{701}. **ad:** CS/Imperial, Holdfast/King II.
Si-H1{528}. [*Isa 1*{528}]. 2H{528}. **ad:** CS/Betzes.

Si-B2{701}. 1BS{701}. **su:** Bersee (Koga II).
Si-D2{701}. 1DS{701}. **v:** Koga II.
Si-H2{528},{701}. [*Ica 1*{528},*Ica 2*{528}]. 1H{528}. **ad:** CS/Betzes.
Si-R2{529},{701}. 1R{529}.1RS{701}. **ad:** CS/Imperial{529}. **tr:** Gabo 1BL.1RS{701}.
Si-S^{l}2{701}. 1S^{l}{701}. **ad:** CS/*Ae. longissima*.
Si-U2{701}. 1U{701}. **ad:** CS/*Ae. umbellulata*.

Considerable genetic variation for *Si-2* was noted in {701}. A chromosome location for *Si-H2* on 1HL was inferred in {528} but questioned in {701}.
Three subunits of the wheat tetrameric inhibitor of insect a-amylase, CM1, CM3 and CM16, with homology to the dimeric and monomeric a-amylase inhibitors and the trypsin inhibitors, were located by Southern analysis of cDNAs pCT1, pCT2, and pCT3 to 4A, 4B, 4D; 7A, 7B, 7D; and 4A, 4B, 4D, respectively {427}.
Genes encoding proteins which inhibit the action of mammalian and insect, but not cereal, a-amylases, were located in chromosomes 3BS, 3DS and 6DS of Chinese Spring {1260}. Also, genes encoding inhibitors of insect a-amylases were located in *H. chilense* chromosomes 4H^{ch} and 7H^{ch} {1262}.

82.4.4. Trypsin inhibition

Ti-H1. [*Itc 1*{528}]. 3H{528}. **ad:** CS/Betzes.

Ti-R1. 3R{529}. **ad:** CS/Imperial.

Ti-A2{699}. 5AL{699}. **v:** CS.

Ti-B2{699}. 5BL{699}. **v:** CS.

Ti-D2{699}. 5DL{699}. **v:** CS.

Ti-D2a{699}. **v:** CS.

Ti-D2b{699}. **v:** Champlein.

Ti-D2c{699}. **v:** Synthetic.

Ti-Ag^{i}2{699}. 5Ag^{i}{699}. **ad:** Vilmorin 27/ *Th. intermedium*.

Ti-M^{t}2{699}. 5M^{t}{699}. **ad:** CS/*Ae. mutica*.

Ti-R2{699}. 5RL{699}. **ad:** CS/Imperial. **su:** CS/King II.

Ti-S^{l}2{699}. 5S^{l}L{699}. **ad:** CS/*Ae. sharonensis*.

Ti-U2{699}. 1U{699}. **ad:** CS/*Ae. umbellulata*.

82.5. Other proteins

82.5.1. Grain softness protein

Gsp-1{1185}.

Gsp-A1{614}. [*GSP*{614}]. 5A{614,0383}. **v:** CS{614,0383}; Rosella (GenBank AF177218){0383}.

In {1185} partial-sequence clone TSF61 from cv. Soft Falcon (GenBank X80380) was identical to this allele.

Gsp-B1{614}. [*GSP*{614}]. 5B{614}. **v:** CS{614}; Glenlea{0385}.

In {1185} sequence of clone TSF33 from cv. Soft Falcon (GenBank X80379) was identical to this allele, as are ESTs for cv. CS (dbEST BJ235798) and cv. CNN (dbEST BE423845).

Gsp-D1{614}. [*GSP*{614}]. 5DS{614}.

Gsp-D1a. **v:** CS{614}; Glenlea{0385}. **dv:** *Ae. tauschii* CPI1110799 (GenBank AF177219){0383}. **ma:** Co-segregation of *Gsp-D1* and *Ha*{614}.

In {1185} the sequence of clone TSF69 from cv. Soft Falcon (GenBank S72696) is identical, as are ESTs for cv CS (dbEST BJ237450) and cv CNN (dbEST BE422565). This locus has a large deletion encompassing genes *Pina-D1, Pinb-D1* and *Gsp-D1*{10077}.

Gsp-D1b{03105}. **dv:** *Ae. tauschii* TA1583 (GenBank AY252079) *Pina-D1a, Pinb-D1a*{03105}; TA2475 (GenBank AY252087) *Pina-D1a*, *Pina-D1i*{03105}.

Gsp-D1c{03105}. **dv:** *Ae. tauschii* TA2369 (GenBank AY252081) *Pina-D1c, Pinb-D1h*{03105}; CPI110799 (GenBank AF177219){0383}.

Gsp-D1d. **dv:** *Ae. tauschii* TA2536 (GenBank 252093) *Pina-D1c*, *Pinb-D2i*{03105}; TA2374 (GenBank AY252046) *Pina-D1d, Pinb-D1i*{03105}; TA2458 (GenBank AY252084) *Pina-D1e, Pinb-D1i*{03105}; TA2436 (GenBank AY252048) *Pina-D1f, Pinb-D1i*{03105}.

Gsp-D1e. **dv:** *Ae. tauschii* TA2527 (GenBank AY252066) *Pina-D1c, Pinb-D1h*{03105}; TA2512 (GenBank AY252092) *Pina-D1d, Pinb-D1i*{03105}; TA2495 (GenBank AY252091) *Pina-D1e, Pinb-D1i*{03105}.

Gsp-D1f. **dv:** *Ae. tauschii* TA1649 (GenBank AY252063) *Pina-D1d, Pinb-D1h*{03105}; TA2455 (GenBank AY252073) *Pina-D1d, Pinb-D1i*{03105}.

Gsp-D1g. **dv:** *Ae. tauschii* TA1599 (GenBank AY252062) *Pina-D1a, Pinb-D1j*{03105}.

Gsp-D1h. **dv:** *Ae. tauschii* TA1691 (GenBank AY252064) *Pina-D1a, Pinb-D1j*{03105}.

Gsp-D1i{03105}. **v:** Yecora Rojo (GenBank AY255771) *Pina-D1b, Pinb-D1a*{03105}.

Gsp-D1j{10077}. **s:** CS*/Red Egyptian 5D, *Pina-D1, Pinb-D1* and *Gsp-D1*{10077}.

82.5.2. Histone H1 Proteins

HstH1-A1{0215}. 5AL{0215}. **v:** CS{0215}.
HstH1-B1{0215}. 5BL{0215}. **v:** CS{0215}.
HstH1-D1{0215}. 5DL{0215}. **v:** CS{0215}.
  HstH1-D1a{0215}. **v:** CS{0215}; 18 others{0215}.
  HstH1-D1b{0215}. **v:** Grekum 114{0215}; Kirgizsky Karlik{0215}.

HstH1-A2{0215}. 5AL{0215}. **v:** CS{0215}.
  HstH1-A2a{0215}. **v:** CS{0215}.
  HstH1-A2b{0215}. Null allele{0215}. **v:** Mara{0215}; 10 others{0215}.
HstH1-B2{0215}. 5BL{0215}. **v:** CS{0215}.
  HstH1-B2a{0215}. **v:** CS{0215}; 19 others{0215}.
  HstH1-B2b{0215}. **v:** Excelsior{0215}.
HstH1-D2{0215}. 5DL{0215}. **v:** CS{0215}.

The relationship of this gene series with a *Hst-A1, Hst-B1, Hst-D1* series in group 5 chromosomes {0216} based on DNA hybridization studies was not established.

82.5.3. Iodine binding factor

A monomeric water soluble protein from mature grain which preferentially binds iodine {818}.

Ibf-A1{818}. 5AL{818}. **v:** CS.
  Ibf-A1a{818}. **v:** CS.
  Ibf-A1b{818}. **v:** Cappelle-Desprez.
  Ibf-A1c{818}. **v:** Hope.
  Ibf-A1d{818}. **v:** Chris.
  Ibf-A1e{818}. **v:** Sears' Synthetic.
Ibf-B1{818}. 5BL{818}. **v:** CS.
  Ibf-B1a{818}. **v:** CS.
  Ibf-B1b{818}. **v:** Cappelle-Desprez.
  Ibf-B1c{818}. **v:** Ciano 67.
  Ibf-B1d{818}. **v:** Sears' Synthetic.
Ibf-D1{818}. 5DL{818}. **v:** CS.
  Ibf-D1a{818}. **v:** CS.
  Ibf-D1b{818}. **v:** Cappelle-Desprez.
  Ibf-D1c{818}. **v:** Purple Pericarp.
  Ibf-D1d{818}. **v:** Sears' Synthetic.
Ibf-Ag^{i}***1***{818}. 5Ag^{i}{818}. **ad:** Vilmorin/*Th. intermedium*.
Ibf-E1{818}. 5EL{818}. **ad:** CS/*E. elongata*.
Ibf-H1{818}. 4H{818}. **ad:** CS/Betzes.
Ibf-R1{818}. 5RL{818}. **ad:** CS/Imperial, CS/KingII.
Ibf-S^{l}***1***{818}. 5S^{l}{818}. **ad:** CS/*Ae. sharonensis*.
Ibf-U1{818}. 5U{818}. **ad:** CS/*Ae. umbellulata*.

82.5.4. Lipopurothionins

Pur-A1{351}. 1AL{351}. **v:** CS{351}.
  A PCR marker specific for *Pur-A1* was developed in {9976}.
Pur-B1{351}. 1BL{351}. **v:** CS{351}.
  A PCR marker specific for *Pur-B1* was developed in {9976}.

Pur-D1{351}. 1DL{351}. **v:** CS{351}.

A locus in chromosome 5DS affects the level of lipopurothionin {351}.

PCR marker specific for *Pur-D1* was developed in {9976}.

Pur-R1. 1RL{1261} = 1RS.1BL.. **ad:** CS/Imperial. **su:** Several 1R(1B) lines. **tr:** Aurora, Kavkaz.

A PCR marker specific for *Pur-R1* was developed in {9976}.

82.5.5. Lectins

Lec-A1. 1AL{1427}. **v:** CS.

Lec-B1. 1B{1427}. **s:** CS*/Hope 1B.

Lec-D1. 1DL{1427}. **v:** CS.

Lec-U1. 1U{1427}. **ad:** CS/*Ae. umbellulata*.

82.5.6. Puroindolines and grain softness protein

Puroindolines a and b are the major components of friabilin, a protein complex that is associated with grain texture (see 'Grain Hardness'). The name 'puroindoline' and the complete amino acid sequence of puroindoline a were given in {0382} from cv Camp Remy. Hard grain texture in hexaploid wheat results from unique changes in the puroindoline amino acid sequence or, currently, four null forms {0295} of the completely linked genes (max. map distance 4.3 cM) {452}. Tetraploid (AABB, AAGG) wheats lack puroindolines and are consequently very hard {03103}. A searchable database of wheat varieties and their puroindoline genotype is available at http://www.wsu.edu/~wwql/php/puroindoline.php. Grain softness protein-1 is a closely related gene which is closely located to the puroindoline genes {03111,1185}. 'GenBank' and 'dbEST' refer to sequence databases available at NCBI (also available throught EMBL and DDB).

Recent reviews {10522, 10523} provide comprehensive descriptions of the molecular genetics and regulation of puroindolines. Morris and Bhave {10524} reconciled the D-genome puroindoline alleles with DNA sequence data. Bonafede et al. {10525, 10526} developed a CS line (PI 651012) carrying a 5A^{m}S.5AS translocation from *T. monococcum*; the translocated chromatin carries A-genome *Pina, Pinb* and *Gsp-1* alleles that confer softer kernel texture.

Pina-A1{03103,03108,03104}. **dv:** *T. urartu* unspecified accession {03103}; TA763(GenBank AJ302094){03108,03104}; TA808(GenBank AJ302095){03108,03104}.

Pina-D1{452}. 5DS{452}. **v:** CS (GenBank DQ363911){03108}; Capitole (GenBank X69914){03110}.

This locus has a large deletion encompassing genes *Pina-D1, Pinb-D1* and *Gsp-D1*. This allelic combination confers a harder kernel texture than *Pina-D1a/Pinb-D1b* {10077}.

Pina-D1a{452}. **v:** Bellevue{0249}; Capitole (GenBank X69914){03110}; Courtot{0249}; Fortuna{0249}; Galaxie{0249}; Heron{1035}; Renan (GenBank CR626934){10440}; Soissons{0249}. **v2:** Aurelio *Pinb-D1a*{0249}; Bezostaja *Pinb-D1b*{0249}; Bilancia *Pinb-D1a*{0249}; Bolero *Pinb-D1a*{0249}; Brasilia *Pinb-D1b*{0249}; Centauro *Pinb-D1a*{0249}; Cerere *Pinb-D1b*{0249}; CS *Pinb-D1a*{452,0249}; Colfiorito *Pinb-D1b*{0249}; Cologna 21 *Pinb-D1b*{0249}; David *Pinb-D1b*{0249}; Democrat *Pinb-D1b*{0249}; Etruria *Pinb-D1b*{0249}; Francia *Pinb-D1b*{0249}; Gemini *Pinb-D1b*{0249}; Genio *Pinb-D1b*{0249}; Gladio *Pinb-D1b*{0249}; Lampo *Pinb-D1a*{0249}; Leone *Pinb-D1a*{0249}; Leopardo *Pinb-D1a*{0249}; Libero *Pinb-D1a*{0249}; Livio *Pinb-D1a*{0249}; Marberg *Pinb-D1b*{0249}; Mentana *Pinb-D1a*{0249}; Mieti *Pinb-D1b*{0249}; Mose *Pinb-D1a*{0249}; Neviana *Pinb-D1a*{0249}; Newana *Pinb-D1b*{0249}; Oscar *Pinb-D1a*{0249}; Pandas

Pinb-D1b{0249}; Pascal *Pinb-D1b*{0249}; Penawawa *Pinb-D1a*{03104}; Sagittario *Pinb-D1b*{0249}; Salgemma *Pinb-D1b*{0249}; Saliente *Pinb-D1b*{0249}; Salmone *Pinb-D1b*{0249}; Serena *Pinb-D1a*{0249}; Serio *Pinb-D1b*{0249}; Veda *Pinb-D1b*{0249}; Zena *Pinb-D1b*{0249}. **dv:** *Ae. tauschii* upspecified accession (GenBank AJ249935){03103}; TA2475 (GenBank AY252037) *Pinb-D1i, Gsp-D1b*{03105}; TA1599 (GenBank AY252011) *Pinb-D1j, Gsp-D1g*{03105}; TA1691 (GanBank AY252013) *Pinb-D1j, Gsp-D1h*{03105}; *Ae. tauschii* unidentified accession (GenBank AJ249935){03103}; *Ae. tauschii* CPI 110799 (GenBank CR626926){10440}.

Pina-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats that carry a hardness mutation in puroindoline b {452,1035,0082,0204,0295}.

Pina-D1b{1035}. Null allele. **i:** Falcon/7*Heron, Heron/7*Falcon{03109}; Gamenya sel.{0298,0203}; Heron/7*Falcon sel.{0298,0203}; PI 644080 (Alpowa/ID377s//7*Alpowa){10429}; Near-isogenic pairs were developed in McNeal, Outlook, Hank, Scholar and Explorer{10527}. **v:** Butte 86{1035}; Eridano{0249}; Falcon{1035}; Glenlea (GenBank AB262660). This BAC clone also contains *Pinb-D1a*{10431}; Kalyansona{0249}; Super X{0249}; Yecora Rojo{0204}. **v2:** Amidon *Pinb-D1a*{0249}; Ciano *Pinb-D1a*{0249}; Dorico *Pinb-D1a*{0249}; Golia *Pinb-D1a*{0249}; Guadalupe *Pinb-D1a*{0249}; Barra *Pinb-D1a*{0249}; Inia 66 *Pinb-D1a*{0249}; Indice *Pinb-D1a*{0249}; Jecora *Pinb-D1a*{0249}; Manital *Pinb-D1a*{0249}; Mendos *Pinb-D1a*{0249}; Padus *Pinb-D1a*{0249}; Prinqual *Pinb-D1a*{0249}; Sibilia *Pinb-D1a*{0249}.

Present only in some hard hexaploid wheats. *Pina-D1b* is associated with harder texture than *Pinb-D1b* {0177,0206}.

This allele is now defined as a 15,380 bp deletion versus other possible puroindoline a nulls {10428,10391}.

Pina-D1c{03105}. **dv:** *Ae. tauschii* TA2369 (GenBank AY252031) *Pinb-D1h, Gsp-D1c*; TA2527 (GenBank AY252015) *Pinb-D1h, Gsp-D1e*{03108}; *Ae. tauschii* TA10 (GenBank AY649746){03108}.

Pina-D1d{03105}. **dv:** *Ae. tauschii* PI452131 (GenBank AJ302098) *Pinb-D1i*{03104}; PI554318 (GenBank AJ302099) *Pinb-D1k*{03104}; TA1649 (GenBank AY252012) *Pinb-D1h, Gsp-D1f*{03105}; TA2374 (GenBank AY251996) *Pinb-D1i, Gsp-D1d*{03105}; TA2512 (GenBank AY252042) *Pinb-D1i, Gsp-D1e*{03105}; TA2455 (GenBank AY252022) *Pinb-D1i, Gsp-D1f*{03105}; TA2536 (GenBank AY252043){03105}; *Ae. tauschii* TA 1704 (GenBank AY649744){03108}.

Pina-D1e{03105}. **dv:** *Ae. tauschii* TA2458 (GenBank AY252034) *Pinb-D1i, Gsp-D1d*{03105}; TA2495 (GenBank AY252041) *Pinb-D1i, Gsp-D1e*{03105}.

Pina-D1f{03105}. **dv:** *Ae. tauschii* TA2436 (GenBank AY251998) *Pinb-D1i, Gsp-D1d*{03105}.

Pina-D1g{03105}. **dv:** *Ae. tauschii* TA1583 (GenBank AY252029) *Pinb-D1a, Gsp-D1b*{03105}.

Pina-D1h{10118}. **v:** *X. aegilotriticum* CIGM86.946-1B-0B-0PR-0B (GenBank AY573898) *Pinb-D1o*{10118}.

Pina-D1i{10118}. **v:** *X. aegilotriticum* CIGM87.2784-1B-0PR-0B (GenBank AY573899) *Pinb-D1k*{10118}.

Pina-D1j{10118}. **v:** *X. aegilotriticum* CIGM88.1363-0B (GenBank AY573900) *Pinb-D1o*{10118}.

Pina-D1k{10077}. [*homonym:Pina-D1b/Pinb-D1h(t)*]. **s:** CS*/Red Egyptian 5D substitution line, *Pinb-D1q, Gsp-D1i*{10077}. **v:** Bindokku{10305}; Cheyenne-A{10305}; Chosen 68{10305}; Gaiyuerui{10316}; KT020-584{10432}; Saiiku 18{10305}; Saiiku 44{10305}; Safangmai{10316}; Tachun2 {10316}; ZM2851{10316}; ZM2855{10316}.

This allele is currently used to denote a large deletion of undetermined size that involves

Pina-D1, Pinb-D1 and *Gsp-D1* {10077}. The deletion of both puroindolines is associated with harder kernel texture than other known puroindoline hardness alleles {10077,10305, 10432).

Pina-D1l{10168}. [*Pina-D1c*{10168}]. **v:** Baikezaomai Chinese landraces{10208}; Chengduguangtou{10208}; Guangtouxiaomai{10208}; Sanyuehuang{10208}; Xiaoyuhua{10208}. **v2:** Fortuna (USA) *Pinb-D1a*{10168}; Glenman *Pinb-D1a*{10168}.

Pina-D1l has a C deletion leading to an open reading frame shift and premature stop codon; PINA null, hard kernel texture {10208}.

Pina-D1m{10208}. **v:** Hongheshang (GenBank EF620907){10208}.

C-to-T substitution: Proline-35 to serine; hard kernel texture {10208}.

Pina-D1n{10208}. **v:** Baimangchun{10208}; Hongheshang (GenBank EF620907){10208}; Xianmai (GenBank EF620908){10208}; Yazuixiaomai Chinese landraces{10208}; Yazuizi{10208}; Zhuantoubaike{10208}.

G-to-A substitution: Tryptophan-43 to stop codon; PINA null hard kernel texture {10208}.

Pina-D1o{10311}. **dv:** *Ae. tauschii* RM0182 (GenBank AY608595){10311}.

Pina-D1p{10316}. **v:** *T. aestivum* Jing 771 (GenBank AY599893){10316}.

Pina-D1q{10316}. **v:** U29 (GenBank AB181238){10316}; Muu-27 (homonym 'a2', *Pina-D1p*){10316}.

Pina-A^{m}1{0083}. 5A^{m}S{0083}. **dv:** *T. monococcum* DV92(cultivated), G3116 (spp. *aegilopoides*) (GenBank AJ242715){0083}; unspecified acession (GenBank AJ249933){03103}; PI277138 (GenBank AJ302093){03104}; PI418582 (GenBank AJ302092){03104}; *T. monococcum* spp. *monococcum* TA2025, TA2026 (GenBank AY622786), TA2037 (GenBank AJ242715){03108}; *T. monococcum* spp. *aegilopoides* TA183, TA291, TA546, TA581 (GenBank AY622786){03108}.

In *T. monococcum Pina-A^{m}1* is completely linked to *Gsp-A^{m}1*{0083}.

Pina-S1{03108}. **dv:** *Ae. speltoides* PI 393494 (GenBank AJ302096){03104}; PI 369616 (GenBank AJ302097){03104}; *Ae. speltoides* spp. *speltoides* TA2368 (GenBank AY622787), TA1789 (GenBank AY622788){03108}; *Ae. speltoides* spp. *ligustica* TA1777 (GenBank AY622789){03108}.

Pina-S^{b}1{03108}. **dv:** *Ae. bicornis* spp. *typica* TA1954, TA1942{03108}.

Pina-S^{l}1{03108}. **dv:** *Ae. longissima* spp. *longissima* TA1912 (GenBank AY622790){03108}; *Ae. longissima* spp. *nova* TA1921 (GenBank AY622791){03108}.

Pina-S^{s}1{03108}. **dv:** *Ae. searsii* TA1837, TA1355 (GenBank AY622792){03108}.

Pina-S^{sh}1{03108}. **dv:** *Ae. sharonensis* TA1999 (GenBank AY622796){03108}.

Pinb-A1{03108,03104}. **dv:** *T. urartu* TA763 (GenBank AJ302103){03104}; TA808 (GenBank AJ302104){03108,03104}.

Pinb-D1. 5DS{452}. **v:** CS{452}; Capitole (GenBank X69912){03110}.

Pinb-D1a{452}. **v:** Hill 81{452}. **v2:** Adder *Pina-D1a*{0317}; Amidon *Pina-D1b*{0249}; Aurelio *Pina-D1a*{0249}; Barra *Pina-D1b*{0249}; Bilancia *Pina-D1a*{0249}; Bolero *Pina-D1a*{0249}; Centauro *Pina-D1a*{0249}; CS *Pina-D1a*{452,0249}; Ciano *Pina-D1b*{0249}; Dorico *Pina-D1b*{0249}; Fortuna (USA) *Pina-D1b*{0249}; Glenman *Pina-D1b*{0249}; Golia *Pina-D1b*{0249}; Guadalupe *Pina-D1b*{0249}; Inia 66 *Pina-D1b*{0249}; Jecora *Pina-D1b*{0249}; Idice *Pina-D1b*{0249}; Karl *Pina-D1a*{0317}; Lampo *Pina-D1a*{0249}; Leone *Pina-D1a*{0249}; Leopardo *Pina-D1a*{0249}; Libero *Pina-D1a*{0249}; Livio *Pina-D1a*{0249}; Manital *Pina-D1b*{0249}; Mendos *Pina-D1b*{0249}; Mentana *Pina-D1a*{0249}; Mose *Pina-D1a*{0249}; Neviano *Pina-D1a*{0249}; Oscar *Pina-D1a*{0249}; Padus *Pina-D1b*{0249}; Penawawa *Pina-D1a*{03104}; Prinqual *Pina-D1b*{0249}; Serena *Pina-D1a*{0249}; Sibilia *Pina-D1b*{0249}; Sigyn II *Pina-D1a*{0317}. **dv:** *Ae. tauschii* unspecified accession (GenBank AJ249936){03103}; TA1583 (GenBank AY251981) *Pina-D1a, Gsp-D1b*{03105}.

Pinb-D1a is present in all soft hexaploid wheats and possibly all hard hexaploid wheats carrying the *Pinb-D1b, -D1c, -D1d, -D1e, or -D1f* mutations {452,1035,0082,0204,0295}.

Pinb-D1b{452}. 5DS{452}. **i:** Paha*2/Early Blackhull/5*Paha{0298,0203}; Early Blackhull der./5*Nugaines sel.{0298,0203}; hard sib sel. from Weston{03107}; PI 644081 (Alpowa/ND2603//7*Alpowa){10429}. **s:** CS*7/Cheyenne 5D{452}. **v:** Thatcher{0204}; Wanser{452}; hard component of Turkey{0204}; Cheyenne (GenBank DQ363914){10315}; Renan (GenBank CR626934){10440}. **v2:** Bastion *Pina-D1a*{0317}; Bezostaya *Pina-D1a*{0249}; Brasilia *Pina-D1a*{0249}; Cerere *Pina-D1a*{0249}; Colfiorito *Pina-D1a*{0249}; Cologna 21 *Pina-D1a*{0249}; David *Pina-D1a*{0249}; Democrat *Pina-D1a*{0249}; Etruria *Pina-D1a*{0249}; Francia *Pina-D1a*{0249}; Gemini *Pina-D1a*{0249}; Genio *Pina-D1a*{0249}; Gladio *Pina-D1a*{0249}; Marberg *Pina-D1a*{0249}; Mieti *Pina-D1a*{0249}; Newana *Pina-D1a*{0249}; Pandas *Pina-D1a*{0249}; Pascal *Pina-D1a*{0249}; Sagittario *Pina-D1a*{0249}; Salgemma *Pina-D1a*{0249}; Saliente *Pina-D1a*{0249}; Salmone *Pina-D1a*{0249}; Serio *Pina-D1a*{0249}; Veda *Pina-D1a*{0249}; Zena *Pina-D1a*{0249}.

Pinb-D1b is a "loss-of-function" mutation resulting from the replacement of a glycine by a serine at position 46 {452}.

Pinb-D1c{0082}. **i:** PI 644082 (Alpowa/Red Bobs//7*Alpowa){10429}. **v:** Avle{0082}; Bjorke{0082}; Portal{0082}; Reno{0082}; Tjalve{0082}.

Pinb-D1c is a "loss-of-function" mutation resulting from the replacement of a leucine by a proline at position 60 {0082}.

Pinb-D1d{0082}. **i:** PI 644083 (Alpowa/Mjolner//7*Alpowa){10429}. **v:** Bercy{0082}; Mjolner{0082}; Soissons (homonym 'b1'){10433}.

Pinb-D1d is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a arginine at position 44 {0082}.

Pinb-D1e{0204}. **i:** PI 644084 (Alpowa/Canadian Red//7*Alpowa){10429}. **v:** Gehun{0204}; Canadian Red{0204}; Chiefkan{0204}; Yunxianxiaomai{10427}.

Pinb-D1e is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a stop codon at position 39 {0204}.

Pinb-D1f{0204}. **i:** PI 644085 (Alpowa/Sevier//7*Alpowa){10429}. **v:** Abyssinia AV12.4{10430}; The hard component of Utac{0204}.

Pinb-D1f is a "loss-of-function" mutation resulting from the replacement of a tryptophan by a stop codon at position 44 {0204}.

Pinb-D1g{0204}. **i:** PI 644086 (Alpowa/Andrews//7*Alpowa){10429}. **v:** Andrews{0204}.

Pinb-D1g is a "loss-of-function" mutation resulting from the replacement of a cysteine by a stop codon at position 56 {0204}.

Pinb-D1h{03105}. **dv:** *Ae. tauschii* TA2369 (GenBank AY251983) *Pina-D1c, Gsp-D1c*{03105}; TA2527 (GenBank AY251965) *Pina-D1c, Gsp-D1e*{03105}; TA1649 (GenBank AY251963) *Pina-D1d, Gsp-D1f*{03105}; TA10 (GenBank AY649748){03108}; CPI110799 (GenBank AY159804){10037}.

Pinb-D1i{03105}. **dv:** *Ae. tauschii* TA2475 (GenBank AY251989) *Pina-D1a, Gsp-D1b*{03105}; TA2536 (GenBank AY251993) *Pina-D1c, Gsp-D1d*{03105}; TA2374 (GenBank AY251948) *Pina-D1d, Gsp-D1d*{03105}; TA2512 (GenBank AY251992) *Pina-D1d, Gsp-D1e*{03105}; TA2455 (GenBank AY251972) *Pina-D1d, Gsp-D1f*{03105}; TA2458 (GenBank AY251986) *Pina-D1e, Gsp-D1d*{03105}; TA2495 (GenBank AY251991) *Pina-D1e, Gsp-D1e*; TA2436 (GenBank AY251947) *Pina-D1f, Gsp-D1d*{03105}; *Ae. tauschii* TA1704 and TA2381 (GenBank AY649747){03108,10315}; *Ae. tauschii* isolate Q03-002 (GenBank DQ257553) (referred to as allele 2){10314}; *Ae. tauschii* CPI 110799 (GenBank CR626926){10440}.

Q03-002, TA1704, and TA2381 were incorrectly assigned *Pinb-D1w* in the 2006 supplement.

Pinb-D1j{03105}. **dv:** *Ae. tauschii* TA1599 (GenBank AY251962) *Pina-D1a, Gsp-D1g*{03105}; TA1691 (GenBank AY251964) *Pina-D1a, Gsp-D1h*{03105}; *Ae. tauschii* TA1691 (GenBank AY251946){03108}.

Pinb-D1k. **dv:** *Ae. tauschii* PI554318 (GenBank AJ302108) *Pina-D1d*{03104}.

Pinb-D1l{10119}. **v:** GaoCheng8901{10119}.
{10208} reported *Pinb-D1b* in Gaocheng 8901.

Pinb-D1m{10118}. **v:** *X. aegilotriticum* CIGM87.2783-1B-0PR-0B (GenBank AY573901) *Pina-D1c*{10118}.

Pinb-D1n{10118}. **v:** *X. aegilotriticum* CIGM92.1708 (GenBank AY573902) *Pina-D1d*{10118}.

Pinb-D1o{10118}. **v:** *X. aegilotriticum* CIGM93.247 (GenBank AY573903) *Pina-D1e*{10118}.

Pinb-D1p{10121}. [*Pinb-D1z*{10316}]. **v:** Dahuangpi (GenBank AY581889){10316}; Nongda 3213{10121}; Nongda 3395{10121}; Qindao landrace{10305}; Qitoubai{10305}; Shijiazhuang 34{10305}; Zigan{10305}.
The single nucleotide A deletion occurs in the AAAA at position 210-213 and is assigned to the last position at 213. Homonym: *Pinb-D1i(t)* {10305}. This homonym sequence (allele) was incorrectly assigned *Pinb-D1z, 'b3', Pinb-D1u*

Pinb-D1q{10077}. **s:** CS*/Red Egyptian 5D substitution line, *Pina-D1k, Gsp-D1i*{10077}. **v:** Jingdong 11 (GenBank EF620909){10313}.
This allele was used originally (2004 supplement) in combination with *Pina-D1k* and *Gsp-D1i* to denote the large deletion that encompasses *Pina-D1, Pinb-D1, and Gsp-D1* {10077} (cf. *Pins-D1k*). The haplotype nomenclature of this deletion is under review. *Pinb-D1q* is currently used to denote the C-to-G SNP at position 218 {10313}.

Pinb-D1r{10209}. [*Pinb-D1h*{10209}]. **v:** Hyb65 (NCBI AJ619022){10209}.
G insertion: open reading frame shift and premature stop codon; hard kernel texture {10209}.

Pinb-D1s{10209}. **v:** NI5439 (NCBI AJ619021){10209}.
G insertion as in *Pinb-D1r* and an A-to-G substitution; hard kernel texture {10209}.

Pinb-D1t{10208}. **v:** Guangtouxianmai (GenBank EF620910){10208}; Hongmai{10208}.
G-to-C substitution: Glycine-47 to arginine; hard kernel texture {10208}.

Pinb-D1u{10427}. **v:** Tiekemai (GenBank EF620911){10427}; 31 hard Yunnan endemic wheats (*T. aestivum* ssp. *yunnanense* King){10427}.
Possesses a G deletion at position 127 leading to a shift in ORF {10427}.

Pinb-D1v{10305,10316}. [*Pinb-D1i(t)*{10305},*Pinb-D1r*{10316}]. **v:** Qingdao Landrace 1{10305}; Qitoubai{10305}; Shijiazhuang 34{10305}; Tachun 3 (GenBank AY598029){10316}; Zigan{10305}; homonym 'b5'{10316}.
The original assignment of this allele in the 2006 supplement was incorrect; the sequence/varieties in {10305] are *Pinb-D1p* as listed above for that allele. The following variety/sequence was assigned *Pinb-D1y* in the 2006 supplement; but the original assignment of {10316} is now unchanged.

Pinb-D1w{10314}. [*Pinb-D1q*{10316}]. **v:** Jing 771 (GenBank AY640304, AB180737){10316}; homonym 'b4'{10316}. **dv:** *Ae. tauschii* 002 (GenBank DQ257553){10314}; *Ae. tauschii* ssp. *tauschii* TA1704 (GenBank AY649747){10315}; *Ae. tauschii* ssp. *anathera* TA2381 (GenBank AY649747{10315}.
This variety/sequence was incorrectly assigned *Pinb-D1x* in the 2006 supplement; the original assignment of {10316} is now unchanged.
Ae. tauschii isolate Q03-002 (GenBank DQ257553) (referred to as allele 2) {10314}; *Ae. tauschii* TA1704 and TA2381 (GenBank AY649747) {10315}; *Ae. tauschii* CPI 110799

(GenBank CR626926) {10440} were incorrectly assigned this allele in the 2006 supplement; they are *Pinb-D1i* as listed above.

Pinb-D1x{10528}. **v:** Kashibaipi (GenBank AM909618){10528}.

Pinb-D1y.

The original assignment of this allele in the 2006 supplement was incorrect; the sequence for Tachun 3 in {10305} is *Pinb-D1v* as listed above. The original assignment of {10316} is now unchanged. Currently there is no assignment for this allele.

Pinb-D1z.

This allele/sequence is identical to, and listed under *Pinb-D1p*. Currently there is no assignment for this allele.

Pinb-D1aa{10391}. **v:** Changmangtoulongbai (GenBank EF620912){10391}; Hongtutou 1{10391}; Hongtutou 2{10391}.

Pinb-D1ab{10432}. **v:** KU3062{10432}; KU3069{10432}; Tuokexunyihao{10528}.

Pinb-D1ac{10570}. **v:** Kashibaipi{10570}; Red Star{10570}.

G to A substitution at position 257 and C to T substitution at position 382 {10570}.

Pinb-A^{m}***1***{0083}. 5A^{m}S{0083}. **dv:** *T. monococcum* DV92 (cultivated) cds (GenBank AJ242716) complete BAC sequence (GenBank AY491681), G3116 (spp. *aegilopoides*){0083}; is identical to allele *Pina-D1h*{03105}; PI277138 (GenBank AJ302102){03104}; PI418582 (GenBank AJ302101){03104}; *T. monococcum* TA2025 (GenBank AY622797){10315}; *T. monococcum* TA2026 (GenBank AY622798){10315}; *T. monococcum* TA183 (GenBank AY622799){10315}.

In *T. monococcum Pinb-A*^{m}*1* is 0.1 cM proximal to *Pina-A*^{m}*1* and both loci are less than 36 kb apart {0083}.

Pinb-S1{03108}. **dv:** *Ae. speltoides* PI393494 (GenBank AJ302105){03104}; PI 369616 (GenBank AJ302106){03104}; *Ae. speltoides* spp. *speltoides* TA2368 (GenBank AY622797), TA1789 (GenBank AY622802){03108}; *Ae. speltoides* spp. *ligustica* TA1777 (GenBank AY622803){03108}.

Pinb-S^{b}***1***{03108}. **dv:** *Ae. bicornis* spp. *typica* TA1954 (GenBank AY622807), TA1942 (GenBank AY622808){03105}.

Pinb-S^{l}***1***{03108}. **dv:** *Ae. longissima* spp. *longissima* TA1912 (GenBank AY622800){03108}; *Ae. longissima* spp. *nova* TA1921 (GenBank AY622804){03108}.

Pinb-S^{s}***1***{03108}. **dv:** *Ae. searsii* TA1837 (GenBank AY622805), TA2355 (GenBank AY622806){03105}.

Pinb-S^{sh}***1***{03108}. **dv:** *Ae. sharonensis* TA1999 (GenBank AY622809){03105}.

Pinb-D1b, Pinb-D1c, Pinb-D1d, Pinb-D1e, Pinb-D1f, or *Pinb-D1g* are present in hard hexaploid wheats not carrying the *Pina-D1b* (null) mutation {452,1035,0082,0204}.

Wheats with *Pinb-D1b* were slightly softer and a little superior to those with *Pina-D1b* in milling and bread-making characteristics although there was considerable overlap {0206}.

Transgenic rice with the *Pina-D1a* and *Pinb-D1a* alleles possessed softer grain {0207}.

Genotypes for a selection of North American wheats are given in {0204}.

In *T. monococcum* the gene order was reported to be : tel - *Gsp-1* - *Pina* - *Pinb* {0083, 10122} whereas in *Ae. squarrosa* it was : tel - *Gsp-1* - *Pinb*- *Pina* {10037}.

The soft kernel trait was transferred to durum {10899}.

Ikeda et al. {10305} reported a double-null with apparently no *Pina-D1* or *Pinb-D1* genes present in **v:** Bindokku, Cheyenne 'A', Chosen 68, Saiiku 18, Saiiku 44, and tentatively assigned it *Pina-D1b/Pinb-D1h(t)*. How this deletion compares with the double null mutation reported by Tranquili et al. {10077} which was assigned *Pina-D1k/Pinb-D1q* is unknown. Lines possessing the alien-derived genes *Lr57* and *Yr40* lack puroindoline genes and therefore should be hard phenotypes {10770}.

82.5.7. Endosperm-specific wheat basic region leucine zipper (bZIP) factor storage activator

Spa-A1{10908}. 1AL{10909}. **v:** Recital{10909}.

Spa-B1{10908}. 1BL{10909}. **v:** Recital{10908}. **ma:** *Glu-B1* - 1.3 cM - *Spa-B1*{10909}.

Spa-B1a{10908}. **v:** Chinese Spring{10909}; Recital{10908}; Australian genotypes listed in{10908}.

Spa-B1b{10908}. **v:** Renan{10909}; Australian genotypes listed in{10908}.

Spa-D1{10908}. 1DL{10909}. **v:** Recital{10909}.

After testing an ealier hypothesis that SPA genes affected wheat quality, analyses conducted by both {10908} and {10909} obtained no evidence supporting a significant effect and attributed any variation to the closely linked *Glu-B1* locus.

82.5.8. Salt soluble globulins

GLO-1 are endosperm proteins (23-26 kDa) soluble in salt but not in water {455}.

Glo-A1{455}. 1AS{455}. **v:** CS. **ma:** Distally located: *Glo-A1*(distal) - 5.2 cM - *Gli-A1*{1077}.

Glo-B1{455}. 1BS{455}. **v:** CS.

Glo-D1{455}. 1DS{455}. **v:** CS. **ma:** Distally located: *Glo-D1*(distal) - 2.9 cM - *Gli-D1*{1077}.

Glo-E1{455}. 1ES{455}. **ad:** CS/*E. elongata*.

Glo-R1{455}. 1RS{455}. **ad:** CS/Imperial. **su:** 1B/(1R), eg., Salzmunde 14/44.

82.5.9. Serine protease inhibitors

Serine proteinase inhibitors or serpins are salt soluble proteins (-43 kDa) representing about 4% of the total protein in wheat and barley endosperms. They may have a role in plant defense.

Srp-A1{10754}. 5AL{10754}.

Srp-B1{10754}. [*Srp5B*{10754}]. 5BL{10754}.

Srp-B1a{10754}. [*Srp5Ba*{10754}]. **v:** Etawah{10755}; Federation{10755}; Frame{10755}; Pugsley{10754}; Stylet{10755}.

Srp-B1b{10754}. Null allele **v:** Correll{10755}; EGA Eagle Rock{10755}; Gladius{10755}; Yitpi{10755}.
This allele reduced milling yield by 0.4% {10755}.

Srp-D1{10754}. 5DL{10754}.

82.5.10. Starch granule proteins

The proteins, designated SGP-1, are starch synthases, encoded by *SsII-A1*, *SsII-B1* and *SsII-D1* {0042}.

Sgp-A1{1615}. 7AS{1615}. **v:** CS.

Sgp-A1a{1615}. **v:** CS.

Sgp-A1b{1615}. Null allele. **v:** Chosen 30, Chosen 57.

Sgp-A1c{1615}. **v:** Hua Non 9.

Sgp-B1{1615}. 7BS{1615}. **v:** CS.

Sgp-B1a{1615}. **v:** CS.

Sgp-B1b{1615}. Null allele. **v:** K79.

Sgp-B1c{1615}. **v:** Gnatruche.
Sgp-B1d{1615}. **v:** Waratah.
Sgp-D1{1615}. 7DS{1615}. **v:** CS.
Sgp-D1a{1615}. **v:** CS.
Sgp-D1b{1615}. Null allele. **v:** T116.

Sgp-A2{1615}. **v:** CS.
Sgp-B2{1615}. **v:** CS.
Sgp-D2{1615}. **v:** CS.

Sgp-A3{1615}. 7AS{1615}. **v:** CS.
Sgp-A3a{1615}. **v:** CS.
Sgp-A3b{1615}. Null allele. **v:** Norin 61.
Sgp-B3{1615}. 7BS{1615}. **v:** CS.
Sgp-B3a{1615}. **v:** CS.
Sgp-B3b{1615}. Null allele. **v:** Crest.
Sgp-B3c{1615}. **v:** Spica.
Sgp-D3{1615}. 7DS{1615}. **v:** CS.

The proteins, designated SGP-3, are identical to wheat starch synthase I, encoded by *SsI-A1*, *SsI-A2* and *SsI-D1* {0041}.

A triple null stock (SGP-1 null wheat) is reported in {0137}. Deletion mapping indicated that the gene order on the 7S arms is; centromere - *Sgp-1* - *Sgp-3* - *Wx*{1615}.

82.5.11. Starch synthase

SsI-A1{0041}. 7A{0041}.
SsI-B1{0041}. 7B{0041}.
SsI-D1{0041}. 7D{0041}.

Starch synthase I proteins are identical to the starch granule proteins SGP-3 {0041}.

SsII-A1{0042}. 7A{0042}.
SsII-B1{0042}. 7B{0042}.
SsII-D1{0042}. 7D{0042}.

Starch synthase II proteins are identical to the starch granule proteins SGP-1 {0042}.

82.5.12. Water soluble proteins

WSP-1 are monomeric grain endosperm proteins identified by their high pI's {817}.

Wsp-A1{817}. 7AL{817}. **v:** CS.
Wsp-A1a{817}. **v:** CS.
Wsp-A1b{817}. **v:** Huntsman.
Wsp-A1c{817}. **v:** Hope.
Wsp-A1d{817}. **v:** Sicco.
Wsp-A1e{817}. **v:** Condor.
Wsp-B1{817}. 7BL{817}. **v:** CS.
Wsp-B1a{817}. **v:** CS.
Wsp-B1b{817}. **v:** Hope.
Wsp-B1c{817}. **v:** Condor.
Wsp-D1{817}. 7DL{817}. **v:** CS.
Wsp-D1a{817}. **v:** CS.
Wsp-D1b{817}. **v:** Sears' Synthetic IPSR 1190903.
Wsp-D1c{893}. **v:** T4 = Agatha{893,890}; Indis{890,892}.
Wsp-E1{817}. 7E{817}. **ad:** CS/ *E. elongata*.

Wsp-H1{817}. 7H{817}. **ad:** CS/Betzes.
Wsp-H^{ch}1{817}. 7H^{ch}{817}. **ad:** CS/*H. chilense.*
Wsp-S^{l}1{817}. 7S^{l}{817}. **ad:** CS/*Ae. sharonensis.*
Wsp-V1{817}. 7V{817}. **ad:** CS/*D. villosum.*

82.5.13. Waxy proteins

Waxy protein (granule-bound starch synthase = ADP glucose starch glycosyl transferase, EC 2.4 1.21 = GBSSI) is tightly bound within endosperm starch granules and is involved in the synthesis of amylose {1616}. Waxy variants, characterised by starch granules containing increased amylopectin and reduced amylose, are preferred for Japaness white salted or "udon" noodles {1650}. Similar waxy phenotypes are controlled by orthologous genes in barley, maize and rice but are not known to occur in rye {725}. All combinations of the null alleles were produced in Chinese Spring {0018}. Partial genomic clones of various diploid, tetraploid, and hexaploid wheats were sequenced {0278,0279}.

A multiplex PCR assay for identifying waxy genotypes is described in {10032}.

Wx-A1{180,1053}. [*Xwx-7A*{179,180},*Wx-B1*{1053,1054}]. 7AS{180,1053}. **v:** CS. **ma:** Variation in the microsatellite gene *Xsun1-7A* provides a co-dominant marker for this locus{0116}.

The complete genomic sequences for the *Wx-A1a* allele from CS {0073} and the cDNA sequence for the *Wx-A1b* allele from Kanto 107 {0075} were determined.

Wx-A1a{1054}. [*Wx-B1a*{1054}]. **v:** CS; Hoshuu.

Wx-A1b{1054}. [*Wx-B1b*{1054}]. Null allele. **v:** California{10032}; Kanto 79; Kanto 107 ; Shino{10032}; Shirodaruma{1617}; Sturdy{1617,10032}. **v2:** Mochi-Otome *Wx-B1b Wx-D1b*{10032}; Nebarigoshi *Wx-b1b*{10032}. **tv:** Asrodur{0111}; MG826{03101}; A variant allele was present in one Iranian and one Italian accession{03101}.

Wx-A1c{1617}. **v:** Pakistan Zairaishi selection{10629}; QT105{1617}; WB6{1617}.

Wx-A1d{1616}. **tv:** *T. dicoccoides* KU 8937B{1616}.

Wx-A1e{1616}. **tv:** KU 3659{10629}; *T. durum* KU 3655 and KU 3659{1616}.

Wx-A1f{10187}. Null allele **v:** Turkey-124{10187}; Turkey-140{10187}; Turkey-171{10187}; Turkey-280{10187}; Turkey-299{10187}.

Lines with this allele produce a PCR product with a 173 bp insertion in an exon {10187}.

Wx-A1g. *Wx-A1'* {10587}. **v:** PI 348476{10587}; Spelt accessions PI 348576{10587}; 2778 Epeautre Noir Velu{10587}.

Wx-A1h{10763}. Null allele **tv:** Buck Topacio{10763}.

This is probably a unique allele possessing a 1 bp deletion in exon 6 leading to frameshift and a stop codon: partial sequence GQ120523 {10763}.

Wx-B1{180,1053}. [*XWx-4B*{179,180},*XWx-4A*{961},*Wx-A1*{1053,1054}]. 4AL{180,1054}. **v:** CS. **tv:** A variant allele was present in three accessions{03101}.

A dominant PCR marker for identifying heterozygotes at the *Wx-B1* locus is reported in {10732}.

Wx-B1a{1054}. [*Wx-A1a*{1054}]. **v:** CS; Joshuu.

The complete genomic sequence for *Wx-B1a* from CS was determined {0073}.

Wx-B1b{1054}. [*Wx-A1b*{1054}]. Null allele. **v:** Kanto 79{1617}; Kanto 82{1617}; Kanto 107{1617}; Norin 98{1617}; Gabo{1617}; Reward{10032}; Satanta{1617}; Yukon{10032}. **v2:** Mochi-Otome *Wx-A1b Wx-D1b*{10032}; Nebarigoshi *Wx-A1b*{10032}. **v:** For list of Australian wheats, see{1650}. **tv:** Blaquetta (BG-13701){0111}.

An ELISA-based method was developed for distinguishing wheat lines carrying this null allele {10325}.

Wx-B1c{1617}. **v:** AF24{10629}; Chousen 40{0094}; Cikotaba{1617,10629}; Junguk 12{1617,10629}.

Wx-B1d{1616}. **tv:** *T. durum* KU 4213D{1616}; KU 4213D{10629}; KU 4224C{1616}.

Wx-B1e{0027}. **v:** Blue Boy II{0027}; Canthatch{0027}; Eureka{0027}; Gotz{0027}; Norin 44{0027}; Turkey Red{0027}.

Wx-B1f{0111}. **tv:** BG-12413{0111}; BG-12415{0111}.

Wx-B^{S}1g{10587}. **al:** *Ae. speltoides* 33{10587}.

Wx-B^{SL}1h{10587}. **al:** *Ae. longissima* 12{10587}.

Wx-D1{180,1053}. [*XWx-7D*{179,180}]. 7DS{180,1053}. **v:** CS.

Wx-D1a{1054}. **v:** CS.

Wx-D1b{1617}. Null allele. **v:** Bai Huo (Baihuomai){1617}; DHWx12 {0117}. **v2:** Mochi-Otome *Wx-A1b Wx-B1b*{10032}. **ma:** STS marker *Xsun1-7D* produces a distinct band of about 260bp (compared with the standard 840bp), indicative of a smaller PCR product, but the gene is non-functional{0116,0117}; *Xsun4(Wx)-7D* is a perfect marker{0118}.

Wx-D1c{1617}. **v:** Scoutland{1617}.

Wx-D1d{0118}. **v:** K107Wx1{0118}; K107Wx2{0118}; One Iranian and one Italian accession{03101}.

Wx-D1e{0117}. Null allele{0117}. **v:** NP150{0117}.
STS marker *Xsun1-7D* fails to produce a PCR product {0117}

Wx-D1f. [*Wx-d1e*{0234}]. **v:** Tanikei A6599-4{0234}; Relative to Kanto 107, Tanikei A6599-4 carries an alanine to threonine substitution at position 258 in the mature protein{0234}.
Various hard and soft wheats with the alleles *Wx-A1b, Wx-B1b* and *Wx-D1b* are listed in {0304}.

Wx-D^{DN}1g{10587}. **al:** *Ae. ventricosa* 12{10587}.

Lists of cultivars, lines and landraces of tetraploid and hexaploid wheats with different, mostly null, alleles at the *Wx* loci are given in {9910,9911,9912,1053,1054,9913,9915, 9916,1650,9917}.

The complete genomic sequence for *Wx-D1a* from CS {0073} and the cDNA sequence for the *Wx-D1b* allele from Bai Huo {0075} were determined.

Isolation of a wheat cDNA encoding *Wx-A1* and *Wx-D1* was reported in {0123} and {0167}, respectively. Isolation of genomic sequences for the genes encoding granule-bound starch synthase (*GBSSI* or *Wx*) in *T. monococcum, Ae. speltoides* and *Ae. tauschii* was reported in {0168}. Cloning of a second set of *GBSSI* or *waxy* genes, *GBSSII*, which were shown to be located on chromosomes 2AL, 2B and 2D, was reported in {0167}.

Various hard and soft wheats with the alleles *Wx-A1b, Wx-B1b* and *Wx-D1b* are listed in {0304}. Fifteen percent of Chinese wheats possessed *Wx-B1* null alleles {10357}.

83. Abiotic Stress Responses:Dehydrin-response Element Binding Factors

DREB proteins are a large family of transcription factors induced by abiotic stresses. Using genome-specific primers as probes for an orthologous *Dreb1* gene series was placed on chromosomes 3A, 3B and 3D {10729}. SNPs in *Dreb-B1* permitted mapping in chromosome 3BL in the ITMI (Opata 85 / W7984) mapping population.

Dreb-A1{10729}. 3A{10729}.

Dreb-B1{10729}. 3BL{10729}. **ma:** *Xmwg818-3B* - 27.3 cM - *Dreb1* - 11.2 cM - *Xfbb117-3B*{10729}.

Dreb-B1a{10729}. **v:** Opata 85{10729}.

Dreb-B1b{10729}. **v:** W7984{10729}.

Dreb-D1{10729}.   3D{10729}.

Pathogenic Disease/Pest Reaction

For disease/pest reaction gene guidelines see Introduction, no. 8.

Note: In listings of multiple alleles, the chromosome locations and ma: citations will generally be given with the particular allele that was located or mapped.

84. Reaction to Barley Yellow Dwarf Virus

Disease: Cereal yellow dwarf

Bdv1{1363,1379}. 7D{1379}.7DS{1363}. **i:** Jupeteco 73R (compared to Jupeteco 73S){1363}. **v:** Anza{1379}; Condor BW3991{1379}; Tyrant BW3872{1379}; Hahn BW4097{1379}; Parrot BW10817{1379}; Siren BW18643{1379}; Many CIMMYT genotypes. *Bdv1* is completely linked with *Ltn*, *Sr57*, *Lr34* and *Yr18*. See *Ltn*, *Lr34*, *Yr18*. Note: BW = CIMMYT wheat accession number.

Bdv2{058}. Derived from *Th.* intermedium 7DL = T7DS.7DL-7Ai#1L{552,0182}.7D = T7DS-7Ai#1S.7Ai#1L group. **tr:** TC14{059,0201}; H960642{0182}. **v:** Glover (with TC6){10491}; Mackellar = LH64C (from tissue culture){10177}; TC14*2/Hartog{0225}; TC14*2/Spear{0201}; TC14*2/Tatiara{0225}; Yw243, Yw443, Yw642 and Yw1029 (derived by *ph1* induced recombination) see{10177}. **ma:** Distal 10% of 7DL, translocation point between RFLP markers *Xpsr680* and *Xpsr965*{0182}; Complete association with *Xpsr129-7D*, *Xpsr548-7D*, *XksuD2-7D*, *XcslH81-7D*, and *Xgwm37-7D* selected as a diagnostic marker{0225}; Two RGAP and 1 RAPD markers developed for the Yw series also effective for at least TC14{10177}.
7D = T7DS-7Ai#1S.7Ai#1L{552}. **tr:** TC5, TC6, TC8, TC9, TC10{059}.
1B = T1BS-7A#1S.7Ai#1L{552}. **tr:** TC7{447}.
7Ai#1S{552}. **su:** TAF2{059}; Lines 5395 & 5395-243AA{552}.

Bdv3{10159}. Derived from *Th. intermedium* cv. Ohahe {10158} 7DS.7DL-7EL{10157}. **v:** P961341 PI 634825{10157}; P98134{10159}. **ad:** P107{10159}. **su:** P29 (7D{7E}){10156}. **ma:** A SSR-BDV marker is described in {10159}.
Bdv3 in wheat shows distored inheritance that varies with genetic background. Further translocation lines with *Bdv3* are described in {10882}.

85. Reaction to *Bipolaris sorokiniana*

Diseases: Spot blotch and common root rot.

Spot blotch

QTL

Yangmai 6 (R)/Sonalika (S): RIL population: AUDPC was controlled by four QTLs derived from Yangmai 6, viz. *QSb.bhu-2AL* (*Xbarc353-2A* - *Xgwm445-2A*, R^2=0.148), *QSb.bhu-2BS* (*Xgwm148-3B* - *Xgwm375-2B*, R^2=0.205), *QSb.bhu-5BL* (*Xgwm67-5BL* - *Xgwm371-5BL*, R^2=0.386) and *QSb.bhu-6DL* (*Xbarc173-6D* - *Xgwm732-6DL*, R^2=0.225) {10719}.

Sb1{10855}. Partial resistance 7DS{10855,10856}. **i:** HUW234Ltn+{10855}. **v:** Saar{10856}; Lines with *Lr34/Yr18/Pm38/Sr57* - see Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*, Reaction to *Blumeria graminis*, Reaction to *Puccinia graminis*, Leaf tip necrosis.. **ma:** Pleiotropic or closely linked with *Lr34/Yr18/Pm38/Sr57* located between *Xgwm1220-7DS* and *Xswm10-7DS* (1.0 cM interval){10856}; see also Reaction to *Puccinia* *triticina*, Reaction to *Puccinia striiformis*, Reaction to *Puccinia graminis* and Reaction to *Blumeria graminis*. **c:** Putative ABC transporter{10862}.

86. Reaction to *Blumeria graminis* DC.

Disease: Powdery Mildew.

Resistance genes and their molecular associations are reviewed in {10141}.

86.1. Designated genes for resistance

Note: Chancellor, used as a susceptible genetic background, for some near-isogenic lines probably carries *Pm10* and *Pm15* {1479}.

33 NILs, including 22 resistance genes and 3 genetic backgrounds are listed in {10389}.

Pm1.

Pm1a{562}. [*Pm1*{130},*Mlt*{1175},*Mla*{348}]. 7A{1293}.7AL{1305}. **i:** Axminster/8*Chancellor{132}; CI 14114 = As II/8*Chancellor{132}; CI 13836/8*Chancellor{132}; Kenya C6041/5*Federation{1168}; Norka/8*Chancellor{132}. **s:** CS*5/Axminster 7A{1293}. **v:** Anfield{098}; As II{130}; Axminster{130,1175}; Birdproof{165}; Bonus{1554}; CI 13836{130}; Converse{1175}; Fedka{939}; Festival{1554}; Fram I{130}; Huron CI 3315{1175,1554}; Kenora{1554}; Kenya W744 = C6041{130,1175}; Norka{130,1175}; Pika{130}; Sweden W1230{1554}; Thew{1175}; TU 4{130}; Zhengzhou 871124{570}. **v2:** Anfield *Pm9*{1287}; BGRC 44514 *Pm3a*{1628}; Mephisto *Pm2 Pm9*{540}; Normandie *Pm2 Pm9*{165}; Pompe *Pm9*{1287}; Ring *Pm9*{1287}; Sappo *Pm2 Pm4b* (Carries *Lr20*){310}; Solo *Pm2 Pm4b*{052}. **ma:** Co-seg. with *Xcdo347-7A* using NILs{864}; Co-segregation or close linkage with three RAPDs; one RAPD converted to a STS{570}; Note: In Solo, *Pm1* is translocated to chromosome 7D{052}; Complete cosegregation of several markers including *Xcdo347-7A, Xpsr121-7A, Xpsr680-7A, Xpsr687-7A, Xbzh232(Tha)-7A, Xrgc607-7A* and *Xsts638-7A* with *Pm1* and *Lr20* was reported in {0323}.

Pm1b{562}. **v:** MocZlatka{562}.

Pm1c{562}. [*Pm18*{853,562}]. **v:** Blaukorn{0011}; M1N{1628,562}; In {540} M1N was described as an undesignated subline of Weihenstephan M1. **ma:** AFLP marker 18M2 was diagnostic for *Pm1c*{0011}.

Pm1d{562}. **v:** *T. spelta* var *duhamelianum* TRI2258{562}. **ma:** AFLP marker 18M1 - various *Pm1* alleles 0.9 cM{0011}.

T. spelta duhamelianum also possesses *Pm10* and *Pm11* which confer resistance to certain hybrids cultures of *B. g. tritici* and *B. g. agropyri*.

Pm1e{0322}. [*Pm22*{1134}]. **v:** Elia{1134}; Est Mottin{1134}; Ovest{1134}; Tudest{1134}; Virest{1134}.

Pm2{130}. [*Mlu*{1175},*Mlx*{1088}]. 5D{1007}.5DS{945}. **i:** CI 14118 = Ulka/8*Chancellor{132}; CI 14119 = CI 12632/8*Chancellor{132}; Federation*4 /Ulka{1168}. **v:** Avalon{096}; Bounty{096}; Fenman{096}; Galahad{1531}; H8810/47{130}; Longbow{1531}; Maris Beacon{1592}; Maris Nimrod{1592}; Maris Sportsman{096}; Maris Templar{1592}; Norman{096}; Orestis{1079}; PI 92378{1168}; PI 181374{1168}; Sea Island{130}; Sentry{096}; S2303{945}; Synthetic(Iumillo/*Ae. tauschii*){1168}; TP 114/2*Starke deriv{626}; Ulka{130,1175}; XX186 = *T. durum* Santa Maria/*Ae. squarrosa* BGRC 1458 *Pm19*{853}. **v2:** Apollo *Pm4b Pm8*{541}; Brigand *Pm6*{096}; Brimstone *Pm6*{1531}; CI 12632 *Pm6*{130}; CI 12633 *Pm6*{133}; Compal *Pm4b*{854}; Crossbow *Pm5 Pm6*{098}; Gawain *Pm6* {1531}; Halle Stamm 13471 *Mld*{097}; Heiduck *Pm6*{541}; Hustler *Pm6* {096}; Hornet *Pm8*{1531}; Kinsman *Pm6*{096}; Mardler *Pm6*{096}; Maris Dove *Mld*{1592}; Maris Fundin *Pm6*{096}; Maris Huntsman *Pm6*{1592}; Mephisto *Pm1 Pm9*{540}; Normandie *Pm1 Pm9*{165}; Parade *Pm5*

Pm6 {1531}; Rendezvous *Pm4b Pm6* {1531}; Solo *Pm1 Pm4b* {052}; Timmo *Pm4b*{096}; TP 114 *Pm6*{626}; Virtue *Pm6*{096}; Walter *Pm4b Pm6* {1428}. **dv:** *Ae. squarrosa* BGRC 1458{853}; Forty accessions of *Ae. tauschii*{852}. **ma:** *Pm2* - 3.5 cM - *Xbcd1871-5D* using F2s{864}; *Xcfd81-5D* - 2.0 cM - *Pm2*{10366}.

Pm3. 1A. **ma:** *Xgdm33-1A* - 2.3 cM - *Pm3/Xpsp2999-1A*{0313}.

Genotype list: {0313, 10405, 10406} The *Pm3a, Pm3b, Pm3d* and *Pm3f* alleles form a true allelic series based on sequence analysis {10292}.

Following the cloning and sequencing of *Pm3b* {10064], 6 other alleles were sequenced {10405}. The Chinese Spring (susceptible) allele, *Pm3CS*, considered to be ancestral and present in many hexaploid and tetraploid wheats, was also transcribed {10405, 10406}. Other wheats possessed a truncated sequence (e.g. Kavkaz), or were null {10405,10406}. Unique markers were developed for all 8 transcribed alleles, and for individual alleles {10405}.

Alleles *Pm3b, Pm3d,* and *Pm3f* were detected in Scandinavian varieties using allele-specific markers {10681}.

Pm3a{130,132}. [*Mla*{1168}]. 1A{1007}.1AS{943,947}. **i:** Asosan/8*Chancellor {132} = CI 14120; Asosan/3*Federation{1168}. **v:** Asosan{130,1168}; BGRC 44514 *Pm1a*{1628}; Coker 797{786}; Florida 301{786}; Florida 302{786}; Hadden{097}; Halle Stamm{097}; Madrid{10843}; Merker{10843}; Norin 3{1134}; Norin 29{1134}; PI 46890{1439}; Robigus{10843}; Saluda{786}; Tabasco{10843}; Tyler{1419}. **ma:** *Xbcd1434-1A* - 1.3 cM - *Pm3* using NILs{864}; *Xwhs179-1A* - 3.3 cM - *Pm3*{522}. Sequence AY939880 {10292}.

Pm3b{130,132}. [*Mlc*{165},*Pm3j*{10405}]. 1A{1007}. **i:** Chul*8/Chancellor = CI 14121{132}; *T. sphaerococcum**8/Chancellor = CI 15887{539}. **v:** Chul{165}; Enorm{10843}. **ma:** *Xbcd1434-1A* - 1.3 cM - *Pm3b* using NILs{864}. **c:** The isolation of *Pm3b* is reported in {10064}. The *Pm3b* gene (GenBank AY325736) is a coiled-coil NBS-LRR type of disease resistance gene{10064}.

Pm3c{130,132}. [*Mls*{1175},*Pm3i*{10405}]. 1A{134,1007}. **i:** Sonora/8*Chancellor{132} = CI 14122; Sonora/4* Federation{1168}; Triticale/8*Chancellor{539}. **s:** CS*7/Indian 1A{134}. **v:** Borenos{854}; Cawnpore{1628}; CI 3008{130}; CI 4546{130}; Hindukush{1628}; Indian{1175}; Sonora{130,1168}; Sturgeon{1175}. **c:** Sequence DQ251587, DQ517917{10405}.

Pm3d{1628}. [*Ml-k*{540},*Mlk*{434},*Pm3h*{10405}]. 1A{1628}. **v:** Axona{0313}; Cornette{0313}; Herold{540}; Indian 4{0313}; Kadett{0313}; Kanzler{0011}; Kleiber{0313}; Kolibri{540,542,1628}; Ralle{540}; Socrates {heterogeneous}{540}; Star {heterogeneous}{540}; Syros{540}; Vergas{10843}. **v2:** Kadett *Pm4b*{540}; Turbo *Pm4b*{540}.

Sequence AY9398881 {10292}. DQ251488, DQ517518 {10405}.

Pm3e{1628}. **v:** Sydney University Accession W150 =AUS 6449{939,1628}. **v2:** Cortez *Pm5* allele{10843}. **ma:** *Pm3e* - 7.1 cM - *Xwmc818-1A*{10843}.

Pm3f{1628}. **i:** Michigan Amber/8*Chancellor{1628}; This allele was distinguished from *Pm3c* with only one of 13 pathogen cultures. **v:** Viza{10843}. **c:** Sequence DQ071554{10292}.

Sequence DQ071554 {10292}.

Pm3g{0070}. [*Mlar*{854}]. 1A{0070}.1AS{0313}. **v:** Avo{1629}; Aristide{1629}; Champetre{0313}; Courtot{1629}; Lutin{0313}; Oradian{0313}; Rubens{0313}; Soissons{0313}; Valois{0313}. **ma:** *Pm3g* - 5.2 cM - *Gli-A5* - 1.9 cM - *Gli-A1*{0070}; *Pm3g* was completely linked to microsatellite *Xpsp2999*{0313}. **c:** Sequence DQ251489, DQ517919{10405}.

Pm4{131}.

Pm4a{1464}. [*Pm4*{131}]. 2AL{1464}. **i:** CI 14123 = Khapli/8*Chancellor{131}; CI 14124 = Yuma/8*Chancellor{131}. **v:** Steinwedel*2/Khapli{939}; Yangmai

10{10176}; Yangmai 11{10176}. **tv:** Khapli{131}; Valgerado{097}; Yuma{131}. **ma:** Co-seg with *Xbcd1231-2A.2* & *Xcdo678-2A* using F2s{864}; *Xbcd1231-2A.1* - 1.5 cM - *Pm4* - 1.56 cM - *Xbcd292-2A*{864}; *Pm4a* - 3.5 cM - AFLP markers 4aM1 and 4aM2{0011}; *Xbcd1231-2A* was converted to a STS marker{0069, 10176}; and to a *Pm4a*-specific dominant PCR marker{10176}; *Xgwm356-2A* - 4.8 cM - *Pm4a*{10176}.

Pm4b{1464}. [*Mle*{1591}]. 2A{052}.2AL{1464}. **i:** Federation*7/*T. carthlicum* W804{1464}. **v:** Achill{540}; Ajax{540}; Arkas{540}; Armada{096}; Atlantis{0011}; Boheme{0011}; Botri (heterogeneous){854}; ELS{1591}; Facta{854}; Factor (heterogeneous){854}; Fakon{854}; Fazit{854}; Hermes{540}; Horizont{540}; Maris Halberd; Max{540}; Olymp{540}; Orbis{540}; RE714{1220}; Renan{0016}; Ronos{1079}; S-25{052}; S-28{052}; TP 229{626,1591}; Weihenstephan M1{1591}; VPM1{097}. **v2:** Apollo *Pm2 Pm8*{541,802}; Boxer *Pm5*{541}; Compal *Pm2*{854}; Kadett *Pm3d*{540}; Kronjuwel *Pm8*{541}; Mission *Pm5* {78,541,1531}; Rang *Pm1*{052}; Rendezvous *Pm2 Pm6*{1531}; Solo *Pm1 Pm2*{052,540}; Sorbas *Pm6*{541}; Timmo *Pm2 Pm6*{096}; Turbo *Pm3d*{540}; Walter *Pm2 Pm6*{1428}. **ma:** *Pm4b* - 4.8 cM - *Xgbx3119b-2A*{0272}; *Xgwm382-2A* - +/- 10 cM - *Pm4b* - +/- 2 cM - *XgbxG303-2A*{0354}; STS241 - 4.9 cM - *Pm4b* - 7.1 cM - SRAP $Me8/Em7_{220}$ - 4.7 cM - *Xgwm382-2A*{10553}.

Pm4c{10583}. *Pm23* {1618} 2AL{10583}.earlier reported on 5AL{1618}. **v2:** 81-7241 *Pm8* suppressed{10583,1618}. **ma:** *Xbarc122-2A* - 1.4 cM - *Pm4c* - 3.5 cM - *Xgwm356-2A*{10583}.

Pm4d{10744}. 2AL{10744}. **bin:** 2AL1-0.85-1.00. **dv:** *T. monococcum* Tm27{10744}. **v:** Tm27d2 = WW St2022/Tm27//Amor = TRI 29584{10744}. **ma:** A 218 bp fragment was amplified with STS marker *ResPm4* as were other *Pm4* alleles{10744}.

Pm5.

Pm5a{0257}. *Pm5a* was transferred to hexaploid wheat from *T. dicoccum* via Hope and H-44. Recessive. [*Pm5*{787},*mlH*{771}]. 7B{964}.7BL{771}. **i:** Hope/8* Chancellor = CI 14125{570}. **s:** CS*6/Hope 7B{771,964}. **v:** Alidos{854}; Aotea{964}; Caldwell{786}; Ga 1123{786}; Galaxie{0257}; Glenwari{964}; Hardired{786}; Hope{964}; H-44{964}; Kontrast{854}; Kormoran{1079}; Kutulukskaya{0257}; Lambros{0257}; Lawrence{964}; Navid{0257}; Pagode{0257}; Redcoat{097}; Redman{964}; Regina{0257}; Renown{964}; Selpek{540}; Sicco{096,0257}; Spica{964}; Tarasque{0257}; Warigo{964}; Zolotistaya{0257}. **v2:** Arthur *Pm6*{786}; Coker 983 *Pm6*{786}; Double Crop *Pm6*{786}; Granada *Pm8*{541}; Saar *Pm38 Pm39*{10481}; Sensor *Pm8*{541}.

Pm5b{0257}. [*Mli*{540,558}]. **v:** Aquila{096,541}; Carimulti{541}; Cariplus{541}; Cucurova{0257}; Dolomit{541}; Falke{541}; Flanders{096}; Fruhprobst{0257}; Ilona{0257}; Ibis{096}; Kirkpinar-79{0257}; Kontrast{0257}; Kormoran{541}; Krata{541}; Markant{541}; Mercia{1531}; Milan{541}; Nadadores{0257}; Reiher{541}; Rektor{541}; Rothwell Perdix{096}; Siete Cerros{0257}; Severin{541}; Sicco{096}; Sperber{541}; Tukan{541}; Una{0257}; Urban{541}; Wattines{541}; Wettiness{0257}. **v2:** Bert *Pm6*{541}; Boxer *Pm4b*{541}; Crossbow *Pm2 Pm6*{098}; Kristall *Pm8*{541}; Mission *Pm4b*{541,1531}; Parade *Pm2 Pm6*{1531}.

Pm5c{0257}. 7B{0257}. **v:** *T. sphaerococcum* cv. Kolandi{0257}.

Pm5d{0257}. 7B{0257}. **bin:** 7BL 0.86-1.00{10542}. **i:** IGV 1-455 = CI 10904/7*Prins{0257}; CI 10904/7*Starke{0257}. **v:** Dream{10542}. **ma:** *Xgwm611-7B* - 2.1 cM - *Pm5d* - 2.0 cM - *Xgwm577-7B* - 1.0 cM - *Xwmc581-7B*{10542}.

Pm5e{0258}. Recessive and hemizygous effective {0258}. [*mlfz*{0259}]. **v:** Fuzhuang 30{0258}. **ma:** *Xgwm1267-7B* - 6.6 cM - *Pm5e* - 12.6 cM - $Xubc405_{628}$-*2B*{0258}.

Pm6{627}. [*Mlf*{626}]. 2B{1088}. **i:** CI 13250/7*Prins{0069}; CI 12559/8*Prins{0069}; Eight Prins derivatives{10576}; PI 170914/7*Prins 6 NILs based on Prins {0139}.{0069}. **v:** 1969 IVGS Line C{626}; Abe{097,1256}; Coker747{786,1079}; Mengavi{097};

Oasis{786}; Timgalen{098}; TP 114/2*Starke deriv. B{626}. **v2:** Arthur *Pm5a*{097,786}; Brigand *Pm2*{096}; Brimstone *Pm2*{1531}; CI 12632 *Pm2*{626,1088}; CI 12633 *Pm2*{626,1088}; Crossbow *Pm2 Pm5*{098}; Double Crop *Pm5a*{786}; Garwain *Pm2*{1531}; Greif *Pm5a*{0011}; Heiduck *Pm2*{541}; Hustler *Pm2*{096}; Kinsman *Pm2*{096}; Mardler *Pm2*{096}; Maris Fundin *Pm2*{096}; Maris Huntsman *Pm2*{1592}; Parade *Pm2 Pm5*{1531}; Rendezvous *Pm2 Pm4b*{1531}; Sorbas *Pm4b*{541}; Timmo *Pm2 Pm4b*{096}; TP 114 *Pm2*{626}; Virtue *Pm2*{096}; Walter *Pm2 Pm4b*{1428}. **ma:** Close linkage with *Xbcd135-2B* (1.5+-1.4 cM), *Xbcd307-2B* (4.7+-2.5 cM) and *Xbcd266-2B* (4.5+-2.4 cM){0069}; Mapped to the interval *Xbcd35-2B-Xpsr934-2B*{0139}; However, the fact that Timgalen and a 'CI12632/Cc' line lacked the critical *T. timopheevii* markers {0139} is cause for concern; RFLP marker *Xbcd135-2B* was converted to STS markers $NAU/STS_{BCD135\text{-}1}$ and $NAU/STS_{BCD135\text{-}2}$ which showed linkage of 0.8 cM with *Pm6*{10576}.

Pm7. Derived from *S. cereale* cv. Rosen. 4BL{270,271,389} = T4BS.4BL-5RL{543}, but more recently revised to T4BS.4BL-2R#IL{380,389}. **i:** Transec/8*Chancellor. **v:** Transfed{269}; Transec{273}.

Pm8. Derived from Petkus rye - see *Yr9, Lr26, Sr31.* 1R{1B}.1BL.1RS. **i:** MA1 and MA2, four-breakpoint double translocation lines 1RS-1BS-1RS-1BS. 1BL in Pavon{0084}. **v:** Corinthian{1531}; Dauntless{1531}; Ambassador{1531}; Disponent{541}; GR876{753}; Halle Stamm{097}; Hammer{098}; Others{1208}; ST1-25{201}; Slejpner{1531}; Stetson{1531}; Stuart{096}. **v2:** Apollo *Pm2 Pm4b*{541}; Granada *Pm5*{541}; Hornet *Pm2*{1531}; Kristall *Pm5*{541}; Kronjuwel *Pm4b*{541}; Sensor *Pm5*{541}. **tv:** Cando*2/Veery = KS91WGRC14{381}.

1BS/1RS recombinants 2.9 cM proximal to *Gli-B1/GluB3*{0084}. Crosses between three lines with *Pm8* and Helami-105, a 1BL.1RS line with *Pm17*, indicated that *Pm8* and *Pm17* were allelic{524}. Earlier, these genes were reported to be genetically independent{1463}. A STS marker distinguished *Pm17* from *Pm8*{0286}.

Pm9{347}. 7A{347}.7AL. **v:** N14{562}. **v2:** Anfield *Pm1a*{1287}; Mephisto *Pm1a Pm2*{540}; Normandie *Pm1a Pm2*{347}; Pompe *Pm1a*{1287}; Ring *Pm1a*{1287}.

Pm10{1482}. 1D{1482}. **v:** Norin 4{1482}; Norin 26{1482}; Norin 29{1482}; Penjamo 62{1482}; Shinchunaga{1482}. **v2:** *T. spelta duhamelianum Pm11*{1481}.

Pm10 was detected using a culture derived from a hybrid of *B. g. tritici* and *B. g. agropyri*.

Pm11{1481}. 6BS{1481}. **v:** Chinese Spring{1481}; Salmon{1481}; *T. compactum* No. 44{1481}. **v2:** *T. spelta duhamelianum Pm10*{1481}.

Pm11 was detected using a culture derived from a hybrid of *B. g. tritici* and *B. g. agropyri*

Pm12{1017}. Derived from *Ae. speltoides*.

The earlier location of 6A {1017} was not correct. 6B = 6BS-6SS.6SL{598,572}.6S^{1}S{598}. **v:** Wembley*6/*Ae. speltoides* #31{1017,598}. **al:** *Ae. speltoides* CL214008 = K{1017}. **ma:** *Pm12* was mapped to a translocated segment proximal to *Xpsr551-6B*{598}; Secondary recombination analysis indicated that *Pm12* was located in the long arm of 6S between *Xwmc105* and *Xcau127*{10517}.

Pm13. Derived from *Ae. longissima* **ma:** STS marker *Xutv13*{0036}; several other markers located in introgressed segments{0036}.

3B{173} = T3BL.3BS-3S^1#1S{389}. **v:** R1A{174}; R1B{0055}; R4A{0055}; R6A{0055}. **ma:** *Pm13* was mapped to a translocated 3S^{1}S segment distal to *Xcdo-460-3B*{0036}.

3D{173} = T3DL.3DS-3S^1#1S{389}. **v:** R2A{0055}; R2B{0055}. **tv:** R1D{174}.

3S^1#1S. **al:** *Ae. longissima*.

Pm14. 6B{1478}. **v2:** Akabozu *Pm10Pm15*{1478}; Kokeshikomugi *Pm15*{1478}; Norin 10 *Pm15*{1478}.

Pm14 and *Pm15* were detected using hybrids between *B. g. tritici* and *B. g. agropyri* cultures.

Pm15. 7DS{1478}. **v2:** Akabozu *Pm14*{1478}; Chinese Spring *Pm11*{1478}; Kokeshikomugi *Pm14*{1478}; Norin 4 *Pm10*{1478}; Norin 10 *Pm14*{1478}; Norin 26 *Pm10*{1478}; Shinchunaga *Pm10*{1478}; *T. macha subletschumicum Pm10*{1478}; *T. compactum* No. 44

Pm11{1478}.

Pm14 and *Pm15* were detected using hybrids between *B. g. tritici* and *B. g. agropyri* cultures.

Pm16{1201}. 4A{1201}.5B{10217}. **v:** Line 70281 = Norman/*3 Beijing 837{10217}; Norman lines with resistance from *T. dicoccoides* CL1060025{1201}. **tv:** *T. dicoccoides* CL1060025{1201}. **ma:** *Pm16* - 5.3 cM - *Xgwm159-5B*{10217}.

To account for the different chromosome locations a 4A-4B translocation was suggested {10217}. Based on the 5B location and similar disease responses *Pm16* and *Pm30* may be the same {10217}.

Pm17{097,838,544}.

1AS = T1AL.1R#2S{1624,185,389}. **v:** Amigo{561}; Century{216}; McCormack{10758}; Nekota{0021}; Neobrara{0021}; TAM107{216}; TAM200{216}; TAM201{216}; TAM202{0021}; TAM303{10758}; Tribute{10758}.

1BS = T1BL.1R#2S{561}. **v2:** Helami 105 *Pm5*{561}. **ma:** A STS marker distinguished *Pm17* from *Pm8*{0286}; *Pm7* - 7.8 cM - *Xmwg68-1R* - 10.9 cM - *Sec-1* in 1RS{10167}.

Pm8 and *Pm17* were reported to be allelic {524}, see note under *Pm8*.

Pm18. Deleted, see *Pm1c*.

Pm19{853}. 7D{853}. **v:** *T. durum* 'Moroccos 183'/*Ae. tauschii* AE 457/78{853}. **v2:** Synthetic XX186 *Pm2*{853}. **dv:** *Ae. tauschii*{853}.

Pm20{386}. [*M1P6L*{543}]. 6BL = T6BS.6R#2L{543,386,389}. **v:** KS93WGRC28 = PI 583795{386,382}; 6RL. **su:** 6R{6D}{543}. **ad:** 6R addition{543}. **al:** Prolific rye{543}.

Pm21{1177}. 6AS = T6AL.6VS{1177}. **bin:** 6VS 0.45-0.58{10859}. **v:** 9 independent translocations{1177}. **ma:** RAPD *OPH17*$_{1900}$ (synonym 'OPH17-1900') was associated with *Pm21* and RAPD *OPH17*$_{1000}$ (synonym OPH17-1000') with its absence{1176}; RAPD OPH17$_{1400}$ and SCAR markers SCAR$_{1400}$ and SCAR$_{1265}$ associated with *Pm21* are described in{0014}; Marker NAU/Xibao15, developed from a serine/threonine gene upregulated by powdery mildew infection, acts as a co-dominant marker for lines carrying *Pm21*{10519}; Potentially useful markers are provided in {10918}. **c:** *Pm21* is likely the serine/threonine kinase gene *Stpk-V*{10859}.

Three lines, Pm97033, Pm97034 and Pm07035, with a 6DL.6VS translocation were developed from a different source of *H. villosa* {10194}. These may carry *Pm21*.

Pm22{1134}. Deleted. See *Pm1e*

Pm24{571}. 6D{571}.1DS{0150}. **v:** Chiyacao{571}. **ma:** *Xgwm789-1D/Xgwm603-1D* - 2.4 cM - *Pm24* - 3.6 cM - *Xbarc229-1D*{10109}.

Pm25{1343}. [*PmTmb*{1343,1344}]. 1A{1343}. **v:** PI 599035 = NC94-3778{1344}. **v2:** NC96BGTA5 = Saluda*3/PI 427662 *Pm3a*{1343}. **dv:** *T. monococcum* PI 427662{1343}. **ma:** Linked with 3 RAPDs, the nearest, OPAG04950, at 12.8 +/- 4.0 cM{1343}; Associated with 3 RAPDs{1344}.

Pm26{0001}. Recessive {0001}. 2BS{0001}. **s:** Bethlehem*8/*T. turgidum* var. *dicoccoides* 2BS{0001}. **tv:** *T. turgidum* var. *dicoccoides* TTD140{0001}. **ma:** Co-segregation with *Xwg516-2B*{0001}.

Pm27{0002}. 6B (6B-6G){0002}. **v:** Line 146-155-T{0002}. **tv:** *T. timopheevii* var. *timopheevii* K-38555{0022}. **ma:** 6BS......*Xpsr8/Xpsr964-6B* - *Pm27* - *Xpsr154/Xpsr546-6B* ......6BL{0002}; Co-segregation with *Xpsr3131-6B*{0002}.

Pm28{0022}. 1B{0022}. **v:** Meri{0022}.

Pm29{0129}. Derived from *Ae. ovata* 7DL. **v:** Pova{0129}. **ma:** Location confirmed by co-segregation with molecular markers{0129}.

Pm30{0163}. [*MIC20*] 5BS{0163}. **v:** 87-1/C20//2*8866 Seletion{0163}. **ma:** *Pm30* - 5.6 cM - *Xgwm159-5B*{0163}.

Pm30 could be the same as *Pm16* {10217}.

Pm31{0301}. [*mlG*{0301}]. 6AL{0301}. **v:** G-305-M/781//3*Jing411{0301}. **tv:** *T. dicoccoides* G-305-M{0301}. **ma:** cent....*Pm31* - 0.6 cM - *Xpsp3029.1-6A* - 2.5 cM -

Xpsp3071-6A{0301}.

This gene designation {0301} is not valid; subsequent studies {10918} showed the gene was *Pm21*.

Pm32{10025}. Derived from *Ae. speltoides* {10025}. 1B=1BL.1SS{10025}. **v:** L501 = Rodina*6/*Ae. speltoides*{10025}.

Pm33{10205}. [*PmPS5B*{10205}]. 2BL{10205}. **v:** Am9 = *T. carthlicum* PS5/*Ae. umbellulata* Y39{10205}. **tv2:** *T. carthlicum* PS5 *PmPS5A*{10205}. **ma:** *Xgwm536-2B* - 18.1 cM - *Pm33* - 1.1 cM - *Xwmc317-2B* - 1.1 cM - *Xgwm111-2B* - 1.8 cM - *Xgwm383-2B*{10205}.

Pm34{10241}. 5DL{10241}. **v:** PI 604033 = NC97BGTD7 = Saluda*3/*Ae. tauschii* TA2492{10241}. **dv:** *Ae. tauschii* TA2492{10241}. **ma:** *Xbarc177-5D* - 5.4 cM - 2.6 cM - *Xbarc144-5D*{10241}.

Pm35{10342}. 5DL{10342}. **v:** NC96BGTD3 = PI 603250 = Saluda*3/TA2377{10342}. **dv:** *Ae. tauschii* ssp. *strangulata* TA2377{10342}. **ma:** *Xcfd26-5D* - 11.9 cM - *Pm35*{10342}.

Pm36{10356}. 5BL{10356}. **bin:** 5BL6-0.29-0.76{10356}. **tv:** MG-FN14999, a durum backcross line 5BIL-29{10356}; *T. turgidum* ssp. *dicoccoides* MG29896{10356}. **ma:** *Xcfd7-5B* - 10.7 cM - *Pm36* - 0.8 cM - *EST BJ261636* - 8.9 cM - *Xwmc75-5D*{10356}.

Pm37{10372}. 7AL{10372,10274}. **v:** PI 615588 = NC99BgTAG11 = Saluda*3/PI 427315{10372}. **tv:** PI 427315=*T. timopheevii* ssp. *ameriacum*{10372}. **ma:** *Pm37* (PmAG11) was about 15 cM proximal to a cluster of markers that earlier co-segregated with *Pm1*{10372}; A cross indicated linkage between *Pm37* and *Pm1*{10372}; *Xgwm332-7A* - 0.5 cM - *Pm37* - 0.5 cM - *Xwmc790-7A* - 15.5 cM - *Pm1*{10372}.

Pm38{10373}. Adult plant resistance 7DS{10374}. **i:** RL6058=Tc*6/PI 58548{10374}. **v:** Lines with *Sr57/Lr34/Yr18* - see Reaction to *Puccinia triticina*, Reaction to *Puccinia striiformis*. **v2:** Saar *Pm5a Pm39*{10481}. **ma:** *Xgwm1220-7D* - 0.9 cM - *Lr34/Yr18/Pm38* - 2.7 cM{10374}; see also, Reaction to *Puccinia graminis.* Reaction to *Puccinia triticina* and Reaction to *Puccinia striiformis*. **c:** See *Lr34*.

This gene is identical to *Yr18, Sr57, Lr34* and *Ltn* and confers stem rust resistance in some genetic backgrounds.

Pm39{10481}. Adult plant resistance 1BL{10480,10481}. **i:** Avocet-R+Lr46/Yr29 = Avocet-R*3//Lalb mono 1B*4/Pavon 76{10480}. **v:** Genotypes with *Lr46/Yr29*; see Reaction to *Puccina triticina*, Reaction to *P. striiformis*. **v2:** Saar (CID: 160299, SID: 188) *Pm5a Pm38*{10481}. **ma:** *Xwmc719-1BL* - 4.3 cM - *Lr46/Yr29/Pm39* - 2.5 cM - *Xhbe248-1BL*{10481}.

Pm40{10539}. Derived from *Th. intermedium* {10539}. 7BS{10539}. **v:** GRY19{10539}; Partial amphiploid TAI7047{10539}; Yu{10539}; Yu24{10539}. **ma:** *Xwmc426-7B* - 5.9 cM - *Xwmc334-7B* - 0.2 cM - *Pm40* - 0.7 cM - *Xgwm297-7B* - 1.2 cM - *Xwmc364-7B*{10539}.

Pm41{10551}. Derived from *T. dicoccoides*. 3BL{10551}. **bin:** 0.63-1.00. **v:** XXX = 87-1*4/Langdon/IW2{10551}. **tv:** Langdon/IW2 Seln. XXX{10551}; *T. dicoccoides* IW2{10551}. **ma:** *BE489472* - 0.8 cM - *Pm41* - 1.9 cM - *Xwmc687-3B*{10551}.

Pm41 and associated marker alleles showed strongly distored inheritance with reduced frequencies relative to Langdon alleles {10551}.

Pm42{10559}. Derived from *T. dicoccoides* Recessive. 2BS{10559}. **bin:** 2BS-0.75-0.84. **v:** P63 = Yanda 1817/G303-1M/3*Jing 411{10559}. **tv:** *T. dicoccoides* G303-1M{10559}. **ma:** *BF146221* - 0.9 cM - *Pm42* - *Xgwm148-2B*{10559}.

Pm43{10560}. Derived from *Th. intermedium*. 2DL{10560}. **v:** Line CH5025 = 76216-96/TAI7045//2*Jing 411{10560}; Partial amphiploid TAI7045{10560}. **al:** *Th. intermedium* Z1141{10560}. **ma:** *Xwmc41-2D* - 2.3 cM - *Pm43* - 4.2 cM - *Xbarc11-2D*{10560}.

Pm44{10790}. 3AS{10790}. **v:** Hombar{10790}. **ma:** Flanked by SSR marekers distally located in chromosome 3AS{10790}.

Pm45{10791}. [*Pm57-6D*{10790}]. 6DS{10791}. **v1:** Line NWG0099{10791}. **v2:** D57{10791}. **ma:** Close linkages are reported in the draft manuscript.

Pm46{10847}. Partial resistance 4DL{10847,10678}. **bin:** Distal to break point 0.56 FL{10678}. **i:** RL6077=Thatcher*6/PI250413{10847,10678}. **ma:** Pleiotropic or closely linked with *Lr67/Yr46/Sr55* and aassociated with *Xgwm165-4D* and *Xgwm192-4DL*{10847,10678}.

Pm47{10912}. Reccessive [*PmHYLZ*{10912}]. 7BS{10912}. **bin:** 7BS-1 c-0.27. **v:** Hongyanglazi{10912}. **ma:** *Xgpw2097-7B* - 0.9 cM - *Pm47* - 3.6 cM - *Xgwm46-7B*{10912}.

A further gene derived from *T. monococcum* PI 427772 was identified in BCBGT96A = PI 599036 = Saluda*3/PI 427772 {10479}.
A single resistance gene was identified on chromosome 7AL in hexaploid germplasm NC96BGT4 (a *T. monococcum* derivative). This gene was proximal to *Pm1* and considered to be different from *Pm37*, although possibly allelic {10274}.
Genotype lists:Chinese wheats{1608,572}; Finnish wheats {0028}; French wheats{1629}; Hungarian wheats {02104}; Western Siberian wheats{1101}
Complex genotypes:
Drabent {heterogeneous} *Pm2 Pm4bPm9/Pm1 Pm2 Pm4b Pm9* {1287};
Nemares *Pm1 Pm2Pm4b Pm6 Pm9* {1287};
Planet, Sappo & Walter *Pm1 Pm2 Pm4b Pm9* {096,097,540,1287,1428}

Scandinavian wheats {10681}.

86.2. Suppressors of *Pm*

Some wheats which, on the basis of cytological and rust tests carry 1RS from Petkus rye, do not express resistance due to presence of a suppressor {385}. Zeller & Hsam {1625} located a suppressor of *Pm8* and *Pm17* in chromosome 7D of Caribo. Mildew resistance was suppressed in Florida, Heinrich, Ikarus, Olymp and Sabina, which are derivatives of Caribo with 1BL.1RS. According to Ren *et al.* {1209}, *SuPm8* does not suppress *Pm17*. Hanusova *et al.* {492} listed 16 wheats that carry a suppressor of *Pm8*; 111 wheats did not carry the suppressor. In contrast, a high frequency of suppression occurred in CIMMYT wheats {108,1208}. Further genotypes are identified in {491}. Although Line 81-7241 carries *Pm8* as well as *Pm23*, evidence was presented to indicate that *Pm8* was suppressed in Line 81-7241{1618} and , by inference, indicated that Chinese Spring possessed *SuPm8*.

SuPm8{1209}. 1AS{1209}. **v:** Wheats with *Gli-A1a*{1209} including CS; Lists in{108,491,1208}.

Pm8 was suppressed when locus *Pm3* is transcribed (including Chinese Spring and Thatcher which have no currently detectable *Pm3* resistance alleles) {10828}.

86.3. Temporarily designated genes for resistance to *Blumeria graminis*

Pm2026{10604}. *pm2026* {10604}, Recessive {10604}. 5A^{m}L{10604}. **bin:** 5AL17-0.78-1.00{10604}. **dv:** *T. monococcum* TA2026{10604}. **ma:** *Xcfd39-5A* - 1.8 cM - *Xcfd1493-5A/Xmg2170-5A* - 0.9 cM - *Pm2026* - 2.5 cM - *Xgwm126-5A*{10604}.

PmCn17{10686}. 1BS=1BL.1RS{10686}. **v:** Chuannong 17{10686}. **al:** *S. cereale* R14{10686}.

PmG16{10886}. 7AL{10886}. **bin:** 7AL16 0.86-0.90. **tv:** *T. dicoccoides* G18-16{10886}. **ma:** *Xgwm1061/Xgwm344-7A* - 1.2 cM - *PmG16/wPt-1424/wPt6019* - 2.4 cM - *wPy-0494/wPt9217/Xwmc809-7A*{10886}.

PmHNK{10706}. 3BL{10706}. **v:** Zhoumai 22{10706}. **ma:** *Xgwm108-3BL* - 10.3 cM - *PmHNK* - 3.8 cM - *Xwmc291-3BL*{10706}.

PmHNK54{10897}. 2AL{10897}. **bin:** 2AL1 C-0.85. **v:** Zheng9754{10897}. **ma:** *Xgwm372-2A* - 5.0 cM - *PmHNK54* - 6.0 cM - *Xgwm312-2A*{10897}.

PmLK906{10476}. Resistance is recessive {10476, 10477}. 2AL{10476,10477}. **v:** Lankao 90(6)21-12{10476}; Zhengzhou 9754{10476}. **ma:** *TacsAetPR5-2A/Pm4* - 3.9 cM - *Xgwm265-2A* - 3.72 cM - *Pm39* - 6.15 cM - *Xgdm93-2A*{10476,10477}; *TacsAetPR5-2A* was converted to a STS marker{10477}.

PmPs5A{10205}. 2AL{10205}. **v:** AM4{10205}. **tv2:** *T. turgidum* subsp. *carthlicum* pS5 *Pm33*{10205}. **ma:** *Xgwm356-2A* - 10.2 cM - *PmPS5A*; *PmPS5A* is located at or near the *Pm4* locus{10205}.

PmY39{10367}. 2U(2B){10367}. **su:** Laizhou 953*4/Am9(Am9=*Ae. umbellulata* Y39/*T. turgidum* ssp. *carthlicum* PS5){10367}. **dv:** *Ae. umbellulata* Y39{10367}. **ma:** Associated with 2U markers *Xgwm257, Xgwm296* and *Xgwm319*{10367}.

PmYm66{10619}. 2AL{10619}. **v:** Yumai 66{10619}. **ma:** *XKsum193-2A* - 2.4 cM & 3.6 cM - *PmYm66*{10619}.

Ml3D32{10892}. 5BL{10892}. **bin:** 5BL 0.59-0.76. **tv:** *T. dicoccoides* I222{10892}. **v:** 3D232{10892}. **ma:** *Xwmc415-5B* - 1.3 cM - *Ml3D232* - 3.3 cM - *CJ832481*{10892}; Co-segregation with 8 EST markers including an NBS-LRR analogue{10892}.

MlAB10{10873}. 2BL{10873}. **bin:** 2BL6 0.89-1.00. **v:** NC97BGTAB10 PI 604036{10873}. **tv:** *T. dicoccoides* PI 471746{10873}. **ma:** *Xwmc445-2B* - 7 cM - *MlAB10*{10873}.

Ml-Ad{854}. **v:** Adlungs Alemannen{854}.

Ml-Br{854}. **v:** Bretonischer Bartweizen{854}.

Mld{096}. 4B{097}. **v2:** Halle 13471 *Pm2*{096}; H8810/47 *Pm2*{096}; Maris Dove *Pm2*{096}. **tv:** *T. durum* line{096}.

Ml-Ga{854}. **v:** Garnet{854}; many old German cultivars{854}.

MlIw72{10545}. 7AL{10545}. **bin:** FL 0.86{10545}. **tv:** *T. dicoccoides* IW72{10545}. **ma:** *Xmag1759-7A* - 8.2 cM - *MlIw72* - 3.3 cM - *Xmag2185-7A* - 1.6 cM - *Xgwm344-7A*{10545}.

Mlm3033{10393}. 7AL{10393}. **dv:** *T. monococcum* TA2033{10393}. **ma:** *Xmag1757/Xmag2185* - 2.7 cM - *Mlm2033/Xmag2185* - 1.3 cM - *Xgwm344-7A*{10393}; *Xmag1757* - 5.9 cM - *Mlm2033/Xmag2185/Xgwm344/Xgwm146-7A* - 4.7 cM - *Xmag1986*{10393}; *Xmag1757/Xmag1714/Xmag1759 - Mlm2033* - 0.9 cM - *Xmag2185/Xgwm344-7A*{10393}.

Mlm80{10393}. 7AL{10393}. **dv:** *T. monococcum* ssp. *aegilopoides* M80{10393}. **ma:** *Xmag1757/Xmag1759* - 3.6 cM - *Mlm80* - 0.7 cM - *Xmag2166/Xgwm344-7A*{10393}. *Mlm2033* and *Mlm80* appeared to be allelic and their relative locations suggest they are allelic with *Pm1* {10393}.

mljy{0339}. Recessive, hemizygous-effective {0339} 7B{0339}. **v2:** Jieyan 94-1-1 *Pm8*{0339}.

mlsy{0339}. Recessive, hemizygous-effective {0339} 7B{0339}. **v:** Siyan 94-2-1 {0339}.

mlRd30{10175}. Reccesive 7AL{10175}. **v:** RD30{10175}; TA2682c{10175}. **ma:** *Xgwm344-7A* - 1.8 cM - *mlRD30* - 2.3 cM - *Xksuh9-7A*{10175}.
TA2682c carries a second dominant gene located in chromosome 1A {10175}.

Mlre{1220}. 6AL{0142}. **v2:** RE714 *Pm4b*{0142,1220}. **tv:** *T. dicoccum* 119{1220}. *Mlre* showed a residual effect on the quantitative expression of APR in the presence of *B. graminis* pathotypes considered virulent for *Mlre* in standard seedling tests{0016}. In addition to *Mlre*, a QTL for resistance effective at the seedling stage was associated with microsatellite marker *Xgwm174-5D* {0146}.

Mlxbd{0259}. Recessive and hemizygous-effective {0258} 7B{0259}. **v:** Xiaobaidong{0258}.

MlTd1055{10029}. **tv:** *T. dicoccoides* 1055{10029}.

Mlzec1{10127}. [*MLZec*{10127}]. 2BL{10127}. **v:** Zecoi 1 = Ralle*3/*T. dicoccoides* Mo49{10127}. **tv:** *T. dicoccoides* Mo49{10127}. **ma:** Distally located in chromosome 2BL{10127}; *Xwmc356-2B* - 2.0 cM - *PmZec1*{10127}.

86.4. QTLs for resistance to *Blumeria graminis*

QTL: Several QTLs were detected in two RE714/Hardi populations when tested at two growth stages and with different cultures over three years. The most persistent and effective QTL was located in the vicinity of *Xgwm174-5D* {0272}. Three QTLs, *QPm.vt-1B*, *QPm.vt-2A* and *QPm.vt-2B*, with additive gene action, accounted for 50% of the variation in a population developed from Becker/Massey{0284}.

These QTLs were confirmed by the addition of extra markers to the Becker/Massey map and in a separate analysis of USG 3209 (A Massey derivative)/Jaypee (susceptible) {10505}. USG 3209 possessed *Pm8* (1BL.1RS) and an unknown specific resistance factor and their combination had a positive effect on APR even though neither was effective against the races used to identify the QTL {10505}.

QTLs on chromosomes 1A, 2A, 2B, 3A, 5D, 6A and 7B were detected in a RE714/Festin population in multiple locations and over multiple years. The QTL on chromosome 5D was detected in all environments and all years and was associated with markers *Xgwm639-5D* and *Xgwm174-5D*. Resistance was contributed by RE714. A QTL coinciding with *MlRE* on 6A was also detected in all environments. The QTL on chromosome 5D and 6A accounted for 45% to 61% of the phenotypic variation {0354}.

Avocet R(S)/Saar (R) F6 RILs: QTL located on chromosomes 1BL (close to *Xwmc44-1B*) (*Pm39*), 7DS (*Xgwm1220-7D*) (*Pm38*) and 4BL (*XwPt-6209*) (resistance allele from Avocet R {10481}.

QPm.sfr-1A{0051}. 1A{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0051}. **ma:** Associated with *Xpsr1201-1A* and *Xpsr941-1A*{0051}.

QPm.sfr-1B{0051}. 1B{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xsfr3(LRR)-1B* and *Xpsr593-1B*{0051}.

QPm.sfr-1D{0051}. 1D{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0051}. **ma:** Associated with *Xpsr168-1D* and *Xglk558-1D*{0051}.

QPm.sfr-2A{0051}. 2A{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0051}. **ma:** Associated with *Xpsr380-2A* and *Xglk293-2A*{0051}.

QPm.sfr-2D{0051}. 2D{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0051}. **ma:** Associated with *Xpsr932-2D* and *Xpsr331-2D*{0051}.

QPm.sfr-3A{0051}. 3A{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xpsr598-3A* and *Xpsr570-3A* {0051}.

QPm.sfr-3D{0051}. 3D{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0051}. **ma:** Associated with *Xpsr1196-3D* and *Xsfr2(Lrk10)-3D*{0051}.

QPm.sfr-4A.1{0051}. 4A{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xgwm111-4A* and *Xpsr934-4A* {0051}.

QPm.sfr-4A.2{0051}. 4A{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xmwg710-4A* and *Xglk128-4A*{0051}.

QPm.sfr-4B{0051}. 4B{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xpsr593-4B* and *Xpsr1112-4B*{0051}.

QPm.sfr-4D{0051}. 4D{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xglk302-4D* and *Xpsr1101-4D*{0051}.

QPm.sfr-5A.1{0051}. 5A{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0051}. **ma:** Associated with *Xpsr644-5A* and *Xpsr945-5A*{0051}.

QPm.sfr-5A.2{0051}. 5A{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0051}. **ma:** Associated with *Xpsr1194-5A* and *Xpsr918-5A*{0051}.

QPm.sfr-5B{0051}. 5B{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0051}. **ma:** Associated with *Xpsr580-5B* and *Xpsr143-5B*{0051}.

QPm.sfr-6B{0051}. 6B{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xpsr167-6B* and *Xpsr964-6B*{0051}.

QPm.sfr-7B.1{0051}. 7B{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xpsr593-7B* and *Xpsr129-7B*{0051}.

QPm.sfr-7B.2{0051}. This QTL corresponds to *Pm5* {0051}. 7B{0051}. **v:** Forno/*T. spelta* var. Oberkulmer mapping population; the resistance was contributed by Forno{0051}. **ma:** Associated with *Xglk750-7B* and *Xmwg710-7B*{0051}.

QPm.ipk-2B{0255}. 2BS{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Resistance was contributed by Opata{0255}. **ma:** Associated with *Xcdo405-2B* and *Xmwg950-2B*{0255}.

QPm.ipk-4B{0255}. 4B{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Resistance was contributed by W-7984{0255}. **ma:** Associated with *Xcdo795-4B* and *Xbcd1262-4B*{0255}.

QPm.ipk-7D{0255}. 7DS{0255}. **v:** Opata/W-7984 (ITMI) RI mapping population{0255}; Resistance was contributed by Opata{0255}. **ma:** Associated with *Xwg834-7D* and *Xbcd1872-7D*{0255}.

Bainong 64(R)/Jingshuan 16(S). DH lines: Four QTL from Bainong 64: *Qpm.caas.1A*. *Xbarc148-1A* - *Xgwmc550-1A* interval. R^2=0.074-0.099; *QPm.caas-4DL* proximal to *Xwmc331-4D*. R^2=0.15-0.23; *QPm.caas-6BS*, proximal to *Xbarc79-6BS*, R^2=0.09-0.13; and *QPm.caas-7AL*, proximal to *Xbarc174-7AL*, R^2=0.067-0.071{10680}.
CI 13227(S)/Suwon 92(R), SSD population; APR (field resistance) was closely associated with *Hg*. *Xpsp2999-1A* and *Xpm3B.1* and *Xpm3B.2* designed from the *Pm3b* sequence.

Fukuho-Komugi/Oligoculm, DH population. QTL for adult plant resistance located on 1AS (R^2=22%, *Pm3* region, *Xgdm33* - *Xpsp2999*), 2BL (R^2=8%, *Xwmc877.1-Xwmc435.1)* and 7DS (R^2=10%) derived from Fukuho-komugi, and 4BL (R^2=6% at one of two sites, *Xgwm373-Xgwm251*) from Oligoculm {10335}. The QTL on 7DS, flanked by *Xgwm295.1-7D* and *Ltn*, is likely to be *Lr34/Yr18*.

Lumai 21(R)/Jingshuang 16(S), F_3 lines: Three QTLs from Lumai 21: *QPm.caas-2BS, Xbarc98-2BS* - *Xbarc1147-2BS* interval, R^2=0.106-0.206; *QPm.caas-2BL, Xbarc1139-2BL* -

Xgwm47-2BL interval, R^2=0.052-0.101; and *QPm.caas-2DL, Xwmc18-2DL - Xcfd233-2DL* interval, R^2=0.057-0.116 {10707}.

RE9001(R)/Courtot(S) RIL population:*QPm.inra-2B* (R^2=10.3-36.6%), in the vicinity of *Pm6*, was consistent over environments {10360}. Eleven QTL, detected in at least one environment were identified by CIM {10360}.

87. Reaction to *Cephalosporium gramineum*

Disease: Cephalosporium stripe

QTL:
Coda (more resistant)/Brundage (less resistant): RIL population: 7 QTLs identified based on whiteheads; three from Coda - *QCs.org-2D.1* (nearest marker C, R^2=0.11), *QCs.orp-2B* (nearest marker *Xwmc453-2B*, R^2=0.08), and *QCs.orp-5B* (nearest marker *Xgwm639-5A*, R^2=0.12) and four from Brundage (*QCs.orp-2D.2* (nearest marker *Xbarc206-2D*, R^2=0.04), *QCs.orp-48* (nearest marker *wpt-3908*, R^2=0.05), *QCs.orp-5A.1* (nearest marker *wpt-3563*, R^2=0.08), *QCs.orp-5A.2* (nearest marker *B1*, R^2=0.05) {10836}.

88. Reaction to *Cephus* spp.

Pest: Wheat stem sawfly. North American species *C. cinctus*; European species *C. pygmeus*. Resistance to wheat stem sawfly is associated with solid stem (see also: Stem solidness).

Tetraploid wheat

Qsf.spa-3B{10351}.
See Stem solidness.

89. Reaction to *Cochliobolus sativus* Ito & Kurib.

Disease: Cochliobolus root rot.

Crr{764}. Recessive. 5BL{764,765}. **v:** Apex{764}; Cadet{765}.

90. Reaction to *Diuraphis noxia* (Mordvilko)

Insect pest: Russian aphid, Russian wheat aphid.

Dn1{286}. 7D{1288}.7DS{0211}. **i:** Betta-Dn1:PI 634768{0004,0211,10277}; Caledon{0004}; Gariep{0004}; Karee-Dn1{0211}; Limpopo-Dn1{0004}; Tugela-Dn1:PI591932{0004,0211,10277}. **v:** PI 137739{286}. **ma:** *Xgwm111-7D-7D*$_{210}$ - 3.20 +/- 0.20 cM - *Dn1*{0211}.

Dn2{286}. 7DL{863}.7DS{0211}. **i:** Betta-Dn2:PI 634769{0211,10277}; Karee-Dn2:PI 663774{0211,10277}; Tugela-Dn2: PI 634772{0211,10277}. **v:** PI 262660{286,863}. **ma:** *XksuA1-7D* - 9.8 cM - *Dn2*{863}; Myburg et al.{9968} identified two SCAR markers that mapped 3.3 cM proximal to *Dn2*{9968}; *Xgwm111-7D*$_{200}$ - 3.05 +/- 0.18 cM - *Dn2*{0211}; *XksuA1-7D* - 9.9 cM - *Dn2* - 2.8 cM - *Xgwm437-7D*{0353}.
According to Saidi & Quick {1250}, *Dn1* and *Dn2* are probably allelic. Reference stocks with each gene showed allelism with a gene in PI 262605.

Dn3{1086}. Recessive. **v:** *Ae. tauschii* SQ24/*T. turgidum* TD65{1086}. **dv:** *Ae. tauschii* SQ24{1086}.

Dn4{1250}. 1DL{863}. **i:** Yumar{10397}. **v:** Ankor{10397}; CORWAI{260}; CI 2401{260}; Halt{0209}; PI 151918{260}; PI 372129{1250}; Prairie Red{10397}. **ma:** *Xabc156-1D* - 11.6 cM - *Dn4* {863}; *Xgwm106-1D* - 7.4 cM - *Dn4* - 12.9 cM - *Xgwm337-1D*{0352}; *Xgwm106-1D* - 5.9 cM - *Dn4* - 9.2 cM - *Xgwm337-1D*{10128}.

Dn5{1249}. 7D{259}.7DL{287,10310,10396}.7DS{0211}. **i:** Betta-DN5{0211}; Palmiet derivative 92RL28{287}; Palmiet DN5{0004}. **v:** STARS - 9302W-sib{259}; PI 294994{259}. **ma:** A SCAR marker developed from the RAPD fragment OPF14$_{1083}$ mapped 5.5 cM proximal to *Dn5*{0172}; *Xgwm111-7D*$_{220}$ - less than 3.20 cM - *Dn5*{0211}.

Issues relating to the confused arm location and mapping of *Dn5* is discussed in {10310}. Genetic mapping indicated that *Dn5* is located in chromosome 7DS, but cytological analysis showed it was located in 7DL {10396}. It was also suggested {10396} that the Palmiet Dn5 line {0004} may not have *Dn5* {10396}.

Dn6{1250}. **v:** CI 6501{260}; PI 243781{1250,1249}. **ma:** *Dn6* - 3.0 cM - *Xgwm111*{0352}.

Dn7{9918}. Derived from *S. secale* cv. Turkey 77 {9918} [*Dn2414*{10478}]. 1B = 1BL.1RS{9918}.1R{9918}. **v:** 93M45-14{9918}; 94M370{10188}; ST-ARS 02RWA2414-11{10474}. **ma:** *Xbcd1434-1R* - 1.4 cM - *Dn7* - 7.4 cM - *Xksud14-1R*{10188}; *Xhor2-1R* - 1.7 cM - *Dn7* - 1.0 cM - *Xscb241-1R*{10474}; Marker *Xrems1303*$_{320}$ was amplified only in genotypes resistant to biotype 3 and presumably possessing *Dn7*{10474}.

Dn8{0211}. 7DS{0211}. **i:** Karee-Dn8:PI 634775{10277}. **v2:** PI 294994 *Dn5Dn9*{0211}. **ma:** *Xgwm635-7D*$_{100}$ - less than 3.20 cM - *Dn8*{0211}.

Dn9{0211}. 1DL{0211}. **i:** Betta-DN9:PI 634770{10277}. **v2:** PI 294994 *Dn5Dn8*{0211}. **ma:** *Xgwm642-7D*$_{180}$ - less than 3.20 cM - *Dn9*{0211}.

Dnx{0211}. 7DS{0211}. **v:** PI 220127{0211}. **ma:** *Xgwm111-7D*$_{210}$ - 1.52 +/- 0.15 cM - *Dnx*{0211}.

Dnx was considered to be located at a locus different from *Dn1, Dn2* or *Dn5* {0211}, which were likely to be identical or allelic.

Dn1881{10145}. 7BS{10145}. **tv:** Line 1881{10145}. **ma:** *Xgwm46-7BS* - 10.1 cM - *Dn1881* - 12.8 cM - *Xgwm333-7BL*{10145}.

QTL: QTLs for antixenosis were associated with *Xpsr687-7D* (7DS) and *Xgwm437-7D* (7DL) in CS/CS (Synthetic 7D) {10136}. Separate antibiotic effects were demonstrated for the same chromosome {10136}.

A QTL, *QDn.unlp.6A*, for antixenosis was associated with *Xgwm1393-6AL* and *Xgwm1150-6AL* in a CS/CS(Synthetic 6A) DH population {10216}.

91. Reaction to *Fusarium* spp.

91.1. Disease: Fusarium head scab, scab

Type II resistance. Whereas much of the recent genetic work involved FHB caused by *F. graminearum*, according to {10514}, *F. culmorum* is more damaging than *F. graminearum* in terms of FHB severity, kernel damage, yield reduction and DON/NIV contamination.

Fhb1{10214,10403}. [*QFhs.ndsu-3BS*{9925,0175}]. 3BS{9925}. **i:** HC374/3*98B69-147{10214}; Sumai3*5/Thatcher{10214}. **v:** HC-147-126{10444}. **v2:** BW278 *Fhb2*{10225}; Sumai 3 *Fhb2*{10314}. **ma:** *XSTS3B-80* - 0.2 cM - *Fhb1* - 1.1 cM - *XSTS3B-142*{10214}; Placed in a 1.2 cM interval flanked by *XSTS3B-189* and *XSTS3B-206*{10403}.

W14(R)/Pioneer 2684(S) population: QTL in 3BS and 5AS accounted for 33%, 35% and 31% of the phenotypic variation for disease spread, kernel infection and DON accumulation in greenhouse experiments, and 34% and 26% of variation for FHB incidence and severity in the field {10239}. Flanking markers were *Xbarc133-3B* & *Xgwm493-3B* and *Xbarc117-5A* &

Xbarc56-5A {10239}.

The relationship of *Fhb1* to *Fhs1* or *Fhsb2* {1096} is unknown.

Fhb2{10225}. 6BS{10225}. **v:** pbE85{10444}. **v2:** BW278 *Fhb1*{10225}; Sumai 3 *Fhb1*{10225}. **ma:** *Xgwm133-6B* - 4 cM - *Fhb2* - 2 cM - *Xgwm644-6B*{10225}.

The relationship of *Fhb2* to *Fhs1* or *Fhs2* {1096} is unknown.

Fhb3{10529}. 7DS = T7AL.7Lr#1S{10529}. **v:** TA 5608{10529}. **al:** *Leymus racemosus*{10529}. **ma:** Three PCR markers, *Be586744-STS, BE404728-STS* and *BE586111-STS*, were developed{10529}.

The level of type 2 resistance conferred by *Fhb3* was similar to that of Sumai 3 {10529}.

Fhb4{10884}. [*Qfhi.nau-4B*{10282}]. 4BL{10282,10883}. **bin:** 4BL5-0.86-1.00. **i:** Mianyang 99-323*4/Nanda 2419/Wangshibai{10885}. **v2:** Wangshuibai *Fhb5*{10884}. **ma:** Located in a 1.7 cM segment flanked by *Xhbg226-4B* and *Xgwm149/Xmag4580-4B*{10883}.

Although plants with *Fhb-4* were taller than the recurrent parent, the height difference was not associated with the *Rht-B1* locus {10885}.

Fhb5{10896}. [*Qfhi.nau-5A*{10282}]. 5AS{10896}. **bin:** C-5AS3-0.75. **i:** Mianyan 99-323 and PH691 backcross derivatives selected for *Qfhi.nau-5A*{10896}. **v2:** Wangshuibai *Fh4b*{10896}. **ma:** Mapped to a 0.3 cM interval between *Xbarc117/Xbarc358/Xgwm293/Xgwm304-5A* and *Xgwm415-5A*{10896}.

Fhs1{1096}. **v:** Line A{1096}. **v2:** Ning 7840 *Fhs2*{1096}.

Fhs2{1096}. **v:** Line B{1096}. **v2:** Ning 7840 *Fhs1*{1096}.

A major QTL was associated with several linked AFLP markers tentatively located in chromosome 7BL of Ning 7840{0005}.

QTLs for resistance to *Fusarium graminearum* detected in the cross Renan/Recital {10069}. All resistance alleles, except *QFhs.inra-3A*, were contributed by Renan. LOD scores and percent of variation explained by the QT (R^2) are average of three years of field tests.

QFhs.inra-2A{10069}. **ma:** Associated with *Xgwm382c-2A* (LOD=6.3, R^2=14.4%).

QFhs.inra-2B{10069}. **ma:** Associated with *Xgwm374-2B* (LOD=7.6, R^2=12%).

QFhs.inra-3A{10069}. **ma:** Associated with *Xbcd372-3A* (LOD=3.7, R^2=6.2%).

QFhs.inra-3B{10069}. **ma:** Associated with *Xgwm383b-3B* (LOD=5.4, R^2=10.5%).

QFhs.inra-5A.1{10069}. **ma:** Associated with *Xpsr170a-5A* (LOD=3.8, R^2=5%).

QFhs.inra-5A.2{10069}. **ma:** Associated with *Xgwm639b-5A* 8LOD=6.6, R^2=14%).

QFhs.inra-5A.3{10069}. **ma:** Associated with *B1* (LOD=6.3, R^2=8.5%).

QFhs.inra-5D{10069}. **ma:** Associated with *Xcfd29-5D* (LOD=4.4, R^2=7%).

QFhs.inra-6D{10069}. **ma:** Associated with *Xcfd42-6D* (LOD=2.7, R^2=6.6%).

QFhs.ndsu-2A{9925,0175}. 2AL{9925}. **v:** Sumai 3/Stoa RI mapping population; the QTL was contributed by Stoa{9925}. **ma:** Association with RFLP *XksuH16-2A* (LOD>3){9925,0175}.

QFhs.ndsu-3AS{10482}. 3AS{0372}. **tv:** *T. turgidum* var. *dicoccoides*. Recombinant substitution lines LDN and LDN(Dic-3A). The resistant allele was contributed by *T. dicoccoides*{0372}. **ma:** Associated with *Xgwm2-3A* (explained 37% of the phenotypic variation){0372}; *QFhs.ndsu-3AS* was placed within a 11.5 cM region flanked by TRAP marker loci *Xfcp401-3A* and *Xfcp397.2-3A*{10482}; This gene is unlikely to be a homoeologue of *Qfhs.ndsu-3BS = Fhb1*{10482}.

QFhs.ndsu-3B{9925,0175}. 3BS{9925}. **v:** Sumai 3/Stoa RI mapping population; the QTL was contributed by Sumai 3{9925,0175}. **ma:** Association with *Xbcd907-3B.2* (LOD>3) {9925} and microsatellite markers *Xgwm1533-3B* and *Xgwm493-3B*{0175}; *QFhs.ndsu-3B* from Sumai 3 was associated with microsatellite loci *Xgwm533-3B* and *Xgwm274-3B* in certain Sumai 3 derivatives {10062}. In Ning 894037 the QTL has the same location and similar SSR bands to Sumai 3 {10085}. STS marker SRST.3B1 was mapped between *Xgwm533-3B* and *Xgwm389-3B* and associated with *QFhs.ndsu-3B* {10072}. *QFhs.ndsu.3B* was associated with markers *Xgwm533-3B, Xbard133-3B, Xbarc147-3B* and *Xgwm493-3B*{10073}.

This QTL explained 42% of the variation in Sumai 3/Stoa{0175}.
Two additional QTL for resistance to *Fusarium graminearum* were identified in the cross Sumai3/Stoa {0175}. The QTL on 4BS was associated with *Xwg909-4B* and the QTL on 6BS was associated with *Xbarc101-6B* and *Xbcd1383-6B* {0175}. The QTL associated with markers *Xgwm493-3B/Xgwm533-3B* (explaining 24.8 % of the variation), and *Xbarc101-6B/Xbcd1383-6B* were also identified in a RIL population from the cross ND2603/Butte 86 {0175}. In addition, one QTL on chromosome 3AL associated with *Xbcd941-3A* and one on chromosome 6AS associated with *XksuH4-6A* were identified in RILs from the cross ND2603/Butte 86 {0175}.

Resistance QTL on chromosome 3BS associated with *Xgwm493-3B* and *Xgwm533-3B* was also identified in a DH population of the cross Remus/CM-82036 (a Sumai 3 derivative) {0240}. Additional QTL in this cross were detected on chromosome 5A, associated with *Xgwm293-5A* and *Xgwm304-5A*, and possibly on 1B, associated with *Glu-B1* {0240}.

Two major genes with additive effects were reported in crosses between Sumai 3 (resistant) and two susceptible cultivars{0174}. One of the genes was assigned to 5AL based on linkage to the dominant awn suppressor B1 (RF 15.1-21.4%).

QTLs were located in 3BS, 2BL and 2AS in Ning 7840/Clark. The most effective QTL was probably in the interval flanked by deletions 3BS-3 and -8 and was close to *Xgwm533-3B* and *Xbarc147-3B* {0328}.

A marker study found that 14 of 66 wheats with putative FHB resistance shared markers indicative of the 3BS QTL in Ning 7840, Sumai 3, Wangshuibai and possibly Wuhan 3, plus Japanese landraces Shinchunaga and Shirasu No 1 {10115}. The original source may be the landrace 'Taiwan Wheat' rather than Funo {10115}. Four QTLs on chromosomes 3BS (associated with *Xbarc133-3B*), 3BL (*Xgwm247-3B*) and 3AS (*Xgwm5-3A*) from Huapei 57-2, and 5BL (*Xbarc59-5B*) from Patterson, were reported in the cross Huapei 57-2/Patterson {10026}. Huapei 57-2, Ning 7840 and Sumai 3 carried common alleles in the *Xgwm533-3B, Xgwm493-3B, Xbarc147-3B* and *Xbarc133-3B* region {10026}.

Wuhan-1/Nyubai{10623}: Two QTLs were located on chromosomes 2DL and 3BS (distal) {10020}.

<u>Field resistance</u>

G16-92(R)/Hussar(S): Two QTL for resistance to *F. culmorum* were identified on chromosome 1A (resistance from Hussar) (R^2 = 0.01) and 2B (resistance from G16-92) (R^2 = 0.14) {10588}.

Of 54 lines with reported FHB resistance, 6, including CM-82036, Ning 7840 and Wuhan 3, had the same 5-marker haplotype as Sumai 3, and 4 lines possessed 4 of the markers. Twenty-nine lines, including Frontana, had no marker allele in common with Sumai 3, whereas 13 lines had 1 to 3 alleles in common with it {10113}. *Qfhs.ndsu-3B* and the 5 marker loci were placed in 3BS deletion bin 0.78-0.87 {10144}.

Nanda2419(S)/Wangshuibai(R): 8 QTLs were identified; those with large effects were associated with *Xgwm533-3B.3* - *Xgwm533-3B.1* (W), *Xwmc539-6B* (W) and *Xs1021m-2B* - *Xgwm47-2B* {10190}.

Type I resistance (% infected plants) in this cross was attributed to 10 chromosome regions among which *Qfhi.nau-4B* (*Xwmc349-4B* - *Xgwm149-4B* - r^2=0.75), *XFhi.nau-5A (Xwmc96-5A* - *Xgwm304-5A* - R^2=0.27) and *Qfhi.nau-5B (Xgwm408-5B* - *Xbarc140-5B*) from Wangshuibai were detected in at least 3 of 4 years {10282}. A significant additive effect of QTL on 6D and 2A was also observed {10282}.

Type IV resistance (proportion of Fusarium-damaged kernels) was attributed to five QTLs, four from Wangshuibai. Those with the largest effects included *QFdk.nau-2B* (from Nanda 2419), *QFdk.nau-3B* and *QFdk.nau-4B* {10577} with each accounting for more than 20% of the phenotype variation.

Pelikan (S)/G93010 (=Bussard / Ning 8026) (R). *Qfhs.Ifl-7BS/5BL* and *Qfhs.Ifl-6BS* (probably *Fhb2*) from Ning 8026 reduced disease severity by 30% and 24%, respectively, and by 46% when combined {10594}. Other resistance genes were located on chromosomes 1AS (*Qfhs.Ifl-1AS* from Pelikan), and 2AL and 7AL (from Ning 8026) {10594}.

Spark (MR)/Rialto(S) DH population: Of nine QTLs identified across all environments, seven alleles for resistance came from Spark and two from Rialto. The largest effect on Type 1 resistance (*Xfhs.jic-4D.2*) was associated with the *Rht-D1b* allele in Rialto which made lines more susceptible. Other QTLs occurred on chromosomes 1B (1B.1R), 4D (*Qfhs.jic-4D.2*), 2A,3A (each, 2 QTLs), 5A and 7A. *Xfhs.jic-4D.2* had little effect on Type 2 resistance {10603}.

Wangshuibai/Seri 82:F3:F5 population: QTL on chromosome 3BS (*Xgwm533-3B* - *Xs18/m12-3B*) and 2DL(*Xgwm539-2D* - *Xs15/m24-2D*) accounted for 17% and 11%, respectively, of the phenotypic variance {10264}.
Wangshuibai/Alondra 'S': A stable QTL was associated with *Xgwm533-3B* in each of 3 years, QTLs in 5B (*Xgwm335-5B*), 2D and 7A were detected in 2 years {10268}.

Wangshuibai(R)/Wheaton(S): QTLs located in chromosome 3BS (*Xbarc147-3B*, R^2=37% & *Xbarc344-3B*, R^2=7%), 7AL (*Xwms1083-7A*, R^2=10%) and 1BL (*Xwms759-1B*, R^2=12%) {10200}.

Chokwang (R)/Clark (S):
Qfhb.ksu-5DL.1 associated with *Xbarc239-5D* (R^2=0.24) {10276}, *Qfhb.ksu-4BL.1* associated with *Xbarc1096-4B* (R^2=0.13) {10276}, and *Qfhs.ksu-3BS.1* marginally associated with the region of *Fhb1* (R^2=0.1) {10276}.

Ernie(Res)/MO94-317(Sus): 243 F8 RIL population. Four QTLs from Ernie detected as follows:
Qfhs.umc-2B, linked to *Xgwm278-2BS*, R^2 = 0.04 {10456}.
Qfhs.umc-3B, linked to *Xgwm285-3BS*, R^2 = 0.13 {10456}.
Qfhs.umc-4B, linked to *Xgwm495-4BL*, R^2 = 0.09 {10456}.
Qfhs.umc-5A, linked to *Xgwm165-5A*, R^2 = 0.17 {10456}.
Evidence was provided to suggest the QTL acted additively {10456}

Associations between responce to FHB caused by *F. culmorum* and the semi-dwarfing locus *Rht-D1* in crosses Apache/Biscay, Romanus/Pirat and History/Rubens (Biscay, Pirat and

Rubens carry *Rht-D1b*) were reported in {10574}. Genotypes with the semi-dwarf alleles tended to be more susceptible.

A review of 52 mapping studies is provided in {10593}.

Seedling resistance to *Fusarium graminearum* (FSB). A QTL for FSB resistance in the Wuhan/Nyubai population was associated with the *Qwmc75-5B* locus, R^2 = 0.138. The relationship of this resistance to crown rot resistance is unknown {10624} (see Reaction to *F. pseudograminearum*).

Tetraploid wheat

Langdon/Langdon (DIC-2A) RICL population: Increased susceptibility of the *T. dicoccoides* Israel A substitution line relative to Langdon was mapped to a 22 cM interval spanned by *Xgwm558-2A* and *Xgwm445-2A* {10613}.

QFhs.pur-2D{10085}. **v:** Alondra{10085}. **ma:** Located on 2DS between SSR markers *Xgwm296-2D* and *Xgwm261-2D*{10085}.

QFhs.pur-7El{10489}. 7el$_2${10489}.7DS.7DL-7el$_2${10489}. **su:** K2630{10489}. **v:** K11695 = 7DS.7DL-7el$_2${10489}; KS10-2 = 7el$_2$S.7el$_2$L-7DL{10489}; KS24-1 and KS24-2 = 7DS.7el$_2${10489}. **ma:** *Qfhs.pur-7el$_2$* was flanked by *BE445653* and *Xcfa2270-7D*{10489}; These markers were also present in KS10-2{10489}.

Qfhs.ifa-5A{10076}. Associated mainly with resistance to fungal penetration {10073}. 5A{0240,10076}. **v:** Remus/CM-82036{10076}. **ma:** Associated with markers *Xgwm293-5A*, *Xgwm304-5A*, *Xgwm1057-5A*, *Xbarc117-5A*, *Xbarc186-5A*, *Xbarc100-5A* and *Xbarc40-5A*{10073}.

Qfhs.crc-2BL{10445}. **tv:** Strongfield{10445}. **ma:** Spanning 16 cM, this QTL peaking on *Xgwm55-2B* explained 23% of the phenotypic variation{10445}.

Qfhs.ndsu-3AS{10402}. **sutv:** LDN-DIC3A{10402}. **tv:** *T. dicoccoides*{10402}. **ma:** Located in an interval spanning 29.3 cM this QTL accounted for 37% of the phenotypic variation; peak marker, *Xgwm2-3A*{10402}.

Qfhs.crc-6BS{10445}. **tv:** *T. turgidum* var. *carthlicum* cv. Blackbird{10445}. **ma:** Spanning 23 cM and peaking on *Xwmc397* this QTL accounted for 23% of the phenotypic variation{10445}.

Qfhs.fcu-7AL{10401}. **sutv:** LDN-DIC 7A{10401}. **tv:** *T. turgidum* var. *dicoccoides* PI 78742{10401}. **ma:** Located in an interval 39.6 cM thie QTL accounted for 19% of the phenotypic variation in a RIL population of Langdon/LDN-DIC 7A; nearest marker *Xbarc121-7AL*{10401}.

Strongfield/*T. carthlicum*(Blackbird): Field resistance identified in chromosome 2BL (*Xgwm55-2B*), and 6BL(*Xwmc397-6B*) (coincident with *Fhb2* {10225}.

Patterson (mod sus)/Fundulea 201R RILS: QTLs accounting for 19% and 13% of phenotypic variation were found on chromosomes 1BL (*Xbarc8-1BS* - *Xgwm131-1BL* region) and 3AS (*Xgwm674-3A/Xbarc67-3A* region) {10114}. Two weak QTLs were possibly associated with chromosomes 3D (Patterson allele) and 5AS {10114}.

Arina(R)/Forno(S): Three QTLs, *QFhs.fal-6DL* (R^2=22%), *QFhs.fal-5BL.1* (in Forno, R^2=14%) and *QFhs.fal.4AL* (R^2=10%) and 5 minor QTLs in 2AL, 3AL, 3BL, 3DS and 5DL were detected {10172}.

Arina/Riband DH lines: QTL affecting ADUPC were identified in 1BL(2), 2B, 4DS, 6BL and 7AL (Arina), and 7AL and 7BL (Riband). The most effective was the 4DS QTL that appeared to be an effect of *Rht-D1a* rather than height *per se* {10464}.

Cansas (moderately resistant)/Ritmo (susceptible): Map based analysis across environments revealed seven QTL, *QFhs.whs-1BS* (1RS), *QFhs.whs-3B* (not *Fhb1*), *QFhs.whs-3DL, QFhs.whs-5BL, QFhs.whs-7AL* and *QFhs.whs-7BL* (cumultatively, $R^2 = 0.56$). The chromosome 1D gene was primarily involved in resistance to fungal penetration and the others in resistance to spread {10503}. There were significant correlations of FHB response with height and heading date {10503}. Cansas/Ritmo: After *QFHS.whs-5BL* '(renamed *Qfhs.lfl-1BL* in {10768})'. *Qfhs.lfl-1BL* was verified in $F_{4:7}$ lines and detected in Biscay, History and Pirat {10768}.
More detailed mapping led to the relocation of the 5B QTL to chromosome 1BL. The renamed *Qfhs.lfl-1BL* reduced FHB severity by 42% relative to line lacking it {10698}. This gene was also present in Biscay, History and Pirat {10698}.

Three RGA sequences putatively assigned to chromosome 1A explained 3.37-12.73% of the phenotypic variation in FHB response among F7 and F10 populations {10364}. STS marker FHBSTS1A-160 was developed from one of the RGA.

CS/CS(Sumai 3 7A): *QFhb7AC*, nearest marker *Xwmc17-7A*, explained 22% of phenotypic variance for Type II and 24% of phenotypic variance for Type III resistance {10798}.

Dream(R)/Lynx(S) RIL population. Following inoculation with *F. culmorum* 4 QTL for AUDPC were identified on chromosomes 6AL (R^2=19%), 1B (12%), 2BL (11%) and 7BS (21%). The resistance allele in 1B came from Lynx and was associated with T1BL.1RS {10260}.

Dream*4/Lynx lines were developed by selection of QTL on chromosomes 6AL, 7BS and 2BL. Lines carrying *QFhs.lfl-6AL* and *QFhs.lfl-7BS* were more resistant than lines lacking them; the 2BL QTL effect was not verified {10470}.

Frontana(R)/Remus(S): Major QTLs in chromosomes 3AL (*Xgwm270-3AL - Xdupw227-3A* region) and 5A (*Xgwm129-5A - Xbarc-5A* region) accounted for 16% and 9% of the phenotypic variation (mainly type 1 resistance) over 3 years {10174}.

Frontana(MR)/Seri82(S), F3 and F3:5 populations: QTLs were located in chromosomes 1BL (R^2=7.9%), flanked by AFLP markers, 3AL (R^2=7.7%), flanked by *Xgwm720-3A* and *Xgwm121-3A*, 7AS (R^2=7.6%), flanked by an AFLP and *Xgwm233-7A* {10349}.

Soissons (relative resistant)/Orvantis (susceptible): Increased susceptibility associated with the *Rht-D1b* allele was further confirmed in crosses of semi-dwarf cultivars Apachi, History and Romanus {10793}.

Veery (S) / CJ9306 (R): Four QTLs, *XQFhs.ndsu-3BS* (*Xgwm533b - Xgwm493*), *QFhs.nau-2DL* (*Xgwm157 - Xwmc-041*), *QFhs.nau-1AS* (*Xwmc024 - Xbarc148*) and *QFhs.nau-7BS* (*Xgwm400 - Xgwm573*) accounted for 31, 16, 10 and 7%, respectively, of the average phenotypic variation over three years {10490}

Type I resistance and DON accumulation: Hobbit Sib/*T. macha* 4A DH population: Both traits were assigned to a small region distal to *Xgwm601-4A* and cosegregating with *Xgwm165-4A* {10254}.

DH181(R)(Sumai 3/HY 386 Seln.): QTL identified in 2DS, 3AS, 3BS, 3B Cent. region, 4DL, 5AS, 6BS {10213}.

Field resistance: Wuhan-1/Maringa, QTLs were located on chromosomes 2DS, 3BS (Proximal) and 4B {10020}.

Resistance to DON accumulation: Wuhan-1/Maringa, QTLs were located on chromosomes 2DL and 5DS {10020}.

Veery/CJ 9306 (R): Four QTLs contributed to resistance; *QFhs.ndsu-3BS* nearest marker *Xgwm533b* ($R^2 = 0.23$), *QFhs.nau-2DL*, *Xgwm539* ($R^2 = 0.2$), *QFhs.nau-1AS*, *Xbarc148* ($R^2 = 0.05$) and *QFhs.nau-5AS*, *Xgwm425* ($R^2 = 0.05$) {10496}.

Haplotype diversity among a large number of FHB resistant and susceptible (mainly Canadian) germplasms indicated similarities in Asian, Brazilian and other materials {10173}. Brazilian cv. Maringa was more similar to Asian than to other Brazilian lines {10173}.

For review see{0283}.

Mesterhazy et al.{0006} reported a strong genetic correlation in resistance to different species of *Fusarium*.

Bobwhite plants transformed with AtNPR1, an *Arabidopsis thaliana* gene that regulates activities of SAR, displayed a heritable type II response equal to that of Sumai 3 {10237}.

In cross Patterson (open)/Goldfield (closed) RILs, narrow flower opening was correlated with FHB resistance. The major QTL effect associated with narrow flower opening and low FHB incidence occured in map interval *Xbarc200* - *Xgwm210* (29% of variation in FHB incidence); these genes were probably located in chromosome 2BS {10243}.

Wangshuibai/Annong8455:RIL population: CIM analysis over 2 years detected QTL for FHB response on chromosome 3B (R^2=0.17) and 2A (R^2=0.12) and for DON levels in 5A (R^2=0.13), 2A (R^2=0.85) and 3B (R^2=0.06) {10447}. The regions involved were *Xgwm533-3B* - *Xbarc133-3B*, *Xgwm425-2A*, and *Xgwm186-5A* - *Xgwm156-5A* {10447}.

In a reciprocal backcross analysis of Chris monosomics/Frontana, Frontana chromosomes 3A, 6A and 4D reduced visibly diseased kernels, kernel weight and DON content, whereas Frontana chromosomes 2A, 2B, 4B and 7A increased the same traits {10398}.

Further study of the 3A, 6A and 4D reciprocal substitution lines indicated that chromosome 3A of Frontana had the largest effect on incidence, severity, spread and kernel damage, 4D less so and 6A possibly not at all {10900}.

Soissons (relatively resistant)/Orvantis (susceptible): Soissons carried *QFhs.jic-4D* (R^2=0.106-0.161) associated with *Rht-D1a* (tall allele) {10718}. FHB susceptibility tended to be associated with the *Rht-D1b* allele {10718}. Supporting studies with NILs indicated that the presence of *Rht-B1b* led to reduced type 2 resistance relative to presence of *Rht-D1b* or the tallness alleles at both loci {10718}.

Ernie(I)/MO94-317(S):RIL population: 3 QTLs on chromosomes 3BSc, 4BL and 5AS accounted for 31 and 42% of the total phenotypic variances for DON and Fusarium damaged kernels (FDK), respectively. A minor QTL (R^2=0.04) for FDK was on chromosome 2B {10831}.

Grandin(S)/PI277012(I): DH population: Two QTLs, *Qfhb.rwg-5A.1* on 5AS ($R^2$0.06-0.2) and *Qfhb.rwg-5A.2* on 5AL (R^2=0.12-0.2) conferred type I and II resistance and reduced DON content {0147}. The new QTL on 5AL was closely but not completely linked with gene *q* which is present in PI277012 {10860}.

Nanda 2419 /Wangshuibai:Backcross-derived NILs with *Qfh.nau-2B, Qfhs.nau-3B, Qfhi.nau-4B* (syn. *Fhb4*), and *Qfhi.nau-5A* were developed with Mianyang 99-323 as the recurrent parent {10884}.

Wheaton(I)/Haiyanzhong: RIL population: Four QTLs, *Qfhb.uhgl-7D* [syn. *Qhb.hyz-7D*], nearest marker *Xwmc121-7D*, R^2=0.16-0.2), *Qfhb.uhgl-6B.1* [*Qhb.hyz-6B.1*], R^2=0.4), *Qfhb.uhgl.6B.2* [*Qhb.hyz-6B.2*], R^2=0.07), *Qfhb.uhgl-5A* [*Qhb.hyz-5A*], R^2=0.04-0.07) were from Haiyanzhong, and *Qfhb.uhgl-1A* [*Qhb.hyz-1A*], R^2=0.05) was from Wheaton {10837}.

91.2. Disease: Crown rot caused by *Fusarium pseudograminearum, F. culmorum* and other *Fusarium* species

QTL: Kukri(R)/Janz(S) DH population. Simple interval mapping in the region Pst1 ACG.Mse1 CAC - *Xgwm251-4B* accounted for 48% of the variation in crown rot response {10034}.

Lang (S)/CSCR6(R):RIL population: tested under controlled conditions with *F. pseudograminearum* and *F. graminearum*: *Qcrs.cpi-3BL* from CSCR6, R^2=0.49 and *Qcrs.cpi-4B* from Lang R^2=0.23 {10703}. Six of 9 NIL pairs made by MAS for *Xgwm01081-3B* earlier located near the 3BL QTL {10703} in CSCR6 showed significant differences ($P < 0.01$) in crown rot response {10891}.

Lang/*T. spelta* CSCR6: *Qcrs.cpi-3BL* from CSCR6 was flanked by *wPt8438* and *wPt9495;* R^2 up to 0.49, validated in other crosses {10723}. *Qcrs.cpi-4B* from Lang; R^2 up to 0.23 {10723}.

Sunco/2-49: DH population: Three QTLs for seedling resistance, viz. *QCr.usq-1D.1* and *QCr.usq-4B.1* (R^2=0.19) from 2-49 and *QCr.usq-2B.1* from Sunco {10883}.
2-49/W21MMT70: DH lines: Three QTLs fo seedling resistance, viz. *QCr.usq-1D.1,* and a weaker QTL on chromosome 7A from 2-49 and *QCr.usq-3B.1* (R^2=0.41) from W22MMT70 {10883}.

2-49 (partially resistant) / Janz(susceptible) DH population: Analysis of partial seedling resistance indicated major QTL in chromosomes 1D (R^2=0.21) and 1A (R^2=0.09) and minor QTL in 2A, 2B (from Janz), 4B and 7B {10132}.
W21NMT70/Mendos: DH population: three consistent QTLs for seedling resistance were identified with CIM; these were located in chromosome 5D and 2D (resistance alleles from W21NMT70) and 2B (resistance allele from Mendos) {10358}.

92. Reaction to *Heterodera avenae*Woll.

Cereal root eelworm; cereal cyst nematode.

Cre1. [*Cre*{1388}]. 2B{1388}.2BL{1579,1580}. **i:** AP = Prins*8/AUS10894{1579}. **v:** AUS 10894{1056}; Beulah{10013}; Chara{10163}; Goldmark{10013}; Goroke{10013}; Kellalac{10013}; Loros CI 3779{10013}; Mira{10163}; Mitre{10163}; Ouyen{10013}; RE8670{10013}; Silverstar{10013}; VI252{10013}; VI727{10013}. **ma:** *Xglk605-2B* - 7.3 cM - *Cre1* - 8.4 cM - *Xcdo588-2B/Xabc451-2B*{1579}; A PCR-based assay was developed from *Xglk605-2B*{1580}; Co-segregation with *Xcsl107-2B*. Four of 6 land varieties possessed *Xcsl107-2B*. A variant haplotype of *Xcsl107-2B* was present in AUS4930{10013}; *Xcdo36-2B* - 7.5 cM - *Xbcd1231-2B/XAtPPr5/Xcsl107-2B/Cre1*{10013}.

Cre2{238}. Derived from *Ae. ventricosa* 10 {238,9991}. 6M^{v}{9991} **v2:** H-93-8 *Cre6*{238}. Although H-93-8 is a double M^{v}(5A), 7M^{v}(7D) substitution line, *Cre2* was presumed to be located in a separate undetected translocated 6M^{v} segment{9991}.

Cre3. [*CcnD1*{329},*Ccn-D1*{328}]. 2DL{328}. **v:** Synthetic hexaploids{329}. **dv:** *Ae. tauschii* accessions AUS 18912{328}; AUS 18913{328}; CPI 110809{329}; CPI 110810{328}. **ma:** Co-linearity with 2BL for *Xcdo-36-2D* and *XAtPPr5/Xbcd1231-2D/G4/G12/Cre3* (see *Cre1*){10013}.

Cre4. [*CcnD2*{329},*Ccn-D2*{328}]. 2D{328}. **dv:** *Ae. tauschii* accessions AUS 18914{329}; CPI 110813{328}.

Cre5{0107}. Derived from *Ae. ventricosa* {0107,0009}. [*CreX*{0009,0183}]. 2AS{0107}=2A-2N^{v}-6N^{v}. **v:** VPM1{0107}; Many VPM1 derivatives{0107}; Notable exceptions of lines with *Lr37, Sr38* and *Yr17*, but lacking *Cre5* include Trident and Line L22{0107}; However a contribution of the *Cre5* region was detected in Trident/Molineux{10343}. **su:** Moisson 6N^{v}(6D){0183}. **dv:** *Ae. ventricosa* 10{0183}. **ma:** Associated with the *Xgwm359-2A* (R^2=8%) - *Xwmc177-2A* (R^2=7%) region in Trident/Molineux{10343}.

Two resistance gene analogues similar to the candidate gene *Cre3* were isolated from the *Ae. ventricosa* segment carrying *Cre5*

Cre6{0138}. Derived from *Ae. ventricosa* {0138}. 5N^{v}{0138}. **ad:** Moisson + 5N^{v}{0138}. **v:** H-93-35{0138}. **v2:** H-93-8 *Cre2*{0138}.

Cre7{0104}. Derived from *Ae. triuncialis* {0105}. [*CreAet*{0105}]. **v:** TR353 derivatives{0105}.

Cre8{0220}. [*CreF*{0012,0138}]. 6BL{0220}, on basis of linkage with *Xbcd1-6B* and *Xcdo347-6B*{0220}. **v:** Barunga{0220}; Festiguay{0012,0220}; Frame{0138,0220}; Molineaux{0220}. **ma:** Linked to RFLP loci *Xbcd1-6B* and *Xcdo347-6B*. The 6B location of the *Xcdo347* probe used in this study was confirmed by nulli-tetrasomic analysis{0220}; Associated with the *Xgwm147-6B* (R^2=24%) - *Xcdo247-6B* (R^2=12%) region in Trident/Molineux{10343}.

CreR{0133,0318}. 6RL{0133}. **ad:** Wheat + 6R {0318}; Wheat + 6RL{0318}; Various deletion stocks{0318}. **su:** CS + 6R(6D){0133}. **al:** Rye accession T701-4-6{0133}; Triticale T-701{0318}. **ma:** Cent......*XksuF37* - 3.7 cM - *CreR*{0133}; Deletion mapping indicated *CreR* was located near *Got-R2*{0318}.

CreX{10486}. Derived from *Ae. variabilis* 2AS or 2DS{10486}. **ad:** Line M{10487}. **v:** Line D{10486}. **ma:** RAPD markers $OP02_{1000}$, $OpR4_{1600}$, $OpV3_{450}${10486}.

CreY{10486}. Derived from *Ae. variabilis* 3BL{590}. **v:** Line X{10487}. **ma:** Co-segregation with RAPD $OpY16_{1065}$ {0103} which was converted to SCAR16{10486}. May be the same gene as *Rkn-mn1* (see reaction to *Meloidogyne naasi*).

QCre.pau-1A{10749}. 1AS{10749}. **dv:** *T. monococcum* Tm 14087 *QCre.pau-2A*{10749}. **ma:** *QCre.pau-1A* was mapped in a 3.6 cM interval in a *T. boeoticum* Tb 5088 / Tm 14087 RIL population and was flanked by *Xcfa2153-1A* and *BE444890* {10749}; R^2=0.26{10749}. *QCre.pau-1A* was transferred to tetraploid and hexaploid lines {10749}.

QCre.pau-2A{10749}. 2AS{10749}. **dv:** *T. monococcum* Tm 14087 *QCre.pau-1A*{10749}. **ma:** *QCre.pau-2A* was mapped in a 4.00 cM interval flanked by *BE498358* and *Xwmc358-2A* {10749}; R^2=0.13{10749}.

QTL: ***Qcre.src-1B*** was located to the *Xwmc719-1B* (R^2=12%) - *Xgwm140-1B* (R^2=12%) region in Trident/Molineux {10343}.

93. Reaction to *Magnaporthe grisea* (Herbert) Barr

M. grisea is a pathogen of blast on many graminaceous species, the best known of which is rice. In Brazil it has become a pathogen of wheat. The wheat pathotype(s) is different from those attacking other species such as rice, oat, millets and weeping lovegrass.

Rmg1{0333,10462}. [*Rwt4*{0302}]. 1D{10462}. **s:** CS (Cheyenne 1D){10462}. **v:** Cheyenne{10462}; Norin 4{0302}; Norin 26{10462}; Shin-chunaga{10462}.

Rmg2{10461}. 7A{10461}. **i:** CS (Thatcher 7A){10461}. **v2:** Thatcher *Rmg3*{10461}.

Rmg3{10461}. 6B{10461}. **i:** CS (Thatcher 6B){10461}. **v2:** Thatcher *Rmg2*{10461}.

Rmg4{10639}. 4A{10639}. **v:** Norin 4{10639}; Norin 26{10639}; Norin 29{10639}; P168{10639}; Shin-chunaga{10639}; *T. compactum* No. 24{10639}.
Cofers resistance to *Digitaria* isolate Dig41 at 26C {10639}

Mg5{10639}. 6D{10639}. **s:** CS (Red Egyptian 6D){10639}. **v:** Red Egyptian{10639}. Confers resistance to *Digitaria* isolate Dig41 at 26C {10639}.

A second gene designated *Rwt3* {0302} was present in CS and Norin 4. Genes *Rwt3* and *Rwt4* were detected using hybrids of *Triticum*-virulent and *Avena*-virulent pathogen isolates.

94. Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)

Insect pest: Hessian fly.

H1{1087}. **i:** Dawson/3*Poso, 6179{1087}. **v2:** Big Club 43 *H2*{1441}; Dawson *H2*{166,1087}; Poso 42 *H2*{1441}.

H2{1087}. **i:** Dawson/3*Poso, 6232{1087}. **v2:** Big Club 43 *H1*{1441}; Dawson *H1* {166,1087}; Poso 42 *H1*{1441}.

H3{156}. Recessive. 5A{425,1105}. Based on the location of *H9* on chromosome 1AS, *H3* may also be located on chromosome 1AS{10231,10252}. **i:** Carol = Newton-207*5/Larned{1107}. **v:** Ace{426}; Arthur{426}; Becker{749}; Cardinal{750}; Dual{1273}; Frankenmuth{341}; Georgia 1123{426}; GR855{751}; GR876{753}; Ike{10252}; Ionia{426}; Larned{824}; Logan{426}; Monon{157}; Norkan{904}; Ottawa{547}; Purdue B 36162 A13-12{156}; PI 468960{1439}; Redcoat{1273}; Reed{1273}; Riley{1273}; Roland{148}; Russell{426}; Shawnee{547}; Titan{747}; Todd{426}; W38{156}. **v2:** Clara Fay *H6*{375}. **ma:** Cosegregation of *H3* and a RAPD{296}.
Allan et al.{019} considered that *H3* and *H4* may be allelic. Also suggested by Shands and Cartwright{1317}. Linkage of 10.5 +/- 2% involving *H3* and *Pm3a* in PI 468960 was attributed to a chromosome 1A/5A translocation{1437}.

H4. Recessive. *H4* confered resistance to race A, but not to race B. [*h4*{1441}]. **v:** Dixon{1441}; Java{1441}.

H5{1317}. Temperature sensitive {1413}. 1AS{1222}. **v:** Abe{162}; Arthur 71{162}; Beau{875}; Downy{1223}; Magnum{10252}; Oasis{1109}; Ribeiro{1317}; Sullivan{1110}. **tv:** Giorgio 331-4{1090}; PI 94567-6{1317}; PI 94571-14{1317}. **ma:** Cosegregation of *H5* and two RAPDs{296}.

H6{019}. 5A{425}. Based on the location of *H9* on chromosome 1AS, *H6* may also be located on chromosome 1AS{10231,10252}. **i:** Erin = Newton-207*7/Arthur 71{1107}; Flynn = Newton-207*7/Knox 62{1107}. **v:** Adder{1319}; Benhur{426}; Caldwell{1421}; Compton{1318}; CI 12855{019}; Excel{752}; Fillmore{1106}; Knox 62{426}; Lathrop{426}. **v2:** Clara Fay *H3*{375}. **tv:** Purdue 4835 A4-6{1105}. **tv2:** PI 94587 *H11 H16*{019}. **ma:** Cosegregation with three RAPDs{296}.

H7 & H8{425}. Duplicate factors. *H7* is located in chromosome 5D {026}. **v:** Adena{748}; Seneca{026,425}.

H9{1420}. 5A{162}.1AS{10231,10252}. **i:** Iris = Newton-207*7/Ella{1107}. **v:** Ella{875}; Line 822-34{162}. **v2:** Elva CI 17714 *H10*{162}; Line 812-24 *H10*{1421}; Line 817-2 *H10*{1421}; Stella *H10*{875}. **ma:** Cosegregation with two RAPDs{296}; *STS-Pm* - 1.7 cM - $SOP005_{909}$ - 0.6 cM - *Xksu11/Xcnl76/Xgdm33-1A* - 0.5 cM -

Xgwm176/Xpsp2999/Xcfa2153-1A - 0.5 cM - *Xbarc263-1A* - 1.2 cM - *H9* - *Xwmc24-1A*{10231}; *Xcfa2153-1A* - 0.5 cM - *H9* - 0.3 cM - *Xbarc263-1A*{10252}.

H10{1104}. May be identical to H9 {10252}. 5A{162}.1AS{10252}. **i:** Joy = Newton-207*3/IN76529A5-3-3{1107}. **v:** IN76529{875}. **v2:** Elva CI 17714 *H9*{162}; Line 817-2*H9*{162}; Stella *H9*{875}. **ma:** Cosegregation with one RAPD and close linkage to another RAPD{296}; *Xcfa2153-1A* - 0.5 cM - *H10* - 1.3 cM - *Xbarc263-1A*{10252}; *Xrapd9-2-1000/Xpsp2999-1A/Xgps7072-1A* - 2.2 cM - *H10*{10252}.

H11{1422}. 1A{1222}.1AS{10252}. **i:** Karen = Newton-207*4/IN916-1-3-1-47-1{1107}. **v:** Kay{875,375}; Line 916{1422}; Line 920{1422}; Line 941{1422}. **tv2:** *T. turgidum* PI 94587 *H6 H16*{1422}. **ma:** Close linkage with two RAPDs{296}; *Xcfa2153-1A* - 0.3 cM - *H11* 1.7 cM - *Xbarc363-1A*{10252}.

H12{1092}. 5A{1098}. **i:** Lola = Newton-207*4/Luso{1107}. **v:** Luso{1092}. **ma:** Cosegregation with one RAPD and close linkage of *H12* to another RAPD{296}.

H13{1104}. 6DL{441}.6DS{10251,10388}. **i:** Molly = Newton-207*7/3/KU221-19/Eagle/KS806{1107}. **v:** KS81H1640HF{441}; PI 562619{10388}; SW34=Langdon/*Ae. tauschii* RL 5544{10388}; *T. turgidum* var. *durum* cv. Gulab KU 134/*Ae. tauschii* KU 2076, KU 221-14{525}; *T. turgidum* var. *persicum straminium* KU 138/*Ae. tauschii* KU 2076, KU221-19{525}. **dv:** *Ae. tauschii* KU 2076{525}. **ma:** Cosegregation with a RAPD{296}; *Xgdm36-6D* - 2.7 cM - *H13/Xcfd132-6D* - 1.1 cM - *Xcfd213-6D*{10251}; *Xcfd132-6D* - 3.7 cM - *H13*{10388}.

H14{875}. 5A{875}. **tv:** IN 81601A2-3-3{875}. **tv2:** ELS 6404-160 *H15*{875}. **ma:** Cosegregation with a RAPD{296}.

H15{875}. 5A{875}. Based on the location of *H9* on chromosome 1AS, *H15* may also be located on chromosome 1AS{10231}. **tv:** IN81602C5-3-3{875}. **tv2:** ELS 6404-160 *H14*{875}.

H16{1106}. 5A{1098}. **tv:** IN 80164H5-2-9{1106}; N80164{1097}. **tv2:** PI 94587 *H6 H11*{1106}. **ma:** Cosegregation of *H16* and a RAPD{296}.

H17{1090}. 5A{1090}. **tv:** PI 428435{1090}. **ma:** Cosegregation of *H17* and a RAPD{296}.

H18{1090}. **v:** Marquillo{426,874}; Redlant{10715}; Shield{198}.

H19{1089}. **tv:** PI 422297{1089}; This germplasm possesses a second gene which is allelic or closely linked with *H16*{1089}; IN84702{1097}. **tv2:** PI422297 *H29*{1097}.

H20{025}. 2B{025}. **tv:** Jori{025}.

H21. 2B {383} = 2BS.2R#2L{389}. **v:** Hamlet = KS89WGRC8{1312}; KSWR 69-2-4-3{383}; KS85HF 011-5{383}. **ad:** KSWR 297h-1-1-9{383}. **al:** Chaupon rye{383}. **ma:** A RAPD amplified by primer OPE-13 was shown to co-segregate with *H21*{9938}; A STS primer set SJ07 was developed to identify 2RL, and hence *H21*{0233}.

H22{1199}. 1D{1199}.1DS{10381}. **v:** KS86WGRC1{1199}; KS85WGRC01=*Ae. tauschii* TA1644/Newton//Wichita{1199}; PI 572542{10388}. **ma:** *Xgdm33-1D* - 1.0 cM - *H22* - 0.3 cM - *Xhor2KV-1D* - 0.5 cM - *Xgpw7082-1D*{10381}.

H23{1199}. 6D{442}.6DL{1199}.6DS{10251}. **v:** KS89WGRC03 = TA1642 / 2*Wichita{442,10251}; PI 535766{10388}. **al:** *Ae. tauschii* TA1642{10251}. **ma:** *H23* - 6.9 cM - *XksuH4-6D*{861}; Maps to same region as *H13*{10262}.

H24{1199}. 3D{442,1199}.6DL{861}. **v:** KS89WGRC6{442}; PI 535769{10388}. **ma:** *H24* - 5.9 cM - *Xbcd451-6D/Xcdo482-6D*{861}.

H25.
6B{384} = T6BS.6BL-6R#1L{389}. **v:** 88HF16 = WGRC17{384}.
4B{384} = T4BS.4BL-6R#1L{389}. **v:** 88HF79, 88HF80 = WGRC18, 88HF81, 88HF117 = WGRC19{384}.
4A{384} = Ti4AS.4AL-6R#1L-4AL{389}. **v:** 89HF17, 89HF18, 89HF25, 88HF32, 88HF51, 88HF89 = WGRC20{384}.
6R. **al:** Balbo rye{384}.

H26. 4D{217}.3DL{10388}. **bin:** 3DL3-0.81-1.00. **v:** KS92WGRC26{217}; SW8 = Langdon/*Ae. tauschii* CIae 25{10388}. **dv:** *Ae. tauschii* TA2473{217}. **ma:** *Xcfd211-3D* - 7.5 cM - *H26* - 2.9 cM - *Xwgc7330-3D* - 4.0 cM - *Xgwm3-3D*{10388}.
H26 is very close to *H32* {10846}.

H27{235}. 4M^{v}{235}. **su:** H-93-33{235}. **al:** *Ae. ventricosa* No. 10{235}; *Ae. ventricosa* No. 11{235}.

H28{171}. 5A{171}. **tv:** PI 59190{171}.

H29{1095}. [*H27*{171}]. 5A{1097}. **tv:** PI422297 *H19*{1097}.

H30{0256}. Derived from *Ae. triuncialis* {0256}. **v:** TR-3531{0256}. **al:** *Ae. triuncialis*{0256}.

H31{0332}. 5BS{0332}. **v:** P961696{0332}. **tv:** CI 3984{0332}. **ma:** STS marker *Xupw4148-5B* - 3 cM - *H31*{0332}.

H32{10137}. 3DL{10137}. **bin:** 3DL3-0.81-1.00. **v:** Synthetic W7984{10137}. **ma:** *Xgwm3-3D* - 1.7 cM - *H32* - 1.7 cM - *Xcfd-3D*{10137}; *Xrwgs10-3D* - 0.5 cM - *H32/Xrwgs11-3D* - 0.5 cM - *Xrwgs12-3D*{10846}.
H32 is very close to *H26* {10846}.

Hdic{10262}. 1AS{10262}. **v:** KS99WGRC42{10262}. **tv:** *T. dicoccum* PI 94641{10262}. **ma:** *Xcfa2153-1A* - 1.4 cM - *Hdic* - 0.6 cM - *Xgwm33-1A*{10262}.

H$_{WGRC4}${10251}. 6DS{10251}. **v:** KS89WGRC04 = TA 1695 / 3*Wichita{10251}. **ma:** Allelic with *H13*{10251}.

HNC09MDD14. [*Hf-NC09MDD14*{10844}]. 6DS{10843}. **v:** NC09MDD14 PI 656395{10843}. **dv:** *Ae. tauschii* TA2492 and/or TA2377{10843}. **ma:** *Xgdm36-6D* - 1.5 cM - *HNC09MDD14/Xcfd123-6D*{10843}; *HNC09MDD12* could be allelic to, but is different from, *H13*{10843}.

A recombination value of 12.0% between leaf-rust reaction {possibly *Lr10*} and Hessian-fly reaction in Selection 5240 was reported {018}.

95. Reaction to *Meloidogyne* spp.

Root rot nematode, root knot eelworm

Rkn1{632}. [*Rkn*{632}]. 6D{10799}. **dv:** *Ae. tauschii* G3489. **v:** Prosquare, a synthetic hexaploid of Produra/*Ae. tauschii* G3489{632}.

Rkn2{1621}. Derived from *Ae. peregriina (variabilis)*{1621}. [*Rkn-mn1*{1621}]. 3B{590}. **v:** X8 = CS/*Ae. peregrina* No. 1//Rescler/3/Lutin{1620}; X35{1620,1621}. **ma:** Co-segregation with RAPD *OpY16*$_{1065}$ and close linkage with several markers including *Est-B5*{0103}; converted to SCAR Y16{10486}; May be the same as *CreY* (see reaction to *Heterodera avenae*) on chromosome 3S^{V} from *Ae. variabilis* translocated to 3BL{10800}.

Rkn3{10801}. Derived from *Ae. ventricosa* 2NS translocation into 2AS{10801}. **v:** VPM1, Lassik (PI 653535){10801}. **ma:** Resistances to *M. javanica* and *M. incognita* mapped to the 2NS translocation in BC$_6$F$_3$ near isogenic lines of Anza (PI 638742), Yecora Rojo, and Express with the 2NS translocation{10801}.

96. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter

Disease: Septoria tritici blotch

Stb1. [*Slb1*{1586}]. 5BL{10123}. **v:** Bulgaria 88{1586}; Oasis{1586}; P881072-75-1{10123}; SO852{10123}; Sullivan{1586}. **ma:** Located in FL 5BL-11 - 5BL-14{10123}; Close linkage with 2 RAPD markers at >0.68 and 1.4 cM in P881072-75-1{10123}; Cent.....*Xbarc74-5B* - 2.8 cM - *Stb1*{10123}.

Stb2. [*Slb2*{1586}]. 3BS{10105}. **v:** Nova Prata{1586}; Veranopolis{1586}. **ma:** *Xgwm389-3B/Xgwm533-3B* - 1.0 cM - *Stb2* - 3.7 cM - *Xgwm493-3B*{10105}.

Stb3. [*Slb3*{1586}]. 6DS, according to {10556} this location is not correct{10105}.7AS{10556}. **v:** Israel 493{1586}. **ma:** *Stb3* - 3.0 cM - *Xgdm132-6D*{10105}.

Stb4{1410}. 7D{0326}.7DS{10140}. **v:** Cleo{1410}; Gene{10010}; Tadinia{1410,10140}; Tadorna{1410}. **ma:** *XAGG/CAT10* - 4.0 cM - *Stb4* - 0.7 cM - *Xgwm111-7D* - 1.4 cM - *XATCG/CAAA5* ....Cent{10140}; *Stb4* - 0.7 cM - *Xgwm111-7D*{10140}.
Stb4 segregated independently of *Stb1* but its relationship with *Stb2* and *Stb3* is unknown. Genetic analysis of Tadinia indicated single gene segregation (assumed to be *Stb4*) with a Californian culture but a different single gene segregated with South American isolates {10140}.

Stb5{0186}. Identified using *M. graminicola* IPO94269{0186}. Derived from *Ae. tauschii* accession 37-1 {0186}. 7DS{0186}. **v:** Bezostaya{0187}; Hereward{0187}; Sears' Synthetic{0186}; Shafir{0187}; Vivant{0187}. **su:** CS*8/(Syn7D){0186}. **dv:** *Ae. tauschii* 37-1{0186}. **ma:** *Rc3* - 6.6 cM - *Stb5* - 7.2 cM - *Xgwm44-7D* - Centromere{0186}; *Stb6* - 2 cM - *Xgwm369-3A*{0187}.

Stb6{0187}. Confers resistance to *M. graminicola* isolate IPO323 but not to isolate IPO94269 {0187}. 3AS{0187}. **v:** Amigo{10448}; Arina{10448}; Amada{10448}; Atlas 66{10448}; Ble Seigle{10448}; Bon Fermier{10448}; Chinese Spring{10448}; Bezostaya 1{10495}; Flame{0187}; Gene{10448}; Heines Kolben{10448}; Hereward{10448}; Poros{10448}; Senat{10448}; Shafirm{10448}; Tadinia{10448}. **v2:** Bulgaria 88 *Stb1*{10448}; Israel 493 *Stb3*{10448}; Kavkaz-K4500 *Stb7 Stb10 Stb12*{10011}; TE9111 *Stb7 Stb11*{10012}; Veranopolis *Stb2*{10448}. **ma:** A resistance gene from Senat located at or near the *Stb6* locus was mapped 5 cM from microsatellite *Xgwm369-3A* on chromosome arm 3AS{10067}.

Stb7{0311}. 4AL{0311}. **v:** ST6 = Estanzuela Federal{0310, 0311}. **v2:** Kavkaz-K4500 *Stb6 Stb10 Stb12*{10011}; TE9111 *Stb6 Stb11*{10012}. **ma:** *Xwmc219-4A* - 0.8 cM - *Xwmc-4A* - 0.3 cM - *Stb7*{0311}; *Stb7* was closer to *Xwmc313-4A* than to *Xwmc219-4A*{10011}.

Stb8{0326}. 7BL{0326}. **v:** Synthetic hexaploid W7984 (parent of ITMI population){0326}. **ma:** *Xgwm146-7B* - 3.5 cM - *Stb8* - 5.3 cM - *Xgwm577-7B*{0326}.

Stb9{10027}. Culture IPO89011 2BL{10027}. **v:** Courtot{10027}; Tonic{10027}. **ma:** *Xfbb226-2B* - 3 cM - *Stb9* - 9 cM - *XksuF1b-2B*{10027}.
Information withheld until publication

Stb10{10011}. Confers resistance to cultures IPO94269 and ISR8036, but not to IPO87019 {10011}. 1D{10011}. **v2:** Kavkaz-K4500 L.6.A.4 *Stb6 Stb7 Stb12* = JIC.W9995{10011}. **ma:** Associated with *Xwmd848-1D*{10011}.

Stb11{10012}. Confers resistance to isolate IPO90012 {10012}. 1BS{10012}. **v:** JIC W 9996; TE9111. **v2:** TE9111 *Stb6 Stb7*{10012}. **ma:** Distal to *Xbarc008-1B*{10012}.

Stb12{10011}. Confers resistance to cultures ISR398, ISR8036 and IPO87019 {10011}. 4AL{10011}. **v2:** Kavkaz-K4500 *Stb6 Stb7 Stb10*{10011}. **ma:** *Stb12* was closer to *Xwmc219-4A* than to *Xwmc313-4A*{10011}.

Stb13{10347}. Confers resistance to Canadian cultures MG96-13 and MG2 {10347} 7BL{10347}. **v:** DH line 90S05B*01{10347}; DH line 98S08C*03{10347}. **v2:** Salamouni *Stb14*{10347}. **ma:** *Xwmc396-7B* - 9 cM - *Stb13*{10347}; *Xwmc396-7B* - 7 cM - *Stb13*{10347}.

Stb14{10348}. Confers resistance to Canadian isolate MG2 but not to MG96-13 {10347} 3BS{10348}. **v:** DH line 98S08A*09{10348}. **v2:** Salamouni *Stb13*{10347}. **ma:** *Xwmc500-3B* - 2 cM - *Stb14* - 5 cM - *Xwmc623-3B*{10348}.

Stb15{10341}. Confers resistance to Ethiopian culture IPO88004 {10341} 6AS{10341}. **v:** Riband{10341}. **v2:** Arina *Stb6*{10341}. **ma:** *Stb15* - 14 cM - *Xpsr904-6A*{10341}.

Stb16{10879}. Seedling and adult plant resistance [*Stb16q*{10879}]. 3DL{10879}. **v2:** Synthetic W-7976 *Stb17*{10879}. **ma:** Associated with *Xgwm494-3D* and mapped as a QTL, R^2=0.4-0.7 in seedling tests and 0.28-0.31 in mature plants{10879}.

Stb17{10879}. Adult plant resistance 5AL{10879}. **v2:** Synthetic W-7976 *Stb16*{10879}. **ma:** Associated with *Xhbg247-5A* and mapped as a QTL, R^2=0.12-0.32{10879}.

Stb18{10827}. Confers resistance to IPO0323, IPO98022, IPO98046 {10827} 6DS{10827}. **v2:** Balance *Stb6 Stb11*{10827}. **ma:** Mapped as a QTL located in a 8.8 cM region spanned by *Xgpw3087-6D* and *Xgpw5176-6D*{10827}.

QTL: Four QTLs for resistance to *Mycosphaerella graminicola* were identified in replicated field experiments in a double haploid population from Savannah (susceptible)/Senat(resistant). Senat contributed all the alleles providing resistance {10067}

QStb.riso-2B was mapped on chromosome arm 2BL linked to SSR marker *Xwmc175-2B* (LOD>5, R^2>17%) {10067}.

QStb.riso-3A.2 was mapped on chromosome arm 3AS linked to SSR markers *Xwmc489-3A, Xwmc388-3A* and *Xwmc505-3A* (LOD>4, R^2>18%). Also detected at the seedling stage {10067}. *Xgwm369-3A* is present on chromosome arm 3AS {0187}. A resistance gene from Senat located at or near the *Stb6* locus was mapped 5 cM from microsatellite *Xgwm369-3A* on chromosome arm 3AS {10067}.

QStb.riso-6B was mapped on the centromeric region between SSR markers *Xwmc494-6B* and *Xwmc341-6B* (LOD>16, R^2>68%). Also detected at the seedling stage {10067}.

QStb.riso-7B was mapped on chromosome 7B close to SSR marker *Xwmc517-7B* (LOD>4, R^2>11%) {10067}.

ITMI Population: Three QTL, ***QStb.ipk-1DS, QStb.ipk-2DS*** and ***QStb.ipk-6DS*** conferred seedling-stage resistance to 2 isolates, whereas 2 QTL ***QStb.ipk-3DL*** and ***QStb.ipk-7BL*** conferred separate adult-stage resistances to each isolate {10151}.

A weak QTL, ***QStb.psr-7D.1***, giving partial resistance to Portuguese isolate IPO92006, was detected in the *Xcdo475b-7B - Xswm5-7B* region in chromosome 7DS {10341}.

Apache/Balance: Analyses with a panel of *M. graminicola* cultures identified QTLs on chromosomes 1BS (Apache, considered to be *Stb11*), 3AS (Balance, considered to be *Stb6*), 6DS (Balance, named as *Stb18*), 7DS (Apache, considered to be *Stb4*) and 7DL (Apache) {10827}.

Florett/Biscay(S): RIL population: two QTLs for APR were located on chromosomes 3B and 6D {10901}.

Tuareg/Biscay(S): RIL population: two QTLs for APR were located on chromosomes 4B and 6B {10901}.

97. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano)

Disease: Septoria nodorum blotch, Stagonospra nodorum blotch.

97.1. Genes for resistance

Snb1{856}. 3AL{856}. **v:** Red Chief{856}. **v2:** EE8 *Snb2*{856}.

Snb2{856}. 2AL{856}. **v2:** EE8 *Snb1*{856}.

Snb3{1594}. 5DL{1594}. **s:** CS*/Synthetic 5D{1594}. **v:** Synthetic{1594}. **dv:** *Ae. tauschii*{1594}.

SnbTM{856,857}. 3A{857}.3AL{856}. **v:** Cooker{10210}; Hadden{10210}; Missouri{10210}; Red Chief{10210}; 811WWMN 2095{10210}; 86ISMN 2137{10210}. **tv:** *T. timopheevii* /2*Wakooma{856}; *T. timopheevii* PI 290518. *T. timopheevii* derivatives: S3-6{857}; S9-10{857}; S12-1{857}. **ma:** $UBC521_{650}$ - 15 cM - *SnbTM* - 13.1 cM - $RC37_{510}${0212}.

$UBC521_{650}$ was converted to a SCAR marker{0212}.

Allelism of the hexaploid wheat gene and the *T. timopheevii SnbTM* was suspected but not confirmed.

QTL

A QTL analysis of SNB response in the ITMI population found significant effects associated with chromosome 1B (probably *Snn1*) and 4BL, with an interactive effect involving the 1BS region and a marker on chromosome 2B {10009}. An additional QTL on 7BL was effective at a later stage of disease development {10009}.

Four QTLs, on chromosomes 2B (proximal part of long arm), 3B (distal part of short arm), 5B and 5D, were mapped in a Liwilla / Begra doubled haploid population. Longer incubation period and lower disease intensity were contributed by Liwilla {10045}.

Two QTLs for glume blotch resistance under natural infection were identified on chromosomes 3BS and 4BL in Arina / Forno RILs {10065}. The 3BL QTL, designated *QSng.sfr-3BS*, was associated with marker *Xgwm389-3B* and explained 31.2% of the variation. The resistance was contributed by Arina {10065}. The 4BL QTL, *QSng.sfr-4BL*, was associated with *Xgwm251-4B* and explained 19.1% of the variation. Resistance was contributed by Forno {10065}. A QTL on 5BL, *QSng.sfr-5BL*, overlapped with QTLs for plant height and heading time {10065}. *QSng.sfr-3BS* peaked 0.6 cm proximal to *Xsun2-3B* {10465}. Association mapping involving 44 modern European cultivars indicated that the association was retained in a significant proportion of genotypes {10465}.

A QTL, *QSnl.ihar-6AL*, identified in DH lines of Alba (R) / Begra (S) accounted for 36% of the phenotypic variance in disease severity and 14% of the variance in incubation period {10143}.

Br34 / Grandin: Three QTLs with resistance effects from BR34; *Qsnb.fcu-5BL.1* (*Tsn1*), R^2 = 0.63, *Qsnb.fcu5BL.2,* R^2 = 0.06, and *Qsnb.fcu-1BS* (vicinity of *Snn1*), R^2 = 0.10 {10458}. QTL analysis of the RIL population with Culture Sn6 revealed four QTLs, *Qsnb.fcu-2DS* (R^2 = 0.3 - 0.49) associated with *Snn2*, *Qsnb.fcu-5BL* (R^2 = 0.14 - 0.2) associated with *Tsn1*, *Qsnb.fcu-5AL* (R^2 = 0 - 0.13) associated with *Xfcp13-5A*, and *Qsnb.fcu-1BS* (R^2 = 0 - 0.11) associated with *Xgdm125-1BS* {10507}.

Forno (S) / Oberkulmer spelt (R). Among 204 RILs leaf and glume response were genetically different but correlated (R^2=0.52). Ten QTLs for glume blotch (SNG) resistance were detected, 6 from Forno. A major QTL (R^2=35.8%) was associated with q. Eleven QTLs (4 from Forno) affected leaf blotch; 3 of these (chromosome 3D, 4B and 7B) with R^2>13% were considered potential candidates for MAS {10250}.

ITMI population: A major QTL, coinciding with *Snn1*, was located in chromosome 1BS (R^2 = 0.58, 5 days after inoculation), minor QTL were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL and 7BL {10009}.

P91193D1 (partially resistant) / P92201D5 (partially resistant) RIL populations were tested in Indiana and Western Australia for glume resistance. Two QTL were identified: *Qng.pur-2DL.1* from P91193D1 (R^2 = 12.3 in Indiana and 38.1% in WA, respectively; *Xgwm526.1-2D* - *Xcfd50.2-2D*) and *QSng.pur-2DL.2* from P99201D5 (R^2 = 6.9% and 11.2%, respectively; *Xcfd50.3-2D* - *wPT9848*) {10471}.

HRWSN125(R)/WAWHT2074(S): Constant detection of *QSnl.daw-2DL* for flag leaf resistance, and *QSng.daw-4BL* for glume resistance over two years {10584}.

Tetraploid wheat

Langdon/Langdon (*T. turgidum* ssp. *dicoccoides* Israel-A 5B): *QSnb.ndsu-5B* located 8.3 cM proximal to *tsn1* for tan spot resistance; R^2 = 0.38 {10597}.

A summary of QTL analyses is provided in {10726}.

Salamouni/Katepwa: RIL population: Two QTLs. *QSnb.fcu-1A* (*Snn4*) (R^2=0.24) and *QSnb.fcu-7A* (R^2=0.16) were associated with SNB response to isolate Sn99CH 1A7a {10867}.

97.2. Sensitivity to SNB toxin

A discussion on the origin and role of host-specific toxins is provided in {10726}.

Australian cultivars with *Tsn1* and *tsn1* are listed in {10540}.

Tetraploid wheat

In a reevaluation of this work Faris and Friesen {10688} attributed all of the variation in SNB response to the presence or absence of SnTox1.

ma: *Xbcd183-5B* - 1.2 cM - *Tsn1/Xbcd1030-5B* - 2.4 cM - *Xrz575-5B* {10688}.

Tsn1{10458, 346,10207}. Sensitive to SnToxA, which is functionally identical to Ptr ToxA {10459}. **v:** Cheyenne{0007}; Forno{10725}; Hope{0007}; Jagger{0007}; Kulm{346,10030,10458}; ND495{0007}; Timstein{0007}; Trenton{0315}. **dv:** Two *Ae. speltoides* accessions{10756}. **tv:** Langdon{10458}; Some *T. dicoccoides* accessions{10756}. **c:** *Tsn1* has 8 exons and a S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA{10756}.
See reaction to *Pyrenophora tritici repentis* {10458}.

tsn1{346,10207}. Insensitivity (disease resistance) is recessive {346}. 5BL{346}. **v:** AC Barrie{10153}; AC Cadillac{10153}; AC Elsa{10153}; BR34{0007}; CEP17{0007}; Chinese Spring{0007}; Erik{0007,10030}; Hadden{10155}; Laura{10153}; Line 6B-365{10155}; Red Chief{10155}; 1A807{0007}; 1A905{0007}; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. squarrosa* C122. **v2:** Grandin *Snn2 Snn3*{10507}. **tv:** Altar 84{0007}; D87450{0007}; *T. dicoccoides* Israel A{10506}. **ma:** *Xbcd1030-5B* - 5.7 cM - *tsn1* - 16.5 cM - *Xwg583-5B*{346}; *tsn1* - 3.7 cM - *Xbcd1030-5B*{0007}; *Xfgcg7-5B* - 0.4 cM - *Tsn1/Xfcg17-5B* - 0.2 cM - *Xfcg9-5B*{10207}; *Xfcg17-5B* - 0.2 cM - *Tsn1* - 0.6 cM - *Xfcg9-5B*{10207}; *Xfcp1-5B* and *Xfcp2-5B* delineated *Tsn1* to an interval of about 1 cM

{10337}. *Tsn1* was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1/XBE425878/Xfcc1/XBE443610*{10413}; This interval was reduced to 0.07 cM between *Xfcp620-5B* and *Xfcp394-5B*{10724}.

Genotype list in {10724}.

snn1tsn1. Atlas 66 {10458}; BR34 {10458}; Erik {10458}; Opata 85 {10458}; ND688 {10458}.

Snn1{10008}. Sensitivity to SnTox1 is dominant {10008} 1BS{10008}. **bin:** 1BS.sat.18. **s:** CS-DIC 1B{10008}. **v:** CS{10008}; Grandin{10008}; Kulm{10008}; ND495{10008}. **ma:** *Snn1* - 4.7 cM - *XksuD14-1B*{10008}; *XksuD14.2-1BS* - 0.4 cM - *Snn1/XBE498831/XBF474204* - 0.4 cM *Xpsp3000-1BS/XBE422980/XBE637568/ZBE605202*{10727}; *XksuD14.2* - 0.34 cM - *Snn1/XBE498831/XBF474204* - 0.12 cM - *XBF29322* - 0.04 cM - *Xpsp3000-1BS/XBE422980/XBE637568/XBF605202*{10727}.

snn1. **i:** CS*/*T. dicoccoides* 1B{10008}. **v:** Br34{10008}; Erik{10008}; Opata 85{10008}.

Snn2{10507}. Sensitivity to SnTox2 is dominant {10507}. 2DS{10507}. **v:** BG223{10507}. **v2:** Grandin *Tsn1 Snn3*{10507}. **ma:** *Xgwm614-2D* - 7.6 cM - *Snn2* - 5.9 cM - *Xbarc95-2D*{10507}; *XTC253803* - 3.6 cM - *Snn2* - 0.4 cM - *Xcfd-2D*{10724}.

snn2. **v:** Atlas 66{10724}; Br34{10507}; Cheyenne{10724}; Chinese Spring{10724}; Jagger{10724}; Opata 85{10724}; Salamouni{10724}; TAM 105{10724}.

Snn3{10728,10507}. Sensitivity to SnTox3 is dominant {10728} 5BS{10728,10507}. **bin:** 5BS-6{10507}. **v2:** Grandin *Tsn1 Snn2*{10728,10507}. **ma:** *Snn3* - 1.4 cM - *Xcfd20-5BS*{10507}.

snn3. **v:** BR34{10507}.

Snn4{10725}. Sensitivity to SnTox4 is dominant {10725} 1AS{10725}. **bin:** 1AS3-0.86-1.00{10725}. **v:** Arina{10725}; Katepwa{10867}; Salamouni{10867}. **ma:** *XBG262267/XBG262975* - 0.9 cM - *Snn4* - 1.6 cM - *Xcfd58.1-1AS*{10725}.

snn4. **v:** Forno{10725}.

QTL: ITMI population: A major QTL, coinciding with *Snn1*, was located in chromosome 1BS (R^2=0.58, 5 days after inoculation), minor QTLs were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL and 7BL {10009}.

P91193D1 / P92201D5 RIL population: tested in USA and Australia: *QSng.pur-2DL.1* from P91103D1, R^2=0.123 (Indiana) and 0.381 (South Perth); and *QSng.pur-2DL.2* from P92201D5, R^2=0.069 (Indiana) and 0.112 (South Perth) {10776}.

98. Reaction to *Pratylenchus* spp.

Root lesion nematode; prats

98.1. Reaction to *Pratylenchus neglectus*

Rlnn1{0121}. 7AL{0121}. **v:** Excalibur{0121}; Krickauff{0121}. **ma:** Mapped between markers *Xpsr121-7A* and *Xgwm344-7A* and 9 cM proximal to *Lr20*{0374}.

98.2. Reaction to *Pratylenchus thornei*

QTLs were located on chromosomes 2BS and 6DS {0122}.

99. Reaction to *Puccinia graminis* Pers.

Disease: Black rust; black stem rust; stem rust.

Note: Some near-isogenic lines are based on Marquis. The genes present in the Marquis background are not listed for those NILs.

Sr1. Deleted - see *Sr9d*.

Sr2{38,677}. Recessive allele. Adult plant response. 3BS{499}. **s:** CS*6/Hope 3B{499}. **v2:** HD2009 *Sr30*{10632}; Warigo *Sr7b Sr17*{499}; Suneca *Sr8a Sr17*{485}; Hopps *Sr9d*{499}; Lancer *Sr9d Sr17*{679}; Scout *Sr9d Sr17*{679}; See also{499,1040}. **ma:** *Xgwm389-3B* - 2.7 cM - *Sr2* - 1.1 cM - *Xglk683-3B*{0358}; .....*Xglk683*(STS *Xsun2-3B*) - 0.5 cM - *Xgwm533-3B*{0358}; These SSR loci were located within FL 0.87 - 0.75{0358}; All 27 lines with *Sr2* carried a 120 bp allele at *Xgwm533-3B*; A 120 bp allele in 4 cultivars lacking *Sr2* differed from the *Sr2* associated allele at 4 base positions{0358}; STMs for the *Xgwm533-3B* locus had increased specificity as markers for *Sr2*{10142}; Tightly linked CAPS marker csSr2 based on a SNP proved superior to *Xgwm533-3B* as a marker for *Sr2*{10786}.

Sr2 is associated with pseudo-black chaff{742,1102} and seedling chlorosis (see {149}) and occurs very frequently in commercial wheats, especially in germplasm produced and distributed by CIMMYT. *Sr2* has probably remained effective since the 1920s.

Sr3 & Sr4{047}. **v:** Marquillo - based on early data. No stocks available.

Sr5{047}. 6D{939,1308,1626}.6DS{939}. **i:** I *Sr5*-Ra{828}; I *Sr5*-Rb{828}; Sr5/7*LMPG{685}; Thatcher/10*Marquis{686}. **s:** CS*6/Thatcher 6D{1308}. **v:** Admonter Fruh{072}; Dacia{979}; Dong-Fang-Hong 2{564}; Dong-Fang-Hong 6{564}; Feng-Kong{563}; Hochzucht{046}; Hybrid 80-3{072}; Jubilejna{068}; Juna{076}; Kanred{1308}; Ke-Fang 1{564}; Stabil{072}; Viginta{071}; Vrakunski{072}. **v2:** Amika *Sr31*{076}; An-Hewi II *Sr8a*{564}; Beijing 10 *SrTmp*{564}; Dong-Xie 3 *Sr31*{563}; Dong-Xie 4 *Sr31*{563}; Erythrospermum 974 *Sr8a*{072}; Glenlea *Sr6 Sr9b*{327}; Istra *Sr31*{076}; Jing-Hong *Sr17*{564}; Jing-Hong 2 *Sr17*{564}; N.P.789 *Sr11*{1555}; Qing-Chung 5 *Sr6 Sr11*{564}; Solaris *Sr31*{076}; Victor *Sr6 Sr8a*{979}.

Sr6{687}. [*SrKa1*{1167}]. 2D{1293,1308,1577}.2DS{942}. **bin:** 2DS5 - 0.47 - 1.00{10714}. **i:** I *Sr6*-Ra{828}; Kenya 58/10*Marquis{468,675}; Sr6/9*LMPG{685}. **s:** CS*5/Red Egyptian 2D{1308}. **v:** Africa 43{669}; Eureka{468,844}; Kenya stocks{669,670,673,687,689,1167,1557}; McMurachy{679}; Shield{198}. **v2:** Bowie *Sr8a*{1553}; Eurga *Sr11*{1553}; Fortuna *Sr7a*{679}; Gamut *Sr9b Sr11*{1555}; Glenlea (heterogeneous) *Sr5 Sr9b*{327}; Kentana 52 *Sr7a*{678,1577}; Kiric 66 *Sr7b*{979}; Lerma Rojo 64 *Sr7b Sr9a*{979}; No. 466 *Sr9b Sr10*{689}; Red Egyptian *Sr8a Sr9a*{687,1308}; Siete Cerros *Sr11*{033}; Victor I *Sr5 Sr8a*{979}. **ma:** *Sr6* - 1.1 cM - *Xwmc453-2D* - 0.4 cM - *Xcfd43-2D*{10714}; *Xgwm102-2D* - 0.9 cM - *Xgpw94049-2D* - 5.6 cM - *Sr6* - 1.5 cM - *Xwmc453/Xcfd43-2D*{10870}.

See also {1553}.

Sr7{830}. 4A{671,830,1293}.4AL{939,1308}.

Sr7a{830}. [*Sr7*{687}]. **i:** Egypt Na101/6*Marquis{468}; Kenya 117A/6*Marquis{468}; Sr7a/9*LMPG{685}. **s:** CS*7/Kenya Farmer 4B{830}; CS*8/Sapporo 4B{830}. **v:** Egypt Na101{669}; Kenya stocks{669,670,673,687,689}; Sapporo Haru Komugi Ichigo{689}. **v2:** Egypt Na95 *Sr9b Sr10*{687}; Fortuna *Sr6*{679}; French Peace *Sr9a Sr13*{680}; Kentana 52 *Sr6*{689}; Khapstein *Sr13 Sr14*{674}; W3746 *Sr12*{1371}.

Sr7b{830}. **i:** I *Sr7b*-Ra{828}. **v2:** Warigo *Sr2 Sr17*{499}; Kiric 66 *Sr6*{979}; Roussalka *Sr8a*{979}; Red Bobs *Sr10*{308}; Nell *Sr17*{1565}; Spica *Sr17*{939}; Marquis *Sr18 Sr19 Sr20*{675,830}.

Sr8. 6A{1293,1308}.6AS{929,1368}.

Sr8a{1368}. [*Sr8*{687}]. **i:** I *Sr8a*-Ra{828}; Red Egyptian/10*Marquis{686}; Sr8a/9*LMPG{685}. **s:** CS*5/Red Egyptian 6A{1308}. **v:** Marimp 3{979}; Mentana{844}; Strampelli{979}. **v2:** An-Hewi II *Sr5*{564}; E-Gan-Zao *Sr17*{564}; Erythrospermum 974 *Sr5*{072}; Frontana *Sr9b*{689}; Golden Valley *Sr17*{979}; Hartog

Sr2 Sr12{127}; Magnif G *Sr9b*{689}; Pitic 62 *Sr9b*{033}; Red Egyptian *Sr6 Sr9a*{687}; Rio Negro *Sr9b*{689}; Roussalka *Sr7b*{979}; Suneca *Sr2 Sr17*{485}; Victor 1 *Sr5 Sr6*{979}.

Sr8b{1368}. [*SrBB*]. **v:** Barleta Benvenuto{1368}; Klein Titan{1368}. **v2:** Bezostaya *Sr5*{979}; Klein Cometa *Sr30*{1368}. **tv:** According to Luig {841} one of the genes in Leeds is *Sr8b*. **tv2:** Arrivato *Sr9e Sr13*{10607}. **ma:** *Sr8b* - 4.6 cM - *Xgwm334-6A*{10607}.

This could be the gene located on chromosome 6A in ST464-A1 {10473} and one of the genes present in ST464, a parent of Leeds.

Sr9{676}. 2B{671,677,828,1308}.2BL{944,946,951,1307,1582}.

Sr9a{676}. [*Sr9*{687}]. **i:** I *Sr9a*-Ra{828}; Red Egyptian/10*Marquis{686}; Sr9a/9*LMPG{685}. **s:** CS*4/Red Egyptian 2B{1308}. **v2:** Red Egyptian *Sr6 Sr8a*{687}; French Peace *Sr7a Sr13*{680}; Excel *Sr8a Sr17*{752}. **ma:** *Xbarc101-2B/Xgwm12-2B* - 2.7 cM - *Xgwm47-2B* - 0.9 cM - *Sr9a/Xwmc175-2B*{10472}.

Sr9b{468}. [*Sr9*{687},*SrKb1*{468}]. **i:** Kenya 117A/10*Marquis{686}; *Sr9b*/10*LMPG{685}. **s:** CS*7/Kenya Farmer 2B{939}. **v:** Gamenya{844}; Kenya stocks{669,670,673,687,689,1557}. **v2:** Egypt Na95 *Sr7a Sr10*{636}; Festival *Sr15*{1553}; Frontana *Sr8a*{689}; Gamut *Sr6 Sr11*{1555}; Glenlea *Sr5 Sr6* heterogeneous{327}; Kenora *Sr15*{1553}; Magnif G *Sr8a*{689}; No. 466 *Sr6 Sr10*{689}; Pitic 62 *Sr8a*{033}; Rio Negro *Sr8a*{689}; Robin *Sr11*{879}; Veadeira *Sr10*{687}.

See also {1553}.

Sr9c. Originally reserved for *Sr36*.

Sr9d{678,831}. [*Sr1*{047,676,677}]. **i:** Hope/10*Marquis{677}; H-44/10*Marquis{677}; I Hope 2B-Ra{828}; Sr9d/8*LMPG{685}. **v:** Hopps *Sr2*{1040}. **v2:** Lancer *Sr2 Sr17*{679}; Scout *Sr2 Sr17*{679}. **tv:** Arnautka{939}; Mindum{939}; Spelmar{939}.

Sr9e{951}. [*Srd1v*{642},*Srv*{1391}]. **v:** SST 16{1324}; SST 33{785}; SST 66{785}; SST 3R{1324}; Vernstein{845}. **v2:** Combination III *Sr36*{841}; Sunstar *Sr8a Sr12*{939}. **tv:** ST464-A2{10473}; Vernal emmer{1391}; CI 7778{845}; *Sr9e* occurs in many tetraploid wheats{939,1378}. **tv2:** Arrivato *Sr8b Sr13*{10607}; ST464 *Sr13*{10473}. **ma:** *Xgwm191-2B* - 5.5 cM - *Sr9e* - 0.7 cM - *Xgwm47-2B*{10607}.

Sr9f{826}. **v:** Chinese Spring{826}; Not present in the near-isogenic I *Sr9a*-Ra{826}.

Sr9g{965}. **s:** CS*7/Marquis 2B *Sr16*{965}; CS*4/Thatcher 2B *Sr16*{965}. **v2:** Celebration *Sr12 Sr16*{965}; Eagle *Sr26*{842}; Hochzucht *Sr5 Sr12*{965}; Lee *Sr11 Sr16*{965}. **tv:** Acme{965}; Iumillo{965}; Kubanka{965}.

See also {504}.

Sr10{687}. 2B{686,939}. **i:** Egypt Na95/4*Marquis{468}. **v:** Federation{939}; Geneva{1412}; Hazen{049}; Kenya stocks{669,670,673,687}. **v2:** Egypt Na95*Sr7a Sr9b*{687}; No. 466 *Sr6 Sr9b*{689}; Red Bobs *Sr7b*{308}.

Sr11{468}. [*Sr11*{687},*Sr12*{687}]. 6B{671,1143,1293,1309}.6BL{1297}. **i:** I *Sr11*-Ra{828}; Lee/10*Marquis{686}. **s:** CS*7/Kenya Farmer 6B{830}; CS*9/Timstein 6B{1308}. **v:** Charter{844}; Flevina{072}; Gabo{687}; Kenya stocks{670,673,844,1557}; Sonora 64{033}; Sylvia{071}; Timstein{687,1308}; Tobari 66{033}; Yalta{844}. **v2:** Eurga *Sr6*{1553}; Gamut *Sr6 Sr9b*{1555}; Lee *Sr9g Sr16*{687}; N.P.790 *Sr5*{1555}; Qing-Chung 5 *Sr5 Sr6*{564}; Robin *Sr9b*{879}; Prospect *SrWld*{197}; See also{1553}.

A resistance gene allelic with *Sr11* was found in Chinese Spring {938}, but the *P. graminis* culture for its detection was lost.

Sr12{1332}. Recessive. 3B{1332,682}.3BS{968}. **s:** CS*7/Marquis Selection 3B *Sr16*{1332}; CS*5/Thatcher 3B *Sr16*{1332}. **v:** Marquillo{682}; Tincurrin{939}; Windebri{939}. **v2:** W3746 *Sr7a*{1371}. **tv:** Postulated for several durums{1378}.

Sr12 is more widespread and probably more effective in conferring resistance than is usually acknowledged {939}.

Sr13{674}. 6AL{929}. **bin:** 6AL-8. **i:** Khapstein/10*Marquis{686}; Sr13/9*LMPG{685}. **v2:** French Peace *Sr7a Sr9a*{680}; Khapstein *Sr7a Sr14*{674}; Machete *Sr*{10607}. **tv:** Kronos{10777}; Medora{10777}; Sceptre{10777}; ST464-C1{10473}. **tv2:** Arrivato *Sr8b Sr9e*{10607}; Khapli *Sr14*{674}; ST464 *Sr9e*{10473}. **ma:** *Xwmc59-6A* - 5.7 cM - *Sr13*{10607}; CD926040 - *Sr13* - *BE471213*{10777}.

A gene in Khapstein/9*LMPG and believed to be *Sr13* was mapped in chromosome 6AL by Admassu et al. {10778}. However the map location was more than 50 cM proximal to that reported in {10777}. It was resolved in {10779} that the resistance gene mapped in {10778} could not be *Sr13*.

Sr14{674}. 1BL{933}. **i:** Khapstein/10*Marquis{686}. **v:** Line A{933}. **v2:** Khapstein *Sr7a Sr13*{674}. **tv2:** Khapli *Sr13*{674}.

Sr15{1554}. 7A{1293,1554}.7AL{1305}. **v:** Present in stocks possessing *Pm1 and Lr20*{931,1554}; See Reaction to *Blumeria graminis* and Reaction to *P. triticina*. **ma:** Associated with clustered markers{0323}.

Sr16{830}. [*Srrl2*{1238}]. 2B{830,1308}.2BL{1307}. **i:** I *Sr16*-Ra{828}; I Th3B-Ra{832}. **s:** CS*7/Marquis 2B *Sr9g*{1581}; CS*4/Thatcher 2B *Sr9g*{1308}; CS*5/Thatcher 3B *Sr12*{832}. **v2:** Thatcher *Sr5 Sr9g Sr12*{939}; Lee *Sr9g Sr11*{939}.

Sr16 is allelic with a gene in Kota (*SrKt2*{932}) {939}.

Sr17. Recessive. [*sr17*{964}]. 7B{771}.7BL{964,10565}. **s:** CS*6/Hope 7B{964}. **v:** Forno{10511,10565}. **v2:** E-Gan Zeo *Sr8a*{564}; Golden Valley *Sr8a*{979}; Jing-Hong 1 *Sr5*{564}; Jing-Hong 2 *Sr5*{564}; Lancer *Sr2 Sr9d*{679}; Nell *Sr7b*{1565}; Scout *Sr2 Sr9d*{679}; Suneca *Sr2 Sr8a*{485}; Present in many stocks possessing *Pm5*{964}; See Reaction to *Blumeria graminis*. **ma:** *Xwmc273-7B* - 15.3 cM - *Sr17*{10565}.

Sr18{054}. [*SrG2*{844},*Srrl1*{1238},*Srmq1*{099},*SrPs1*{1263},*SrMn1*{1263}]. 1D{054,1308,1582}. **i:** I Hope 1D-Ra{828}; Sr18/8*LMPG{685}. **s:** CS*6/Hope 1D{1308}. **v:** Present in the majority of wheat stocks{828}; Stocks not possessing *Sr18*: Brevit{054}; Chinese Spring{828}; Eureka{054}; Federation{054}; Gular{054}; Kenya C6042{054}; Koala{054}; Little Club{828}; Morocco{054}; Norka{054}; Prelude{828}; Yalta{054}.

Sr19{029}. [*Srmq2*{099}]. 2B{029}.2BS{1582}. **v:** Mq-B{029}. **v2:** Marquis *Sr7b Sr18 Sr20*{029}.

Sr20{029}. [*Srmq3*{1238},*Srrl3*{1238}]. 2B{029}. **v:** Mq-C{029}; Rl-C{029}. **v2:** Reliance *Sr5 Sr16 Sr18*{029}; Marquis *Sr7b Sr18 Sr19*{029}.

Sr21{1460}. 2AL{1460,1464}. **i:** Sr21/8*LMPG{685}. **v:** Hexaploid derivatives of *T. monococcum*{939}. **tv:** Tetraploid derivatives of *T. monococcum*{939}. **dv:** Einkorn{1460}; Dv92 *Sr35*{10876}; G2919 *Sr35*{10876}; Various *monococcum* accessions. See also *Sr45* which has similar specificity to *Sr21*.

Sr22{1460}. 7A{649}.7AL{1460}. **bin:** 7AL-0.74-0.86; 7AL-13 0.83-0.89{10869}. **i:** Marquis*4//Stewart*3/*T. monococcum*{649,1460}; Sr22/9*LMPG{685}; Others{1112}. **v:** CS/3/Steinwedel*2//Spelmar/*T. boeoticum*{1460}; Schomburgk{880}; Steinwedel*2//Spelmar/*T. boeoticum*{1460}; Others{1112}; Recombinant line reported in{10772,10773}. **tv:** Spelmar/*T. boeoticum*{1460}; Stewart*6/*T. monococcum* RL 5244{649}. **dv:** Various *T. monococcum* accessions{649,1460}. **ma:** Hexaploid derivatives with *Sr22* carried 'alien' segments of varying lengths; the shortest segment was distal to *Xpsr129-7A*{1112}; See also{0158}; *Xcfa2123-7A* - 6 cM - *Sr22* - 5.9 cM - *Xcfa2019-7A*{10263}; Multiplex marker cssu22 based on STS markers derived from cloned fragment csIH81 was developed in {10772}; This marker gave positive results for *Sr22* in all recombinant lines including those reported in{10773}; Recombined lines with shortened introgressions from diploid wheat are reported in{10869}; the shortest was U5616020-154{10869}.

Sr23{950}. The following chromosome locations are consistant with the finding that the first location was based on Rescue monosomics. Rescue differs from CS by a 2B-4B reciprocal translocation {939}. 4B{950}.2BS{939}. **v:** Exchange{950}; Warden{950}; *Sr23* is always associated with *Lr16*{950}. **v2:** Etoile de Choisy *Sr29*{950}.

Sr24{956}. Derived from *Thin. elongatum.*

3DL = T3DS.3DL-3Ae#1L{956,389}. **i:** Sr24/9*LMPG{685}; Sears' 3D/*Ag* translocations{956,1300}. **v:** Agent{956}; Blueboy II{956}; Collin{901}; Cloud{956}; Cody{1284}; Ernest{10845}; Fox{956}; Gamka{785}; Karee{785}; Keene{10845}; Kinko{785}; Palmiet{785}; Sage{825,1024}; SST 23{1324}; SST 25{785}; SST 44 = T4R{1324,785}; SST 102{785}; Torres{128}; Wilga{785}. **v2:** Siouxland *Sr31*{1283}; List of Australian genotypes{0340}.

1BL {185} = T1BL = 1BS-3Ae#1L{600,389}. **tr:** Amigo{1463,600,389}; Teewon{600,389}; Note:Amigo and some derivatives also carry a 1AL.1RS translocation with resistance from rye{1463}.

1BL. **tr:** Millenium{10845}.

3Ae#1. **su:** Chinese Spring 3Ag {3D}{1304}; TAP48{389}. **ma:** *Xbarc71-3Ag* was considered a better marker for *Sr24* than STS Sr24#12{10845}.

Sr24 is completely linked in coupling with *Lr24* {956} and often with red grain colour. See Reaction to *P. triticina*.

Sr25{956}. Derived from *Thin. elongatum*. 7DL = T7DS.7DL-7Ae#1L{291,956,388,657}. **i:** Sears' CS 7D/7Ag translocations{956,1300}; Sr25/9*LMPG{685}. **v:** Agatha *Sr5 Sr9g Sr12 Sr16* {956} = T4{1323}; Mutant 28{388}.

7AL = T7A-7Ae#1L{330}. **v:** Sears' 7A/7Ae#1L No. 12{330,1304}; Sears' 7D/7Ag#11 carries neither *Sr25* nor *Lr19*{939}.

7Ae#1L. **su:** Chinese Spring + 7Ae#1L(7D){1304}.

See *Lr19*, reaction to *Puccinia triticina*.

Sr25/Lr19 often show complete linkage in wheat {956}.

Knott {681} obtained two mutants (28 and 235) of Agatha with reduced levels of yellow pigment in the flour. One of these mutants lacked *Sr25*. Marais {890} reported that a gene very similar to *Sr25* was present in the putative Inia 66 x *Thin. distichum* derivative, Indis. Marais {890,892} also obtained mutants with reduced yellow pigment in Indis derivatives and some of these lacked *Sr25*.

Sr26{956}. Derived from *Thin. elongatum*. 6AL{364} = T6AS.6AL-6Ae#1L{388,389}. **i:** Sr26/9*LMPG{685}. **v:** Avocet{364}; Flinders{1449}; Harrier{939}; Jabiru{956}; King{1451}; Kite{956}; Knott's 6A-6Ae#1L translocation to Thatcher{672}; Takari{253}. **v2:** Bass *Sr36*{1450}; Eagle *Sr9g*{956}. **ma:** Detected with several RFLP probes{0138}; A PCR marker, Sr26#43 was reported in{10257}.

Sr27. Derived from *S. cereale*. 3A (T3A-3R) = T3AS.3R#1S{003,896,389,10162}. **i:** Sr27/9*LMPG{685,10162}. **v:** WRT wheat-rye translocation, available in CS, Thatcher and Pembina backgrounds. Translocated from Imperial rye to Chinese Spring by Acosta{003,10162}; Widespread in triticales{966,1384,10162}.

3A = T3AL.3RS{896}. **v:** W964 = 3RS.3AL.1/4* Inia 66{896}; W968 = 3RS.3AL.1/5* Condor{896}; W970 = 3RS.3AL.88/5*SST3{896}.

3B = T3BL.3R#1S{896}. **v:** W966 = 3RS.3BL.26/4*Inia 66{896}.

Sr28{932}. 2BL{932}. **i:** Line AD{932}. **v2:** Kota *Sr7b Sr18*{932}.

Sr29{313}. [*SrEC*{955}]. 6DL{313}.6DS{1626}. **i:** Prelude/8*Marquis//Etoile de Choisy{313}. **v:** Hana{071}; Hela{076}; Mara{068}; Slavia{076}; Vala{076}. **v2:** Etoile de Choisy *Sr23*{955}.

Sr30{688}. [*SrW*]. 5DL{688}. **i:** Sr30/7*LMPG - Lines 1, 2, and 3{685}. **v:** Festiguay{688}; Mediterranean W1728{1369}; Webster{688}. **v2:** HD2009 *Sr2*{10632}; Klein Cometa *Sr8b*{1368}; Relatively common in Australian and Mexican wheats. Various unnamed accessions{208,1321}. **ma:** *Xcfd12-5D* - 9.0 cM - *Sr30* - 16.6 cM - *Xgwm292-5D*{10858}.

According to {10858} Webster RL6201 carries a second gene *SrW* that confers resistance to the race Ug99 group.

Sr31. Derived from *S. cereale* cv. Petkus. See also Reaction to *P. striiformis, Yr9*: Reaction to *P. triticina, Lr26*

1B = T1BL.1RS = T1BL.1R#1S{389} or 1R(1B). **i:** MA1 and MA2 four-breakpoint double translocation lines 1RS-1BS-1RS.1BL in Pavon{0084}. **v:** Amika {heterogeneous} *Sr5*{076}; Cougar{0267}; Feng-Kang 2{563}; Feng-Kang 8{563}; Gamtoos{785}; GR876{753}; Jing-Dan 106{563}; Jan 7770-4{563}; Lu-Mai 1{563}; Rawhide (heterogenous){0267}; Yi 78-4078{563}. **v2:** Dong Xie 3 *Sr5*{563}; Dong Xie 4 *Sr5*{563}; Istra *Sr5*{076}; Solaris *Sr5*{076}; Siouxland *Sr24*{1283}. **tv:** Cando*2/Veery = KS91WGRC14{381}. **ma:** 1BS/1RS recombinants 4.4 cM proximal to *Gli-B1/Glu-B3*{0084}; Several markers tightly linked with *Sr31* were indentified in{0377}; A SCAR marker, SCSS30.2$_{576}$ was developed{10359}; *Xscm09-1R*$_{208}${10845}.

Sr31 seems to be different from the rye-derived gene in Amigo and related materials {10270}.

Sr32. Derived from *Ae. speltoides*.

2A {939,1304} = T2AL.2S#1L-2S#1S {389}. **v:** C95.24{389}.

2B {1304 }= T2BL-2S#1S{389}. **v:** C82.1 = P80-14.1-2{389}.

2D {1304} = T2DL-2S#1L.2S#1S{389}. **v:** C82.2 = P80-139.1-4{389,1304}; C82.3 = P80-132.2-2{939,1304}; C82.4 = P80-153.1-2{939,1304}; Deben{10283}.

Sr33. [*SrSQ*{650}]. 1DL{650}.1DS{620}. **v:** RL 5405 = Tetra Canthatch/*Aegilops squarrosa* RL 5288{650}. **ma:** linked with *Gli-D1*; *Xmwg60-1D* - 5.8 cM - *Sr33* - 2.2 cM - Xwmg2083-1{0360}.

Sr34{967}. Derived from *Ae. comosa*.

2A {967} = T2AS-2M#1L.2M#1S{389}. **v:** CS 2A-2M 4/2{967}.

2D {967} = T2DS-2M#1L.2M#1S{389}. **i:** Sr34/6*LMPG{685}. **v:** Compair{967}; CS 2D-2M 3/8{967}; Various addition, substitution and translocation lines with *Yr8*{967}.

2M{967}. **su:** Chinese Spring 2M(2A){967}.

Sr35{957}. [*SrTm1*{1522}]. 3AL{957}. **bin:** 3AL8 0.85-1.00. **i:** Marquis*5/G2919{10876}. **v,tv:** Tetraploid and hexaploid derivatives of *T. monococcum*{957}. **dv:** DV92 *Sr21*{10876}; G2919 *Sr21*{10876}; *T. monococcum* C69. 69 Selection{957}; G2919{957}. **ma:** *Sr35* was mapped to a 5.1 cM interval between *XBF483299* and *XCJ656351* in diploid wheat{10712}; Mapped in diploid wheat to a 2.2-3.1 cM region between *Xbf483299* and *XCJ656351* and corresponding to a 174 bp region in *Brachypodium*{10876}.

Sr36{939}. [*SrTt1*{949}]. 2BS{939}. **i:** Sr36/8*LMPG{685}. **v:** Arthur{939}; Arthur 71{1324}; Flemink{1324}; GK Kincso{0235}; Gouritz{1324}; Idaed 59; Maris Fundin{070}; Mengavi{949}; SST 101{1324}; SST 107{785}; Timvera{949}; *T. timopheevii* derivatives{949}; Zaragoza{785}; Others{572,10609}. **v2:** Bass *Sr26*{1450}; Combination III *Sr9e*{939}; Timson *Sr5 Sr6*{939}. **tv:** *T. timopheevii*{949}. **ma:** *Xgwm429-2B* - 0.8 cM - *Sr36/Xstm773-2-2B/Xgwm31-2B/Xwmc477-2B*{10609}; *Xgwm319-2B* - 0.9 cM - *Sr36/Xstm773-2-2B/Xwmc477-2B*{10609}; *Xgwm429-2B* - 0.8 cM - *Sr36/Xstm773-2/Xgwm319/Xwmc477-2B*{10824}; *Xgwm319-2B* - 0.9 cM - *Sr36/Xstm773-2/Xwmc477-2B*{10824}; Of four markers *Xwmc477-2B* was the best, but it is not a perfect marker{10845}.

Sr37{939}. [*SrTt2*{949}]. 4BL{939}. **v,tv:** *T. timopheevii* and derivatives{484,949}; Line W{949}.

Sr38{062}. Derived from *Ae. ventricosa*. 2AS{062}.6M^{v}=2MS-6MS.6ML or 2MS-6ML.6MS{0009}. **i:** RL 6081 =Thatcher + Lr37. This line will carry additional genes from Thatcher. **v:** Moisson derivatives Mx12 and Mx22{0213}; VPM1{062}. **ma:** The 2NS translocated segment carrying *Sr38* replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682* to *XksuH9*; PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682*{10073}.

Sr38 is linked with *Lr37* and *Yr17*. See Reaction to *P. triticina Lr37* and *P. striiformis tritici Yr17*. SCAR markers SC-372 and SC-385 were developed in {10796}.

Sr39{646}. Derived from *Ae. speltoides*. 2B{651}. **v:** RL 5711{646,651}. **tv:** Amphiploid RL 5347 = *Ae. speltoides*/*T. monococcum*{651}. **ma:** *Sr39* is closely linked with *Lr35*{651}; A SCAR marker was developed{9923}.

Lines with shortened alien segments are reported in {10741}. Although *Sr39* produces similar responses to *Sr32*, also derived from *Ae. speltoides*, recombination studies based on three crosses showed independent inheritance {646}. *Sr39* segregated independently of *Lr13* {651}. *Sr39* may be present in DAS15 in combination with *Sr47*. A Ti2BL.2BS-2SS-2BS translocation {10872} separated from *Sr47* in DAS15 could contain *Sr39* -see *SrAEs7t*

Sr40{302}. Derived from *T. araraticum*. 2BS {302} = T2BL/2G#2S{389}. **i:** RL 6087 = RL 6071*7/PGR 6126; RL 6088 = RL 6071*7/PGR 6195{302}. **tv:** *T. araraticum* PGR 6126{302}; PGR 6195{302}. **ma:** *Xwmc661-2B* - 6.4 cM - *Sr40* - 0.7 cM - *Xwmc344-2B* - 2.0 cM - *Xwmc477-2B*{10825}; *Xwmc661-2B* - 7.8 cM - *Sr40* - 2.5 cM - *Xwmc474-2B* - 1.0 cM - *Xwmc477-2B*{10825}.

Sr41{1215}. 4D{1215}. **v:** WDR-B1{1214}. **v2:** Waldron *Sr5* (heterogeneous) *Sr11* (heterogeneous).

Sr42{938}. 6DS{938}. **v2:** Norin 40 *Sr54*{938}.

Sr43. Derived from *Thin. elongatum*.

7DL = T7DL-7Ae#2L.7Ae#2S{657,389}. **tr:** KS10-2{653}.

7D = T7DS.7Ae#2L{657,389}. **tr:** KS23-9{653}; KS24-1{653}; KS24-2{653}.

Sr44{389}. Derived from *Thin. intermedium*.

T7DS-7Ai#1L.7Ai#S 7Ai#1L{389}. **v:** Line 86.187{939}; Several 7A-7Ai#1L translocations{0089}.

7Ai#2, 7Ai#2S. **su:** Group 7 alien substitution lines with 7Ai#1 and 7Ai#1S{939}. **ad:** TAF2 = L1{169}.

Sr45{894}. [*SrD*{934},*SrX*{1805}]. 1D{897}.1DS{894}. **v:** 87M66-2-1{894}; 87M66-5-6{897}; Thatcher + *Lr21*, RL5406{894,934}; Various backcross derivatives developed at PBI Cobbitty{1461}. **dv:** *Ae. tauschii* RL5289{894,934}.

Tests of natural and induced mutants of *P. graminis* f. sp. *tritici* indicated that *Sr45* has identical specificity to *Sr21* {934}.

Sr46{10538}. 2DS{10538}. **v:** L-18913 / Meering selections R9.3{10538}; R11.4{10538}; R14.2{10538}. **v2:** L-18913 = Synthetic Langdon / *Ae. tauschii* var. *meyeri* AUS 18913 *Sr9e*{10538}. **ma:** Co-segregation with RFLP *Xpsr649-2DS* at both the diploid and hexaploid levels{10538}; A PCR-based marker, *csSC46* was developed from a BAC clone containing *Xpsr649*{10538}.

Sr47{10549}. Derived from *Ae. speltoides.* 2B = 2BL-2SL.2SS{10549}.2BS{10872}. **tv:** DAS15{10549}.

2B=2BL-2SL-2BL.2BS. **tv:** RWG35{10872}.

2B=2BL-2SL-2BL.2BS. **tv:** RWG36{10872}. **al:** *Ae. speltoides* PI 369590{10549}. **ma:** Located in the interval *Xgwm47-2B* - *Xgpw4165-2B*{10872}.

Further chromosome engineering on DAS15 showed that the alien segment carried two resistance genes. The gene on 2BL was considered to be *Sr47* based on low infection type. The second gene located in 2BS produced a low infection type similar to *Sr39* and was located in a similar position to that gene {10872}.

Sr48{10564}. [*SrAn1*{10565}]. 2AL{10564,10565}. **bin:** 2AL1-0.85-1.00{10564}. **v:** Arina{10511,10564,10565}. **v2:** Arina *Sr56* AUS 91457{10851}. **ma:** *Xgwm382-2AL* - 0.6 cM - *Xgwm311-2AL* - 2.6 cM - *Xfba8a-2AL* - 1.3 cM - *Xstm673acag* - 1.1 cM - *Yr1* - 16.5 cM - *Sr48*{10564}; *Sr48* is considerably distal to the most distal of published markers, all of which are proximal to *Yr1*.

Sr49{10704}. 5BL{10704}. **v:** AUS 28011{10704}. **ma:** *Sr49* - *Xwmc471-5BL*, 7.8 cM{10704}.

Sr50{10745}. [*SrR*{0377}]. 1DS{10745}. **ad:** CS + Imperial 1R{0377}. **v:** Line T6-1 AUS 91434{10745}. **al:** *S. cereale* cv. Imperial. **ma:** Line T6-1 retains the rye marker AW2-5{10745}.

In rye *Sr50* may be allelic with *Sr31*; however in wheat they can be regarded as separate loci *Sr50* is located in a small interstitial segment not detected by GISH. Line T6-1 lacks the *Sec-1* allele from rye {10745}.

Sr51{10803}. Homoeologous group 3 {10803}; 3S^{S}S {10803}

3A(3AL.3S^{S}S{10803}. **v:** TA5619{10803}.

3B(3BL.3S^{S}S){10803}. **v:** TA5620{10803}.

3D(3DL.3S^{S}S){10803}. **v:** TA5621{10803}.

3D(3DS-3S^{S}S.3S^{S}L){10803}. **v:** TA5622{10803}. **al:** *Ae. searsii* TA2355{10803}. **ma:** 3S^S-specific markers are provided in{10803}.

Sr52{10774}. 6A(6AS.6V#3L){10774}. **v:** TA5617{10775}. **ma:** 6V3-specific EST-STS markers are given in{10775}.

The seedling resonse conferred by *Sr52* is temperature-sensitive.

Sr53{10789}. Derived from *Ae. geniculata* 5D{10789}.

T5DS5DL-5M^{g}L-5DL{10789}. **v:** TA5630(U6154-124){10789}.

T5DL-5M^{g}L-5M^{g}S{10789}. **v:** TA5625(U6200-64){10789}; TA5643(U6200-117){10789}. **al:** *Ae. geniculata* TA10437{10789}.

The three translocation lines are re-engineered derivatives of TA5599 (5DL-5M^{g}L.5M^{g}S {10789}).

Sr54{10816}. 2DL{10816}. **v2:** Norin40 *Sr42*{10816}.

Sr55{10847}. Adult plant resistance 4DL{10847,10678}. **bin:** Distal to break point 0.56 FL{10678}. **i:** RL6077=Thatcher*6/PI 250413{10847,10678}. **ma:** Pleiotropic of closely linked with *Lr67* and *Yr46* and associated with *Xgwm165-4D* and *Xgwm192-4DL*{10847,10678}.

Sr56{10851}. Adult plant resistance [*QSr.sun-5BL*{10565}]. 5BL{10565,10851}. **bin:** 5BL16. **v:** AF533{10851}. **v2:** Arina *Sr48* AUS 91457{0138}. **ma:** *Xgwm118-5BL* - 13.6 cM - *wPt116* - 5.4 cM - *Sr56* - 6.9 cM - *wPt0484*{10851}.

In the earlier QTL analysis of an Arina/Forno population *QSr.sun-5BL* accounted for 12% of the PVE {10565}. In the present study of an Arina/Yitpi RIL population stem rust response segregated as a single gene. The response phenotype was 40-50 MS-S.

Sr57{10861}. Adult plant resistance 7DS{10861}. **bin:** 7DS4. **su:** Lalbahadur(Perula7D) GID 5348503 and GID 5348496{10861,10862}. **v:** Chinese Spring{10861}; Wheat with *Pm38/Lr34/Yr18*, see Reaction to *Blumeria graminis*, Reaction to *Puccinia striiformis*, Reaction to *Puccinia triticina*, Leaf tip necrosis. **ma:** See Reaction to *Puccinia triticina*. **c:** Putative ABC transporter{10862}.

Further evidence for the effects of this gene on stem rust response can be found in {299, 10565, 10733, 10863, 10864, 10865, 10866}.

SrA{323}. **v:** SW55-1{323}; SW56-1{323}. **v2:** SW33-5 *Sr9a Sr13*{323}; SW54-3 *Sr9d Sr13*{323}.

SrAes7t{10872}. 2BS=T2B.2BS-2SS-2BS{10872}. **v:** Line 0797{10872}. **ma:** Sr39#50s{10741,10872}.

SrAes7t may be identical to *Sr39* {10872}.

SrCad{10733}. 6DS{10733}. **v:** AC Cadillac{10733}; AC Crystal{10733}; AC Foremost{10733}; AC Karma{10733}; AC Taber{10733}; AC2000{10733}; Peace{10733}; 5700{10733}. **ma:** Lines with *Bt10*{10733}; *Xcfd49-6D* - 7.7 cM - *SrCad* - 1.5 cM - FSD_RSA/*Bt10* - 14.1 cM - *Xbarc301-6D* - 0.8 cM - *Xbarc173-6D*{10733}; *Xcfd49-6D* - 7.2 cM - *SrCad* - 1.8 cM - FSD-RSA/*Bt10* - 14 cM - *Xcfd75-6D*{10733}.

SrTmp{1230}. **v:** Bai-Yu-Bao{564}; Beijing 9{564}; Beijing 11{564}; Fertodi 293{977}; Martonvasari 5{977}; Mironovska = Mironovskaya 808{068,977}; Nung-Ta 139{564};

Parker{977}; Trison{1230}; Triumph 64{841,1230,977}; Xuzhou 14{564}; Yen-An 15{564}. **v2:** Beijing 10 *Sr5*{564}.
SrWeb{10858}. 2BL{10858}. **v2:** Webster RL6201 *Sr30*{10858}. **ma:** *Xgwm47-2B* - 1.4 cM - *SrWeb* - 12.5 cM - *Xwmc332-2B*{10858}.
SrWld{1230}. **v2:** Prospect *Sr11*{197}.
SrZdar{067}. 1B{067}. **v:** Zdar{067}.
Sr1RS$^{\mathit{Amigo}}${10845}. 1AS(T1AL.1RS){389,1624}. **v2:** Amigo *Sr24*{1464,10845}. **ma:** *Xscm09-1R*$_{224}${10845}.
This alien segment also carries *Pm17* - see *Pm17*

Additional temporary designations are listed in {1230}.
Genotype lists: {323,970,10270,10511,10697}.

Complex genotypes:

AC Taber: *Sr2, Sr9b, Sr11, Sr12*{9905}.
Centurk: *Sr5* {979}, *Sr6* {979}, *Sr8a, Sr9a* {979}, *Sr17* {979}.
Chris: *Sr5* {679,1371}, *Sr7a* {1371}, *Sr9g* {1371}, *Sr12* {1371}.
Egret: *Sr5* {939}, *Sr8a* {939}, *Sr9b* {939}, *Sr12* {939}.
FKN: *Sr2, Sr6, Sr7a, Sr8a* {791}, *Sr9b* {791}.
H-44: *Sr2, Sr7b* {677}, *Sr9d* {677}, *Sr17.*
Hartog: *Sr2* {127}, *Sr8a, Sr9g, Sr12* {939}.
Hope: *Sr2* {677}, *Sr7b* {677}, *Sr9d* {677}, *Sr17.*
Kenya Plume: *Sr2* {1370}, *Sr5* {1370}, *Sr6* {1370}, *Sr7a* {1370}, *Sr9b* {1370}, *Sr12* {1370} *Sr17* {1370}.
Khapstein: *Sr2, Sr7a, Sr13* {674}, *Sr14* {674}.
Lawrence: *Sr2, Sr7b* {939}, *Sr9d, Sr17.*
Lerma Rojo 64: *Sr2, Sr6, Sr7b* {979}, *Sr9a* {979}.
Madden: *Sr2, Sr9b, Sr11, Sr13* {842}.
Manitou: *Sr5* {679}, *Sr6* {679}, *Sr7a, Sr9g* {965}, *Sr12* {939}.
Mendos: *Sr7a* {939}, *Sr11* {879}, *Sr17, Sr36.*
Pasqua: *Sr5, Sr6, Sr7a, Sr9b, Sr12*. Gene *Lr34* acted as an enhancer of APR{9905}.
PI 60599: *Sr7a* {689}, *Sr8a, Sr9b, Sr10.*
Selkirk: *Sr2* {499}, *Sr6* {468}, *Sr7b* {499}, *Sr17, Sr23* {950}.
Redman: *Sr2, Sr7b* {939}, *Sr9d* {939}, *Sr17.*
Reliance: *Sr5* {1308}, *Sr16* {1238}, *Sr18, Sr20.*
Renown: *Sr2, Sr7b* {939}, *Sr9d* {939}, *Sr17.*
Roblin: *Sr5, Sr7a? Sr11, Sr12.*
Timgalen: *Sr5* (heterogeneous) {1555}, *Sr6* {1555}, *Sr8a, Sr36.*
Thatcher: *Sr5* {1308}, *Sr9g* {965}, *Sr12* {939}, *Sr16* {1308}.
WW15 = Anza = Karamu = T4: *Sr5* {939}, *Sr8a* {939}, *Sr9b* {939}, *Sr12* {939}.

QTL:

Arina / Forno:*Qsr.sun-5BL* {10565}; resistance contributed by Arina, associated with *Xglk356-5B*, R^2 = 11-12% {10565}. *Qsr.sun-7DS* {10565}; resistance contributed by Forno, associated with markers *XcsLV34* and *Xswm10* diagnostic for *Lr34/Yr18* {0828}.

HD2009/WL711 RILs: Three of several QTLs gave consistent effects across environments, viz. *QSr.sun-3BS*, R^2 = 0.09-0.15, probably *Sr2*, *QSr.sun-5DL*, R^2 = 0.2-0.44, probably *Sr30*, and *QSr.sun-7A*, R^2 = 0.07-0.13, nearest marker *wPT-4515* {10632}.

RL6071/RL6058(R): RIL population: RL6058, a Tc backcross line with *Lr34/Sr57* is more resistant than Tc. Enhancement of resistance in both Kenya and North America was attributed to a QTL in the region *wPt5044 - Xgwm-2B* in chromosome 2BL {10902}.

100. Reaction to *Puccinia striiformis* Westend.

Disease: Stripe rust, yellow rust.

100.1. Designated genes for resistance to stripe rust

Yr1{851}. [*L*{1622}]. 2A{877,1610}.2AL{940}. **bin:** 2AL1-0.85-1.00{10564}. **i:** AVS+Yr1{970}. **v:** Chinese 166{851}; Corin{230}; Dalee{083}; Durin{1459}; E2025{1267}; E7700{1267}; E8594{1267}; Feng-Kang 13{1610}; Heines 110{604}; Maris Ranger{1459}; Maris Templar{1459}; Odra{073}; Ritmo{10038}. **v2:** Argent *Yr3a Yr4a Yr6*{1067}; Avocet (UK)*Yr2 Yr6*{1459}; Bounty *Yr13*{1459}; Fenman *Yr2*{1459}; Galahad *Yr2* {heterogeneous} *Yr14*{1459}; Galahad *Yr14*{083}; Kraka *Yr32*{10038}; Ibis *Yr2*{604}; Longbow *Yr2 Yr6*{083}; Mardler *Yr2 Yr3a Yr4a Yr13*{604,1459}; Maris Templar *Yr3a Yr4a*{604}; Marksman {heterogeneous} *Yr2 Yr13*{1459}; Mithras *Yr2 Yr6*{1459}; Nudif TP1 *Yr3a*{1431}; Nudif TP3 *Yr3c*{1431}; Nudif TP250 *Yr6*{1431}; Regina *Yr2*{073}; Rothwell Perdix *Yr2*{604}; Savannah *Yr2 Yr3 Yr9 Yr32*{10032}; Sportsman *Yr13*{1459}; Stetson *Yr9*{083}; Sylvia *Yr2*{1430}; Tadorna *Yr2*{1431}; Virtue *Yr13*{083,1459}. **ma:** *Xgwm382-2AL* - 0.6 cM - *Xgwm311-2AL* - 2.6 cM - *Xfba8a-2AL* - 1.3 cM - *Xstm673acag* - 1.1 cM - *Yr1* - 16.5 cM - *Sr48*{10564}.

A report {1267} that Kalyansona and Nadadores carried *Yr1* is not correct.

Yr2{851}. Recessive {1351}. [*U*{1622}]. 7B{746,186,184}. **v:** Derius{230}; Flevina{1431}; Hana{51,58}; HD2329{1352}; Kalyansona{1351,1352}; Laketch{050}; Leda{1430}; Manella{1431}; Merlin{1622}; Odra{071}; PBW54{1352}; PBW120{1352}; Slavia{073,071}; Soissonais Desprez{851}; WG377{1352}; WH147{1352}; WL711{1352}; WL1562{1352}. **v2:** Avocet (U.K.) *Yr1 Yr6*{1459}; Brigand *Yr14*{083}; Cleo *Yr3c*{1457}; Cleo *Yr3c Yr14*{1431}; Fenman *Yr1*{1459}; Flamingo *Yr6*{1430}; Flevina *Yr7*{1430}; Galahad (heterogeneous) *Yr1 Yr14*{1459}; Garant *Yr7*{230}; Hardi *Yr7*{230}; Heines Kolben *Yr6*{611}; Heines Peko *Yr6Yr25*{746}; Heines VII *Yr25*{851}; Ibis *Yr1*{604}; Lely *Yr7*{1430}; Liberator *Yr3c*{1431}; Longbow *Yr1 Yr6*{083}; Mardler *Yr1 Yr3a Yr4a Yr13*{1459}; Maris Beacon *Yr3b Yr4b*{1459}; Maris Huntsman *Yr3a Yr4a Yr13*{604}; Maris Nimrod *Yr13*{1459}; Marksman *Yr1* (heterogeneous) *Yr13*{1459}; Mithras *Yr1 Yr6*{1459}; Nautica *Yr9*{1430}; Norman *Yr6*{083}; Rapier *Yr4*{083}; Rothwell Perdix *Yr1*{604}; Sonalika *YrA*{1352}; Stella *Yr3*{1430}; Sylvia *Yr1*{1430}; Tadorna *Yr1*{1431}; Viginta *Yr3a Yr4a*{073,071}; Wizard (heterogeneous) *Yr14*{1459}; Yamhill *Yr3a Yr4a*{181,182, see also, 184}; Zdar *Yr4a*{073}.

Yr2 originally referred to a gene in Heines VII conferring resistance to European pathotypes. However, Heines VII possesses an additional resistance gene *Yr25* {1351} which can be detected with a geographically wider range of pathogen isolates. *Yr2* is present in Kalyansona {1351} and a range of spring wheats distributed by CIMMYT.

Yr3. Undesignated allele. **v:** Enkoy{050}; Vilmorin 23; Staring{1430}. **v2:** Minister *Yr2*{1430}; Savannah *Yr1 Yr2 Yr9 Yr32*{10016}; Senat *Yr32*{10016}; Stella *Yr2*{1430}.

Yr3a{851}. 1B{185,184}.2B{10370}. **i:** Taichung 29*6/Vilmorin 23{10370}. **v:** Bon Fermier{1431}; Nudif TP1{1431}; Stephens{182,184}; Vilimorin 23{10370}. **v2:** Argent *Yr1 Yr4a Yr6*{1067}; Cappelle-Desprez *Yr4a*{851}; Druchamp *Yr4a*{185,182, see also, 184}; Hobbit *Yr4a Yr14*{604}; Kinsman *Yr4a Yr6*{604}; Mardler *Yr1 Yr2 Yr4a Yr13*{1459}; Maris Huntsman *Yr2 Yr4a Yr13*{604}; Maris Freeman *Yr4a Yr6*{604}; Maris Ranger *Yr4a Yr6*{604}; Nord Desprez *Yr4a*{182,184}; Top *Yr4a*{230}; Viginta *Yr2 Yr4a*; Yamhill *Yr2 Yr4a*{182}; Zdar *Yr4a*{073,071}. **ma:** *Yr3(YrV23) - Xwmc356-2B*, 9.4 cM{10370}.

Yr3b{851}. Chen & Line {182} found that a second gene in Hybrid 46 - presumably this gene - was not located at the *Yr3* locus **v2:** Hybrid 46 *Yr4b*{851}.

Yr3c{851}. 1B{184}. **v:** Minister{851,182,184}. **v2:** Cleo *Yr2*{1430}; Maris Beacon *Yr2 Yr4b*{1459}.

Yr4. Undesignated allele. [*YrRub*{10720}]. 3BS{10720}. **bin:** 3BS3 - 0.87 - 1.00{10720}. **v:** Avalon{10720}; Bolac; Emu S{10720}; Kenya Kubangu{050}; Rubric AUS33333{10720}. **v2:** Avalon *Yr14*{083}; Rapier *Yr2 Yr14*{083}. **ma:** *Yr4* - 2.9 cM - *Xcfb3530-3B* - 2.4 cM - *Xbarc75-3B*{10720}.

The conclusion that *YrRub* is *Yr4* is based on sepcificity similarities and the presence of the *Xcfb3530*$_{150}$ and *Xbarc75*$_{132}$ alleles in the five genotypes listed above. The 3BS location is not consistent with that listed below for *Yr4a and Yr4b*.

Yr4a{851}. 6B{185,184}. **v:** Vilmorin 23{184}. **v2:** Argent *Yr1 Yr3a Yr6*{1067}; Cappelle-Desprez *Yr3a*{851}; Druchamp *Yr3a*{182}; Hobbit *Yr3a Yr14*{604}; Huntsman *Yr2 Yr3a Yr13*{604}; Kinsman *Yr3a Yr6*{604}; Maris Ranger *Yr3a Yr6*{604}; Maris Freeman *Yr3a Yr6*{604}; Mardler *Yr1 Yr2 Yr3a Yr13*{1459}; Nord Desprez *Yr3a*{182}; Top *Yr3a*{230}; Viginta *Yr2 Yr3a*{073,071}; Yamhill *Yr2 Yr3a*{182,185, see also, 184}; Zdar *Yr3a*{073,071}.

Yr4b{851}. 6B{184}. **v:** Avalon{1160}; Opal{1431}; Staring{1430}. **v2:** Hybrid 46 *Yr3b*{851,182, see also, 184}; Maris Beacon *Yr2 Yr3b*{1160,1459}; Nudif TP12 *Yr3c*{1431}; Stella *Yr2*{1430}.

Yr5{877}. Allelic with *Yr7* and *YrSp* {10759} 2BL{034}. **i:** AVS+Yr5{970}. **v:** By 33{03102}; E5557{1267}; E8510{1267}; *T. spelta album*{877}; Seven spelt accessions from Europe and Iran{640}. **ma:** *Yr5* - 10.5 & 13.3 cM - *Xgwm501-2B*{03102}; Completely linked to Resistance Gene-Analog Polymorphism (GRAP) markers *Xwgp17-2B, Xwgp19-2B* and *Xwgp26-2B*{10096}; *Xwgp17-2B* was later converted into a simpler Cleaved Amplified Polymorphic Sequence (CAPS) PCR marker{10097}; Co-segregation with AFLP marker S19N93-140 and 0.7 cM with S23M41-310{10435}; *Xwmc175-2B* - 1.1 cM - *YrSTS-7/8* - 0.3 cM - *Yr5* - 0.4 cM - *Xbarc349-2B*{10826}.

Yr6{877}. [*B*{1622}]. 7B{746}.7BS{331}. **i:** AVS+Yr6{970}. **v:** Austerlitz{230}; Fielder{181}; Heines Kolben{1622}; Koga II{746}; Maris Dove{604}; Recital{230}; Takari{368}. **v2:** Argent *Yr1 Yr3a Yr4a*{1067}; Avocet (UK) *Yr1 Yr2*{1459}; Flamingo *Yr2*{1430}; Heines Peko *Yr2*{746,877}; Kinsman *Yr3a Yr4a*{604}; Kolben *Yr2*{611}; Longbow *Yr1 Yr2*{083,1459}; Maris Freeman *Yr3a Yr4a*{604}; Maris Ranger *Yr3a Yr4a*{604}; Mithras *Yr1 Yr2*{1459}; Norman *Yr2*{083,1459}; Nudif TP241 *Yr7*{1431}; Nudif TP250 *Yr1*{1431}; Orca *Yr3c*{1431}; Pavon 76 *Yr7*{284}; Penjamo 62 (heterogeneous) *Yr18*{1562}. **tv:** Duilio{192}; Latino{192}; Norba{192}; Quadruro{192}; Rodeo (heterogeneous){192}.

Yr7{877}. Allelic with *Yr5* and *YrSp* {10759} 2B{612,1429}.2BL{965}. **i:** AVS+Yr7{970}; Taichung 29*6/Lee{10371}. **v:** Present in many hexaploid wheats with *Sr9g* - see{965}; Brock{083}; Lee{877}; Nudif TP257{1431}; PBW12{1352}; Prinqual{230}; Renard{083}; Talent{230}; Tango{230}; Tommy{083}; WL2265{1352}. **v2:** Donata *Yr9*{1430}; Flevina *Yr2*{1431}; Garant *Yr2*{230}; Hardi *Yr2*{230}; Lely *Yr2*{1430}; Nudif TP241 *Yr6*{1431}; Pakistan 81 = Veery#5 *Yr9*{284}; Pavon 76 *Yr6*{284}; Reichersberg 42 *Yr25*{0010}; Thatcher{965}. **tv:** Iumillo{965}; but not present Acme and Kubanka which also carry *Sr9g*{965}. **ma:** *Yr7 - Xgwm526-2B*, 5.3 cM{10371}.

Yr8{1217,1218}. Derived from *Ae. comosa.* 2D = T2D-2M {1218} = T2DS-2M#1L.2M#1S{389}. **i:** AVS+Yr8{970}. **tr:** Chromosome 2D-2M translocations in Hobbit Sib and Maris Widgeon{1016}; Compair{1217,1218}; CS 3D/2M 3/8{967}; See also *Sr34* and{967}.

2A = 2A-2M = T2AS-2M#1L.2M#1S{389}. **tr:** CA 2A/2M 4/2{967}.

2M-1. **su:** CS 2M#1(2A){967}.

Yr9{878}. Derived from *S. cereale*. See also Reaction to *P. graminis, Sr31*: Reaction to *P. triticina Lr26*

1B=1BL.1RS. **i:** AVS+Yr9{970}. **v:** Almus{998}; Aurora{1623}.

Chromosome status not specified. **v:** Baron{083}; Benno{998}; Bezostaya II{998}; Branka{071}; Clement{1430,1532}; Cougar{0267}; Danubia{068}; GR876{753}; Hammer{083}; Iris{068}; Kavkaz{1623}; Kromerzhizhskaya{1149}; Lyutestsens 15{1149}; Lovrin 10{998}; Lovrin 13{998}; Mildress{1027}; Perseus{998}; Predgornaya{998}; Rawhide (heterogeneous){0267}; Riebesel 47/51{878,1623}; Roxana{068}; Sabina{068}; Salmon{998}; Sarhad 82{284}; Selekta{068}; Shtorm{1149}; Skorospelka 35{998}; Sleipner{10038}; Solaris{068}; St 2153/63{997}; Stuart{083}; Veery{986}; Weique{1627}; Winnetou{998}; Weihenstephan 1007/53{1623}. **v2:** Agra *Yr3*{068,071}; Brigadier *Yr17*{10785}; Donata *Yr7*{1430}; Haven *Yr6*{10038}; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Basribey 95, Seyhan 95 *Yr18 Yr27*{10160}; Lynx *Yr6 Yr17*{10038}; Nautica *Yr2*{1430}; Pakistan 81 = Veery#5 *Yr7*{284}; Savannah *Yr1 Yr2 Yr3 Yr17*{10016}; Stetson *Yr1*{083}; Sparta *Yr3*{071}. **tv:** Cando*2/Veery, KS91WGRC14{381}.

1R(1B){997,1623}. **su:** Burgas 2{998}; Clement{1160}; Lovrin 13{998}; Mildress{998}; Mironovskaja 10{998}; Neuzucht{1623}; Orlando{1623}; Roseana{068}; Saladin{997}; Salzmunder Bartweizen{1623}; St 14/44{998}; Weique{1627}; Wentzel W{1623}; Winnetou{1027}; Zorba{998}; See also{050}. **ma:** Several markers tightly linked with *Yr9* were identified in{0377}; *Yr9* - 3.7 cM - *Xgwm582-1BL*{10365}.

Stripe rust resistant wheat - *S. africanum* derivatives G17 (substitution line with 1R^{a}), L9-15(1BL, 1RS^{a} and L2-20 (putative cryptic translocations) are reported in {10596}.

Yr10{878}. [*YrVav*{0262}]. 1B{641}.1BS{1002}. **i:** AVS+Yr10{970}. **v:** Moro{878}; PI 178383{878}; QLD709 = Janz*2/*T. vavilovii*{0262}; *T. spelta* 415{641}; *T. vavilovii* AUS 22498{0262}. **ma:** A SCAR marker was described in{0261}; QLD709 and *T. spelta* 415, both with white glumes, failed to amplify the SCAR sequence, but both carried unique alleles at the *Gli-B1* and *Xpsp3000-1B* loci {0262}. These differed from the Moro source of *Yr10*. *Yr10* - 1.5 cM - *Gli-B1* - 1.1 cM - *Xpsp3000-1B*{0261}; *Yr10* - 1.2 cM - *Xpsp3000-1B* - 4.0 cM - *Gli-B1*{0321}; Cosegregation between a RGA marker *RgaYr10a* and *Yr10* was reported in {0376}.

Yr11. Adult plant resistance. [*R11*{1157}]. **v:** Joss Cambier{606}. **v2:** Heines VII *Yr2 Yr25* see{970}.

Yr12. Adult plant resistance. [*R12*{1157}]. **v:** Fleurus{1158}; Frontier{1159}; Pride{1157}. **v2:** Armada *Yr3a Yr4a*{1160,081}; Mega *Yr3a Yr4a*{1157,1160}. **v:** Waggoner *Yr3a Yr4a Yr6*{1158}.

Yr13. Adult plant resistance. [*R13*{1157}]. **v2:** Bounty *Yr1 Yr3a Yr4a*{1459}; Brigand *Yr2 Yr3a Yr4a Yr14*{609}; Copain *Yr3a Yr4a*{1158}; Gawain *Yr2 Yr3a Yr4a Yr14*{081}; Guardian *Yr2*{082}; Hustler *Yr1 Yr2 Yr3a Yr4a*{083,1459}; Kinsman *Yr3a Yr4a Yr6*{1459}; Mardler *Yr1 Yr2 Yr3a Yr4a*{1459}; Maris Huntsman *Yr2 Yr3a Yr4a*{083,604,1459}; Maris Nimrod *Yr2 Yr3a Yr4a*{607,1157,1459}; Marksman *Yr1* {heterogeneous} *Yr2 Yr3a Yr4a*{1459}; Pageant *Yr2 Yr3a Yr4a*{082}; Professor Marchal *Yr2 Yr3a Yr4a*{607}; Sportsman *Yr1 Yr3a Yr4a*{1459}; Virtue *Yr1 Yr3a Yr4a*{083,1158,1459}.

Yr14. Adult plant resistance. [*R14*{1157}]. **v:** Kador{1158}; Score{1157}; Wembley{610}. **v2:** Avalon *Yr3b Yr4b*{083,1459}; Brigand *Yr2 Yr3a Yr4a Yr13*{083,609,1459}; Galahad *Yr1 Yr2* (heterogeneous) *Yr3a Yr4a*{083,1459}; Gawain *Yr2 Yr3a Yr4a Yr13*{081}; Hobbit *Yr3a Yr4a*{1459,1157}; Maris Bilbo *Yr3a Yr4a*{1157,1459}; Moulin *Yr6*{083}; Rapier *Yr2 Yr3b Yr4b*{083}; Wizard *Yr2* (heterogeneous) *Yr3b Yr4b*{083,1459}.

Yr15{432,969}. 1BS{939,969}. **i:** AVS+Yr15{970}. **v:** Agrestis{0330}; Boston{0330}; Cortez{0330}; Legron{0330}; Hexaploid derivatives of *T. dicoccoides* G-25{432,466}; V763-2312{969}; V763-254{969}. **tv:** *T. dicoccoides* G-25{432,431,466}; D447 derivatives B1, B2, B9, B10{1434}. **ma:** *Xgwm33-1B* - 5 cM - *Yr15*{9904}; *Xgwm33-1B* - 4.5 cM - *Yr15* - 5.6 cM - *UBC199200* - 5.6 cM *Nor-B1*{0110}; Gene order *Yr15* - *Yr24* -

Xgwm11-1B{10112}; *OPB131420* - 27.1 cM - *Yr15* - 11.0 cM - *Nor-B1*{1434}; *Xwmc128/Xgwm273/Xgwm582-1B* - 0.4 cM - *Yr15/Xwgp34/Xgwm413/Xbarc8*{10826}.

Yr16{1598}. Adult plant resistance. 2D{1598}. **v:** Bersee{1604}; Cappelle-Desprez{1598}.

Yr17{062}. 2AS{062}.2AS-$6M^v$.$6M^v$ = 2MS-6MS.6ML or 2MS-6ML.6MS{0009}. **i:** AVS+Yr17{970}. **v:** Apache{10554}; See *Lr37* (Reaction to *P. triticina*) and *Sr38* (Reaction to *P. graminis*); Arche{0044}; Balthazar{0044}; Bill{10554}; Brigadier{0044}; Caphorn{10554}; Clever{10554}; Clarus{10554}; Cordial{0044}; Corsaire{10554}; Eureka{0044}; Hussar{0044}; Kris{10283}; Pernel{0044}; Rapsodia{10554}; Renan{0044,10554}; Rheia{10554}; RL 6081{939}; Genotype list in{02105}. **v2:** Brigadier *Yr9*{10785}; Lynx *Yr6 Yr9*{0044, 10038}; Savannah *Yr1 Yr2 Yr2 Yr32*{10016}. **ma:** *Yr17* was closely linked to the SCAR marker SC-Y15, developed from RAPD marker OP-$Y15_{580}$, and to *Xpsr150-2N*^{v}{0044}; Characterized by null alleles for *Xwmc382-2A* and *Xwmc407-2A*{10283}; SCAR markers SC-372 and SC-385 were developed in {10796}.

The 2NS translocated segment carrying *Yr17* replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682-2A* to *XksuH9-2A*. PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682* {10073}.

Yr18{1362}. 7D{1362}.7DS{324}. **i:** AVS+Yr18{970}; Thatcher(*Yr7*) near-isogenic lines with *Lr34* including the 13 2-gene combinations reported in{434,937}. **v:** Jupateco 73R; Lerma Rojo 64{1375}; Nacazari 76{1375}; Tesia F 79{1375}; Tonichi S 81{1375}; Wheaton{1375}. **v2:** Parula *Yr29*{10281}; Penjamo 62 *Yr6* (heterogeneous){1375}; Saar *Yr29*{10481}; Wheats with *Lr34* (See *Lr34*); Others{1376}; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Bascribey 95, Seyhan 95 *Yr9 Yr27*{10160}. **ma:** Complete linkage with *Lr34*{937,1362}; *Ltn*{1361}; and *Bdv1*{1363}; *Xgwm120-7D* - 0.9 cM - *Yr18* - 0.7 cM - *Xgwm295-7D*{10259}. **c:** See *Lr34*; Putative ABC transporter{10862}.

This gene is identical to *Lr34, Pm38* and *Ltn* and confers stem rust resistance in some genetic backgrounds. Some AVS NILs also have *Yr18.*

Yr19{183}. [*YrCom*{183}]. 5B{183}. **v2:** Compair *Yr8*{183}.

Yr20{183}. [*YrFie*{181}]. 6D{183}. **v2:** Fielder *Yr6*{183}.

Yr21{183}. [*YrLem*{181}]. 1B{183,10450}. **v:** Lemhi{183}.

A closely linked gene, also in Lemhi, conferred resistance to *P. s. hordei* {10450}. Both genes were mapped relative to RGAP markers. *Yr21* - *YrRpsLem*, 0.3 cM {10450}.

Yr22{183}. [*YrLe1*{183}]. 4D{183}. **v2:** Lee *Yr7 Yr23*{183}.

Yr23{183}. [*YrLe2*{183}]. 6D{183}. **v2:** Lee *Yr7 Yr22*{183}.

Yr24{952}. [*YrCH42*]. 1BS{952}. **i:** AVS+Yr24{970}. **v:** Chuanmai 42{10339}; Meering*3/K733/*Ae. tauschii* AUS18911{952}; Synthetic 769{10339}. **tv:** Decoy 1{10339}; K733{952}. **ma:** Gene order *Yr15* - *Yr24* - *Xgwm11-1B*{10112}; *Xbarc187-1B* - 2.3 cM - *Yr24* - 1.6 cM - *Xgwm498-1B*{10339}.

Yr24 is identical to *Yr26* {10339, 939}

Yr25{158}. 1D{158}. **v:** Carina{0010}; Hugenout{0010}; Strubes Dickkopf{158, 10016}; TP1295{158}; TP981{158}; Tugela{0314}; Tugela-DN{0010,0314}. **v2:** Carstens V *Yr32*{10016}; Heines Peko *Yr2 Yr26*{0010}; Reichersberg 42 *Yr7*{0010}; Spaldings Prolific *YrSP*{10016}.

Yr25 was predicted to be present in Strubes Dickkopf, Heines VII *Yr2*, Heines Peko *Yr2 Yr6*, Reichersberg 42 *Yr7* and Clement *Yr9* {158}. This prediction was confirmed for Heines VII, Heines Peko and Reichersberg 42 {0010} but the pathogen culture used in {0010} was not virulent on Clement(*Yr9*) or on Strubes Dickkopf where another, or a different gene, must be present.

Yr26{617}. 1BS{0285}.The earlier location of 6AS (6AL.6VS){617} is not corect..1BL{10544}. **bin:** C-1BL-6-0.32{10544}. **i:** AVS+Yr26{970}. **v:** Nannong 9918{10544}; Nei 2938{10544}; Nei 4221{10544}; Neimai 9{10544}; Lines R43, R55, R64 and R77{0285}. **tv:** *T. turgidum* Gamma 80-1. **tr:** Yangmai-5{617}. **ma:** *Yr26* - 1.9 cM - *Xgwm11-1B/Xgwm18-1B*{0285}; *Xgwm11/18-1B* - 1.1 cM - *Xwe171/202/210-1B* - 0.4 cM -

Xwe177/201-1B - 0.3 cM - *Xwe173-1B* - 1.4 cM - *Yr26* - 6.7 cM - *Xbarc181-1BL* - 3.0 cM - *Xwmc419-1BL* {10544}.

According to {10554} the markers most closely associated with *Yr26* are actually located in chromosome 1BL.

Yr26 is identical to *Yr24* {10339,939}.

Yr27{928}. [*YrSk*{928}]. 2BS{928}. **i:** AVS+Yr27{970}. **v:** Ciano 79{928}; Inquilab 91{928}; Kauz{928}; McMurachy{928}; Opata 85{928}; PWB343{928}; Selkirk{928}; Webster{928}. **v2:** Attila *Yr27*{928}; Kauz and derivatives, Bakhtawar 94, WH542, Memof, Basribey 95, Seyhan 95 *Yr9 Yr18*{10160}. **ma:** When analysed as a QTL, variation associated with the *Yr27* locus was associated with RFLP markers *Xcdo152-2B* and *Xcdo405-2B*{928}.

Many CIMMYT wheat lines {953}. Recombination *Yr31* - *Yr27*, 0.148, *Yr31* - *Lr23*, 0.295 {0325}.

Yr28{1377}. 4DS{1377}. **v:** Synthetic = Altar 84/*Ae. tauschii* W-219. Synthetic/Opata 85 SSD population. Genotype lists:{1325,970}. **dv:** *Ae. tauschii* W-219{1377}. **ma:** Close association with *Xmwg634-4DS*{1377}.

Yr22 was also reported for chromosome 4D, but in the absence of an appropriate single gene stock and the unavailability of avirulent cultures in most laboratories, tests of linkage with *Yr28* are unlikely in the foreseeable future.

Yr29{0119}. Adult plant resistance {0119}. 1BL{0119}. **s:** Lalbahadur(Parula 1B){10281}. **v2:** Attila *Yr27*{10281}; Parula *Yr18*{10281}; Pavon F76 *Yr6 Yr7 Yr30*{0119}; Saar *Yr18*{10481}; *Yr29* is completely linked with *Lr46*. See *Lr46*{0119}. **ma:** *Xwmc44-1B* - 1.4 cM - *Xbac24prot* - 9.5 cM - *Yr29* 2.9 cM - *Xbac17R .....Xgwm140-1B*{10281}; *Xgwm44-1B* - 3.6 cM - *Yr29* - 2.1 cM - *XtG818/XBac17R.....Xgwm140-1B*{10281}; Associated with *Ltn2* and *Lr46*.

Yr30{0120}. Adult plant resistance {0120}. 3BS{0120}. **v:** Opata 85{0120}; Parula{0120}. **v2:** Inia 66 *YrA*{0120}; Pavon F76 *Yr6 Yr7 Yr29*{0120}; *Yr30* is closely linked with *Sr2* and *Lr27*{0120}.

Yr31{0325}. 2BS. **v:** Pastor{0325}. **ma:** Recombination values: *Yr31* - *Yr27*, 0.148; *Yr31* - *Lr23*, 0.295; *Yr27* - *Lr23*, 0.131{0325}.

Yr32{10016}. [*YrCv*{939},*YrCV*{1430}]. 2AL{10016}. **i:** Avocet S*4/Carstens V{970}; Cook*6/Carstens V{970}; CRW380 = Carstens V/3*Avocet S{10016}; Tres/6*/Avocet S{10016}. **v:** Anouska{1430}; Caribo{1430}; Consort{10021,10023}; Cyrano{1430}; Danis{10023}; Deben{10283}; Hereward{10021,10022}; Okapi{1430}; Oxbow{10021}; Senat{10016}; Solist{10016}; Stakado{10016}; Tres{10016}; Vivant{10023}; Wasmo{10016}. **v2:** Carstens V *Yr25*{10016}; Felix *Yr3*{1430}; Kraka *Yr1*{10021,10038}; Savannah *Yr1 Yr2 Yr3 Yr4 Yr17*{10016}; Senat *Yr3*{10016}; Zdar *Yr3a Yr4a*{067}. **ma:** *Xwmc198-2A* - 2 cM - *Yr32*{10016}; *Yr32* was coincident with one AFLP marker{10016}.

Yr33{10039}. More readily detected in seedling tests at elevated temperatures {10336}. 7DL{10039}. **v:** Batavia{10039}; EGA Gregory; Strezecki. **ma:** Linkage with *Xgwm111-7D* and *Xgwm437-7D*{10039}.

Yr34{10040}. This gene confers a weak seedling resistance (IT 2C to 3C) and a strong adult plant resistance (0 to 10R) {10040} to Australian pathotype 134E16A+, but is not effective against Australian pathotype 110E143A+ {10040}. 5AL{10040}. **v:** AUS22857{10040}; WAWHT2046=AUS91389{10040}. **ma:** *Xgwm410.2-5A* - 8.2 cM - *B1* - 12.2 cM - *Yr34*{10040}.

Yr35{10203}. [*YrS8*{10204}]. 6BS{10203}. **v:** 98M71 = AUS 91388 = *T. dicoccoides* 479/7*CS{10204}. **tv:** *T. dicoccoides* 479{10204}. **ma:** *Xgwm191-6B* - 18.9 cM - *Yr35* - 3 cM - *Lr53* - 1.1 cM - *Xcfd-6B* - 3.4 cM - *Xgwm50-6B*{10780}.

Yr36{10138,10272}. Adult plant resistance 6BS{10138}. **i:** Yecora Rojo NIL PI 638740{10138}. **v:** Glupro{10138}; UC1041+Yr36{10649}. **itv:** UC1113 NIL PI

638741{10138}. **tv:** RSL#65{623,10138,10649}; *T. dicoccoides* FA-15{10138}. **ma:** *Yr36* is between *Xucw74-6B* and *Xucw77-6B* and 3-7 cM proximal to *Nor-B2*{10138}; *Yr36* is closely linked to the high grain protein locus of *T. turgidum* var. *dicoccoides* FA-15{10138}; *Nor-B2 ....Xucw68-6B - Xucw69-6B/Xbarc101-6B/Yr36 - Xucw66-6B*{10272}; *Yr36* is 2-4 cM proximal to *Gpc-B1*{10272}. **c:** ACF33182; *Yr36* is wheat kinase-START-1{10649}; WKS1 is absent in almost all modern tetraploid and common wheats{10649}.

Yr37{10139}. Derived from *Ae. kotschyi*. 2DL{10139}. **v:** Line S14{10139}. **ad:** Line 8078{10139}. **al:** *Ae. kotschyi* 617{10139}.

Yr38{10224}. [*YrS12*{10204}]. 6A (6AL-6L^{sh}.6S^{sh}){10224}. **v:** Line 0352-4 = *Ae. sharonensis*-174/9*CS//3*W84-17/3/CS/4/W84-17{10224}; Recombinants with shorter segments - 07M4-39, 07M4-157 and 07M4-175 are reported in {10691}. **al:** *Ae. sharonensis*-174{10224}.

Yr39{10416}. HTAP resistance 7BL{10416}. **v:** Alpowa{10416}. **ma:** Closely linked to several RGAP markers{10416}.

Yr40{10328}. Derived from *Ae. geniculata* 5DS(5DL.5DS-T5MS^{G}{10328}. **v:** TA 5602{10328}; TA 5603{10328}. **al:** *Ae. geniculata* (=*ovata*) (U^{s}U^{s}M^{g}MM^{g}) TA10437{10328}. **ma:** Completely linked with distinctive alleles of *Gsp, Xfbb276* and *Xbcd873*{10328}; Completely linkd with *Lr57*{10328}; CAPS marker *XLr57/Yr40-MAS-CAPS16*{10770}.

Yr41{10502}. [*YrCN19*{10228}]. 2BS{10228,10502}. **v:** AIM{10228}; AIM6{10228}; Chuannong 19{10228,10502}. **ma:** Complete linkage to a 391 bp allele of *Xgwm410-2BS*{10228}; *Xgwm410-2B* - 0.3 cM - *Yr41*{10502}.

Yr42{10537}. Derived from *Ae. neglecta* 6A = 6AL-6^{Aen}L.6^{Aen}S{10537}. **v:** Line 03M119-71A{10537}. **al:** *Ae. neglecta* 155{10537}.
Associated with *Lr62* {10537}.

Yr43{10673}. 2BL{10673}. **v:** IDO377s=PI 591045{10673}; Lolo{10673}; many IDO377s derivatives{10673}. **ma:** *Xwms501-2B* - 11.6 cM - *Xwgp110-2B* - 4.4 cM - *Yr43* - 5.5 cM - *Xwgp103-2B* - 12.8 cM - *Xbarc139-2B*{10673}.

Yr44{10673}. [*YrZak*{10674}]. 2BL{10674}. **v:** Zak=PI 607839{10674}. **ma:** *XSTS7/8/Yr5* - 12.7 cM - *Yr44* - 3.9 cM - *Xwgp100* - 1.1 cM - *Xgwm501-2B*{10674}.

Yr45{10677}. 3DL{10677}. **v:** PI 181434{10677}. **ma:** *Xbarc6-3D* - 0.9 cM - *Xwmc656-3D* - 6.9 cM - *Xwpl18-3D* - 4.8 cM - *Yr45* - 5.8 cM - *Xwp115-3D*{10677}.
This gene is highly effective and confers resistance to all North American *Pst* pathotypes.

Yr46{10678}. Adult plant resistance. 4DL{10678}. **bin:** Distal to 0.56. **i:** RL6077=Thatcher*6/PI 250413{10678}. **v:** PI 250413{10678}. **ma:** *Xgwm165-4D/Xgwm192-4D* - 0.4 cM - *Yr46/Lr67*{10678}.
Pleiotropic or closely linked with *Sr55* and *Lr67*

Yr47{10679}. 5BS{10679}. **bin:** 5BS - 0.71 - 0.81. **v:** AUS28183 = V336{10679}; AUS28187{10679}. **ma:** 5 +/- 2 cM proximal to *Lr52*{10679}; *Xgwm234-5B* - 10.9 cM - *Lr52* - 4.1 cM - *Yr47* - 9.6 cM - *Xcfb309-5B*{10679}; *Xgwm234-5B* - 10.2 cM - *Lr52* - 3.3 cM - *Yr47* - 8.2 cM - *Xcfb309-5B*{10679}.
This is a seedling resistance gene (IT 1CN), effective against the main Australian groups of *Pst*. V336 is the original source of *Lr52.*

Yr48{10705}. Adult plant resistance. [*Qyr.ucw-5AL*{10705}]. 5AL{10705}. **bin:** 5AL23 0.87-1.00. **v:** UC1110 (MR)/PI 610750(MR) RIL 4=GSTR 13504 & RIL167=GSTR 136{10705}. **ma:** Co-segregated with *Vrn-2A*, BE495011, *Xcfa2149-5AL, Xgpw2181a-5AL, Xwmc74-5AL*, and *Xwmc410-5AL*{10705}; *Xwmc727-5AL* - 3.7cM - *Vrn-A2* - 0.1 cM - *Yr48/BE444566-5AL/Xcfa2149-5AL/Xgpw2181a-5AL/Xwmc410-5AL*{10705}.
PI 610750=Synthetic 205((Crop 1 / *Ae. tauschii*)/Kauz) {10705}.

Yr49{10746}. Adult plant resistance 3DS{10746}. **bin:** 3DS-6(0.55-1.00). **v1:** AvocetS*3 / Chuanmai 18 AUS91433{10746}. **v2:** Chuanmai 18 *Yr18*{10746}. **ma:** *Xgps7321-3D/Yr49* - 1 cM - *Xgwm161-3D*{10746}.

Yr50{10849}. Derived from *Th. intermedium* 4BL{10849}. **v:** CH233{10849}. **ma:** cent...*Xbarc1096-4B* - 6.9 cM - *Yr50* - 7.2 cM - *Xbarc-4B*{10849}.

Yr51{10850}. 4AL{10850}. **bin:** 4AL4-0.80-1.00. **v:** Line 5515 AUS 91456{10850}. **v2:** AUS 27858 Gene 2{10850}. **ma:** *wPt4487* - 9.8 cM - *Yr51* - 4.4 cM - *wPt0763* - 7.9 cM - *Xgwm160-4B*{10850}.

Yr52{10852}. Adult plant resistance 7BL{10852}. **bin:** 7BL-3 0.86-1.00. **v:** PI 183527{10852}; PI 660057=Avocet S/PI 183527 F4-41{10853}. **ma:** *Xbarc182-7B* - 1.2 cM - *Yr52* - 1.1 cM - *Xwgp5258* - 5.7 cM -*Xcfa2040-7B*{10852}.

Yr53{10854}. 2BL{10854}. **tv:** PI 480148{10854}. **v:** Avocet S/PI 480148 F5-128{10854}. **ma:** *Xwmc441-2B* - 5.6 cM - *Yr53* - 2.7 cM - *XLRRrev/NLRRrev*$_{350}$ - 6.5 cM - *Xwmc149-2B*{10853}; *Yr53* was estimated to be 35 cM distal to *Yr5* based on an F2 allelism test, but on an integrated map this distance was about 20 cM.

Sources of additional genes for seedling (designated "12") and adult resistances ("13", "14", "15") are listed in {1430}.

Genotype list: Chinese common wheats {10369}. European wheats {10579}. U.K. wheats {10697}.

100.2. Temporarily designated genes for resistance to stripe rust

North American workers {181,186,184} allocated a number of temporary designations to uncatalogued genes detected with North American *P. striiformis* accessions. Druchamp, Yamhill and Stephens were reported to carry '*Yr3a* or *Yr4a*" because these genes could not be distinguished with the cultures that were used.

YrA. Refers to a phenotype specificity that appears to be controlled by complementary genes {1563}. **v:** Avocet* {*= heterogeneous}; Anza = Karamu = Mexicani =T4 = WW15; Banks*; Condor*; Cocamba; Egret*; Inia 66; Lerma Rojo 64; Lerma Rojo 64A; Nainari 60; Nuri 70; Sanda 73; Sonalika; Zaminder 80. **v2:** Condor selection P44 *Yr6**; Pari 73 *Yr6*; Saric 70 *Yr6*; Yecora 70 *Yr6*{1563}.

YrAlp{10416}. 1BS{10416}. **v2:** Alpowa *Yr39*{10416}. **ma:** *YrAlp* - 15.2 cM - *Xgwm18-1B* - 1.1 cM - *Xgwm11-1B*{10416}; and more closely linked to RGAP markers{10416}.

YrC142{10667}. 1BS{10667}. **v:** Synthetic CI142=Gaza/Boy//*Ae. tauschii* 271{10667}. **ma:** Located in the *Yr24/Yr26* region close to *Xbarc187-1B* and *Xgwm273-1B*{10667}. Although postulated to be unique this gene is likely *Yr24/Yr26*.

YrC591{10606}. 7BL{10606}. **v:** C591{10606}; Zhongzhi 1{10606}. **ma:** *Xcfa20-40-7B* - 8.0 cM - *YrC591* - 11.7 cM - *SCP35M48*{10606}.

YrAS2388{10822}. **dv:** *Ae. tauschii* AS2388{10822}. **ma:** *Xwmc617-4DS* - 34.6 cM - *YrAS2388* - 1.7 cM - *Xwmc285-4DS*{10822}.

YrCle{186}. 4B{186}. **v2:** Clement *Yr9*{186}.

YrCK{10220,10221}. Temperature sensitive {10219} 2DS{10220}. **v:** Cook *Yr34*{10219,10220,10221}; Sunco *Yr34*{10220}.

YrCN17{10562,10686}. Derived from *S. cereale* 1B, 1BL, 1RS{10562,10686}. **v:** Chuannong 17{10686}; CN12{10562}; CN17{10562}; CN18{10562}. **dv:** *S. cereale* R14{10686}. **al:** *S. cereale* L155{10562}.

YrD{185}. 6A{185}. **v:** Druchamp{185,185}.

YrDa1{186}. 1A{186}. **v2:** Daws *YrDa2*{186}.

YrDa2{186}. 5D{186}. **v2:** Daws *YrDa1*{186}.

YrDru{184,185}. 5B{184}.6B{185}. **v:** Druchamp{184,185}.

YrDru2{184}. 6A{184}. **v:** Druchamp{184}.

YrExp1{10601}. 1BL{10601}. **v2:** Express *YrExp2*{10601}. **ma:** *Xwgp78-1B* - 4.2 cM - *YrExp1* - 3.4 cM - *Xwmc631-1B*{10601}.

YrExp2{10601}. 5BL{10601}. **v2:** Express *YrExp1*{10601}. **ma:** *Xgwm639-5B* - 9.2 cM - *Xwgp81-5B* - 1 cM - *YrExp2* - 0.7 cM - *Xwgp82-5B*{10601}.
Based on the presence of the nearest flanking markers *YrExp2* was postulated in Expresso, Blanca Grande, Buck Pronto and Jeff/Pronto {10601}.

YrH46{184}. 6A{184}. **v2:** Hybrid 46 *Yr4b*{184}.
Not the same gene as *YrDru2* {184}.

YrH52{0003}. 1BS{0003}. **tv:** *T. dicocoides* H52{0003}. **ma:** distal ...*Yr15* - 9.6 cM - *YrH52* - 1.4 cM - *Nor-B1* - 0.8 cM - *Xgwm264a* - 0.6 cM - *Xgwm18*{0003}; *Xgmw273a* - 2.7 cM - *YrH52* - 1.3 cM - *Xgwm413/Nor1*...centromere{0108}.

YrHVII{186}. 4A{186}. **v2:** Heines VII *Yr2 Yr25*{186}.

YrMin. 4A{184}. **v:** Minister{184}.

YrMor{186}. 4B{186}. **v2:** Moro *Yr10*{186}. **ma:** The development of an STS marker, derived from an AFLP fragment, that co-segregates with *YrMor* was reported in {0357}.

YrND. 4A{184}. **v2:** Nord Desprez *Yr3a Yr4a*{184}.
May be the same as *YrMin* {184}.

YrP81{10696}. 2BS{10696}. **v:** P81{10696}; Xu29{10696}. **ma:** *Xgwm429-2B* - 1.8 cM - *YrP81* - 4.1 cM - *Xwmc770-2B*{10696}.

YrR61{10914}. [*QYr.uga-2AS*{10914}]. 2AS{10914}. **v:** Pioneer 26R61=PI 612056{10914}.

YrR212{10562}. Derived from *S. cereale* 1B, 1BL.1RS{10562}. **v:** R185{10562}; R205{10562}; R212{10562}. **al:** *S. cereale* R212{10562}.

YrS{185}. 3B{185}. **v:** Stephens{185}.

YrS2199{10618}. 2BL{10618}. **bin:** 2BL0.89-1.00{10618}. **v:** S2199{10618}. **ma:** *Xgwm120-3B* - 11.0 cM - *YrS2199* - 0.7 cM - *Xdp269-2B*{10618}.

YrSte{184}. 2B{184}. **v:** Stephens{184}.

YrSte2. Stephens {184} 3B{184}.

YrSP{10018}. 2BS{10018}. **i:** Cx1=Avocet S*4/Spaldings Prolific{10018}. **v2:** Spaldings Prolific *Yr25*{10018}.

YrSp{10352}. Allelic with *Yr5* and *Yr7* {10759} [*YrSP*{10018}]. 2B{10352,10018}.Probably 2BL. **i:** Avocet*3/Spaldings Prolific{10018}; Taichung*6/Spaldings Prolific{10352}. **v:** Spaldings Prolific{10352,10018}. **ma:** *YrSp* - *Xwmc-2B*, 12.1 cM{10352}.

YrTye{186}. 6D{186}. **v:** Tyee{186}.

YrTr1{186}. 6D{186}. **v2:** Tres *YrTr2*{186}.

YrTr2{186}. 3A{186}. **v2:** Tres *YrTr1*{186}.

YrYam{184,185}. 4B{185}. **v2:** Yamhill *Yr2 Yr3a Yr4a*{185}.

YrZH84{10331}. 7BL{10331}. **v:** Annong 7959{10331}; Zhoumai 11{10331}; Zhoumai 12{10331}. **v2:** Zhou 8425B *Yr9*{10331}. **ma:** *Xwmc276-7B* - 0.6 cM - *Xcfa2040-7B* - *YrZH84* - 4.8 cM - *Xbarc32-7B*{10331}.

YrV23{10370}. Presumed to be *Yr3a* 2B{184}. **v:** Vilmorin 23{10370}; Vilmorin{184}.
Allelic but not the same as *YrSte* {184}.

Yrns-B1{0033}. 3BS{0033}. **v:** Lgst.79-74{0033}. **ma:** *Xgwm493* (distal) - 21 cM - *Yrns-B1*{0033}; As a QTL, *Yrns-B1* was located in a 3 cM interval between *Xgwm493-3B* and *Xgwm1329-3B*{10383}.

Yrxy1{10829}. High temperature resistance **v:** Mingxian 169/Xiaoyan 54 F_3-4-14{10829}. **v2:** Xiaoyan 54 *Yrxy2*{10829}. **ma:** *Xbarc49-7AS* - 15.8 cM - *Yrxy1* with closer flanking RGA markers{10829}.

Yrxy2{10829}. High temperature resistance **v:** Mingxian 169/Xiaoyan 54 F_3-4-30{10829}. **v2:** Xiaoyan 54 *Yrxy1*{10829}. **ma:** *Xwmc794-2AS* - 4.0 cM - *Yrxy2* - 6.4 cM - *Xbarc5-2AL*{10829}.

100.3. Stripe rust QTLs

Two QTLs in Camp Remy/Michigan Amber were located on chromosome 2BL (*QYR1*, LOD score 12) and 2AL (*QYR2*, LOD 2.2) {0287}. Four QTLs were scored in the ITMI population. The most effective (*QYR3*, LOD 7.4) on chromosome 2BS was probably *Yr27*, the others were located in 7DS (*QYR4*, LOD 3.4), 5A (*QYR5*, LOD 2.8), 3D (*QYR6*, LOD 2.8) and 6DL(*QYR7*, LOD 2.4) {0287}.

Camp Remy/Recital: 217 RILs. Six QTLs for APR were detected over 4 years. *QYr.inra-2BL* (R^2=0.42-0.61) corresponded largely to seedling resistance gene *Rsp* and possibly *Yr7*. The other genes were *Qyr.inra-2AL*, *QYr.inra-2BL*, *QYr.inra-2DS* (perhaps *Yr16*), *QYr.inra-5BL.1* and *QYr.inra-5BL.2* {10279}.

Seven QTLs were identified for stripe rust severity in a joint analysis of five datasets from a Fukuhokomugi/Oligoculm doubled haploid population {10060}. Their location, associated marker, percentage variation explained, and genotype contributing to enhanced resistance at that locus, are listed below.

3BS; *Xgwm389-3B*; 0.2-4.9%; Oligoculm {10060}.
4BL; *Xgwm538-4B*; 1.8-12.3%; Oligoculm {10060}.
4DL; *Xwmc399-4D*; 2.5-8.0%; Oligoculm {10060.}
5BL; *Xwmc415-5B*; 2.4-16.1%; Oligoculm {10060}.
6BS(centromeric); *Xgwm935-6B*; 0.5-3.8%; Oligoculm {10060}.
7BS; *Xgwm935-7B*; 1-5.2%; Oligoculm {10060}.
7DS; *Xgwm295-7D*; 10.7-23.7%; Fukuho {10060}; the 7DS QTL was probably *Yr18* {10060}.

Four QTLs were identified for stripe rust infection in a joint analysis of three datasets from a Fukuhokomugi/Oligoculm doubled haploid population {10060}. Their location, associated marker, percentage variation explained and parent contributing to enhanced resistance at that locus are listed below.

2DL; *Xgwm349-2D*; 6.5-9.6%; Fukuho {10060}.
3BS; *Xgwm389-3B*; 15.1-24.5%; Oligoculm{10060}. The 3BS QTL may be *Yr30* {10060}.
5BL; *Xwmc415-5B*; 6.4-12.7%; Oligoculm {10060}.
7BL; *Xwmc166-7B*; 2.5-9%; Oligoculm {10060}.

Otane (R)/Tiritea (S) DH population: QTL in 7DS (probably *Yr18*), 5DL (from Otane) and 7BL (Tiritea) {10150}. Interval mapping of 7DS indicated that the presumed *Yr18* was 7 cM from *Xgwm44-7D* {10150}.

Kariega/Avocet S DH population: Two QTLs ***QYr.sgi-7D*** (probably *Yr18*) and ***QYr.sgi.2B.1*** accounted for 29 and 30%, respectively, of the phenotypic variation for stripe rust response. The nearest marker to the latter was *Xgwm148-2B* {10184}.

Four QTLs were detected in a multiple cross analysis {10283}: Chromosome 2AL (probably *Yr32* in Deben, Kris and Soloist), 2AS (probably *Yr17* in Kris), 2BL (*Xwmc149-2B* - *Xwmc317a-2B* in Deben) and 6BL (*Xwmc397-6B* - *Xwmc105b-6B* in Soloist and Kris).

Avocet S/Pavon 76: QTL identified in 1BL (*Xgwm259*), 3BS (PstAATMseCAC2), 4BL (*Xgwm495*), 6AL (*Xgwm617*), 6BL (PstAAGGMseCGA1) {10443}.

T. monococcum PAU14087 (resistant)/*T. boeoticum* PAU5088 (resistant): RIL population: One adult plant resistance QTL identified in each parent and named *QYrtm.pau-2A* (in a 3.6

cM interval between *Xwmc407-2A* and *Xwmc170-2A*; R^2 = 0.14) and *QYrtb.pau-5A* (in a 8.9 cM interval between *Xbarc151-5A* and *Xcfd12-5A*; R^2 = 0.24) {10518}.

Luke (R) /Aquileja (R): Two QTLs for high-temperature adult plan resistance, *QYRlu.cau-2BS.1* (distal, flanked by *Xwmc154-2B* and *Xgwm148-2B*, R^2 = 0.366) and *QYrl.cau-2BS.2* (proximal, flanked by *Xgwm148-2B* and *Xbarc167-2B*, R^2 = 0.415) from Luke, and *QYraq.cau-2BL* (flanked by *Xwmc175-2B* and *Xwmc332-2B*, R^2 = 0.615) in Aquileja for stripe number {10582}.

Avocet S / Attila: QTLs were located on chromosomes 2BS (probably *Yr27*), 2BL (a race-specific effect) and 7BL (*XP32/M59 - Xgwm344-7B* {10586}.

Guardian / Avocet S: F3 lines. One major QTL, *QPst.jic-1BL* (*Xgwm818-1 - Xgwm259-1B*, R^2 up to 0.45), and two minor resistance QTLs on chromosomes 2D and 4B originating from Guardian {10589}. The major QTL was in the region of *Yr29*.

Stephens / Michigan Amber: Two QTLs for high temperature APR were located in chromosome 6BS; *QYrst.wgp-6BS.1* located in a 3.9 cM region flanked by *Xbarc101-6B* and *Xbarc136-6B* and *QYrst.wgp-6BS.2* located in a 17.5 cM region flanked by *Xgwm132-6B* and *Xgdm113-6B* {10602}.

Pingyuan 50 (R) / Mingxian 169 (S): DH population: APR: *QYrcaas-2BS* (*Xbarc13-2BS) - Xbarc230-2BS*, R^2=0.05-0.09), *QYr.caas-5AL*(*Xwmc410-5AL - Xbarc261-5AL*, R^2=0.05-0.2), *QYrcaas-6BS*(*Xgwm361-6BS - Xbarc136-6BS*, R^2=0.05-0.08) {10693}.

Renan (R) / Recital (S) RIL population: Tested for AUDPC in 1995/6 and 2005/6 with pathogen isolates avirulent and virulent, respectively, for *Yr17*:*QYr.inra-2AS.2*, (=*Yr17*), R^2=0.45, 1995/6; *QYr.inra-2AS.1*, R^2=0.9, 2005/6; *QYr.inra-2BS*, R^2=0.11 & 0.13, *QYr.inra-3Bcent*, R^2=0.06 in 2005/6; *QYr.inra-6B*, R^2=0.04 & 0.06; from Renan; and *QYr.inra-2AS.1*, R^2=0.09; *QYr.inra-3DS*, R^2=0.08 & 0.12 from Recital. Other QTLs were effective only at certain growth stages {10689}.

Express / Avocet S: RIL population: Relative AUDPC for high temperature APR was controlled by *QYrex.wgp-6AS*, R^2=0.326, interval *Xgwm334-6A - Xgwp56-6A*; *QYrex.wgp-3BS*, R^2=0.274, interval *Xgwm299-3B - Xwgp66-3B, QYrex.wgp.1BL*, R^2=0.094, interval *Xwmc631-1B - Xwgp78-1B* {10672}. When rust phenotyping was based on infection type only the 6S and 3BL QTLs were evident {10672}.
Alcedo (R) / Brigadier (S): DH population: Two major QTLs *QPst.jic-2DL* (R^2 up to 0.36) and *QPst.jic-4BL* (R^2 up to 0.29) for percent infection contributed be Alcedo {10785}. A seedling-expressed QTL was located at the same position in 2DL {10774}.

Flinor (R) / Mingxian 169 (S): Two independent QTLs for high temperature (24/18C) seedling resistance located in chromosome 5BL, designated *QYr-tem-5B.1* (*Xbarc89 - Xgwm67*) and *QYr-tem-5B.2* (*Xbarc140n - Xwmc235*) and R^2 = 0.37 and 0.33, respectively {10797}.

Kukri (MR) / Janz (MR): DH population: Tested with pre- and post-2003 Australian *Pst* races in several environments. *QYr.sun-7B* (Kukri) and *Qyr.sun-7D*(=*Yr18*)) (Janz) were consistent over environments; *QYr.sun-1B, -5B* and *-6B* were detected in most environments and *QYr.sun-3B* was identified in only one season. Two genes, *QYR.sun-1A* from Janz and *QYr.sun-2A* from Kukri, were detected only with pre- and post-2003 races, respectively, and likely contributed to differential responses of these cultivars to the two groups of races {10751}.

Pioneer 26R61(R)/AGS2000(S): RIL population: Two QTLs, *QYr.uga-2AS* ($R^2=0.56$) flanked by *Xbarc124-2A* and *Xgwm359-2A* (also named *YrR61*) and *QYr.uga-6AS* ($R^2=0.06$) {10914}. Minor QTLs were also on other chromosomes.

UC1110(MR)/PI 610750(MR): RIL population: *QYr.ucw-3BS* ex UC1110, $R^2=0.22$, associated with *Xgwm522-3B.1*. This marker differs from *Xgwm533-3B.2* that is associated with *Yr30* {10705}; *QYr.ucw-5AL*, $R^2=0.1$, ex PI 61075 - syn. *Yr48* {10705}; *QYr.ucw-2BS*, $R^2=0.045$, ex UC1110, located in the centromeric region near *Xwmc474-2BS* {10705}, *Qyr.ucw-2AS*, $R^2=0.023$, ex PI 61725, near *wPt-5839* {10705}.

Stephens I/Platte(S): RIL population: 13 QTLs were identified across several environments; significant QTL x environment interactions suggested that plant stage specificity, pathogen genotype and temperature as well as host genotype were important in determining rust response {10890}.

101. Reaction to *Puccinia triticina*

Disease: Brown rust, leaf rust.

101.1. Genes for resistance

Lr1{047}. 1B{1409}.5D{954}.5DL{945}. **i:** Centenario/6*Thatcher{317}; Malakoff/6*Prelude{317}; Wichita*4/Malakoff{613}. **v:** Line 87E03-S2B1{10561}; Centenario{317}; Chicora 'S'{143}; Daws (heterogeneous){1019}; Dirkwin{1019}; Glenlea{1255,976}; Halle 9H37{074}; Hyslop{1019}; Luke {heterogeneous}{1019}; Malakoff{047}; McDermid{1019}; Mexico 120{933}; Newton{143,1024,1023}; Norco{1019}; Shabati Sonora{842}; Sonora 64{842}; Tarsa{842}; Uruguay{954}; Walliday{1019}. **v2:** Blueboy *Lr10*{143}; Blueboy II *Lr10 Lr24*{143}; Erythrospermum 142 and 953 *Lr3*{074}; Laura *Lr10 Lr34*{712}; Norka *Lr20*{1552}; Plainsman V *Lr3*{1024}; Suneca *Lr13*{485}. **dv:** Several *Ae. tauschii* accessions{10191}. **ma:** Co-seg. with *Xpsr567-5D* and *Xglk621-5D* in a Frisal/*Lr1* resistant line. pTAG621 was converted to a diagnostic STS{354}; Terminally located{10189}; In *Ae. tauschii* recombination in the region was 5-10X that in common wheat, gene order *Xpsr567-5D - Lr1 - Xabc718-5D*{10191}; Mapped to a 0.7 cM interval in *Ae. tauschii* and a 0.075 cM interval in wheat{10408}; A candidate gene for *Lr1*, *Lr1RGA1*, encoding a CC-NBS-LRR protein, cosegregated with *Lr1*{10408}; Co-segregation with RGA567-5{10561}. **c:** *Lr1* is a member of a multigene family (PSR567), has a CC-NBS-LRR structure, and produces a protein of 1,344 aa, EF567063{10561}.

Lr2. 1B{1409}.2DS{843,942}.

Lr2a{320}. [*Lr2*{047}]. **i:** Prelude*6/Webster{320}; Red Bobs*6/Webster{320}; Webster/6*Thatcher{306}; Wichita*4/Webster{613}. **v:** Eureka CI 17738{143}; Festiguay{843}; Webster{047}. **v2:** Alex *Lr10*{976}; Ck 9835 *Lr9*{10146}; Ck 9663 *Lr2 Lr10*{10146}; Guard *Lr10*{976}; James *Lr10*{976}; Len *Lr10*{976}; Marshall *Lr10*{976}; Mediterranean W1728 *Lr3*{1369}; Shield *Lr3 Lr10*{198}; Waldron *Lr10*{143}.

Lr2b{320}. [*Lr2*^{2}{1409}]. **i:** Prelude*6/Carina{320}; Red Bobs*6/Carina{320}; Thatcher*6/Carina{320}; Wichita/4*Carina{613}. **v:** Carina{613}.

Lr2c{320}. [*Lr2*^{3}{1409}]. **i:** Prelude*5/Brevit{320}; Prelude*6/Loros{320}; Red Bobs*6/Brevit{320}; Red Bobs*6/Loros{320}; Thatcher*4/Brevit{320};

Thatcher*6/Loros{320}; Wichita*4/Brevit{613}; Wichita*4/Loros{613}. **v:** Brevit{613}; Loros{317,1257}.

Lr3{047}. Because *Lr3* appears to be a complex locus {486} Democrat and Democrat/6* Thatcher should be accepted as standards. There is evidence to suggest that the allele in Mentana, and therefore many derivatives, is *Lr3b* {939}. If this is correct, many genotypes listed under *Lr3a* are likely to be *Lr3b*.

Durum cv. Storlom likely carries *Lr3a* or *Lr3b* {10469}. Cv. Camayo was considered to have a closely linked gene, or *Lr3* allele {10469}. Resistance in Storlom co-segregated with an STS derivative of *Xmwg798-6B*. All three Thatcher NILs with named *Lr3* alleles carried the STS marker {10469}.

Lr3a{10028}. [*Lr3*{047}]. 6B{549}.6BL{939}. **i:** Democrat/6*Thatcher{318}; Wichita*4/ Mediterranean{613}. **v:** Belocerkovskaja 289{074}; Bennett{1024}; Democrat{047}; Fertodi 293{074}; Gage{1024}; Hana{068}; Homestead{1024}; Ilyitchovka{075}; Juna{075}; Jubilejne{068}; Kawvale{143}; Lancota{1024}; Mara{068}; Mediterranean{047}; Mediterranean W3732{1369}; Mentana{842}; Mironovskaya 264 & 808{074}; Odra{075}; Osetinskaya{074}; Ottawa{143}; Pawnee{1408}; Ponca{143}; Rannaja 12{074}; Shawnee{143}; Shirahada{842}; Skorospelka 3b{074}; Sledkovicova K1004{074}; Viginta{068}; Warrior{143,1024}; Yubileynaya{075}. **v2:** Amika *Lr26*{076}; Bezostaya 1 *Lr34*{074}; Bowie *Lr14b*{319}; Erythrospermum 142 & 953 *Lr1*{074}; Istra *Lr26*{076}; Mediterranean W1728 *Lr2a*{1369}; Plainsman V *Lr1*{1024}; Shield *Lr2a Lr10*{198}; Solaris *Lr26*{076}; See also{069}. **tv:** Storlom{10469}. **ma:** Co-segregation with *Xmwg798-6B*{9921,10469}; cDNA marker TaR16 was completely linked to *Lr3* in a population of 109 gametes{10058}; *UBC840*$_{540}$ - *Lr3a*, 6 cM{10263}.

Lr3b{486, 10028}. [*Lr3bg*{486}]. **i:** Thatcher*6/Bage; RL6094 = Tc*6/T6{307}. **v:** Bage{486}. **v2:** T6 *Lr16*{307}.

Lr3c{486, 10028}. [*Lr3ka*{486}]. **i:** Tc*6/Klein Aniversario. **v:** Blava{10345}; Klein Aniversario{486}.

Lr4, Lr5, Lr6, Lr7, Lr8{365}. **v:** Purdue Selection 3369-61-1-10 = Waban{365}; Not available as separate single-gene lines.

Lr9{1408}. Derived from *Ae. umbellulata*. 6B{954,1296,1299}.6BL = T6BS.6BL-6U#1L{389}. **i:** T47 = Transfer = CS + *Lr9*{1408}; Thatcher*6/Transfer; Wichita*4/ Transfer{613}; Lines listed in{10244}. **v:** Abe{143}; Arthur 71{1320,1024}; Clemson 201{465}; McNair 701 & 2203{143}; PI 468940{1439}; Riley 67{1320,1024}; Sullivan{1110}; Transfer{1296}. **v2:** Ck 9835 *Lr2a*{10146}; Ck 9663 *Lr2a Lr10*{10146}; Lockett *Lr24*{10146}; Oasis *Lr11*{1109}. **ma:** Co-seg with *XksuD27-6B*{048}; co-seg with *Xmwg684-6B* and STS *Xsfr1*{1272}; *Lr9* - 8 cM - *Xpsr546-6B*{1272}; SCAR markers were developed in {10244}.

The structures of additional translocations are given in {389}.

Lr10{199}. [*LrL*{031}]. 1A{312,546}.1AS{939}. **i:** Exchange/6*Thatcher{306}; Gabo/6*Thatcher{306}; Lee/6*Thatcher{306}; Selkirk/6*Thatcher{306}; Timstein/6*Thatcher{306}. **s:** CS*5/Timstein 1A{939}; CS/7*Kenya Farmer 1A{939}. **v:** Centurk{1024}; Centurk 78{1024}; Concho{143}; Federation{939}; Mayo 52{031}; Mayo 54{031}; Parker{546,1024}; Rocky{1024}; Scout 66{02101}; Sinton{1256}; Tascosa{143}; TAM-105{055}; Unknown accessions{208}; See also{0337}. **v2:** Alex *Lr2a*{976}; Blueboy *Lr1*{143}; Blueboy II *Lr1 Lr24*{143}; Ck 9663 *Lr2a Lr9*{10146}; Era *Lr13*{143}; Exchange *Lr12 Lr16*{031}; Gabo *Lr23*{031}; Guard *Lr2a*{976}; James *Lr2a*{976}; Kenya Farmer *Lr23*{939}; Laura *Lr1 Lr34*{712}; Lee *Lr23*{031}; Len *Lr2a*{976}; Marshall *Lr2a*{976}; Parker 76 *Lr24*{143}; Selkirk *Lr14a Lr16*{031,199}; Shield *Lr2a Lr3*{198}; Timstein *Lr23*{031}; Waldron *Lr2a*{143}; Warden *Lr16*{031}. **tv:** Altar 82{10760}; Russello{10760}. **ma:** *Xcdo426-1A* - 5.1 cM - *Lr10*{1058}; *Lr10* - 8 cM - *Glu-A3*{355}; cosegregation with *Xsfr1(Lrk10-1A)* and *Xsfrp1(Lrk10-1A)*{1270}; complete linkage with

Xsfr1(Lrk10-1A), which encodes a protein kinase{639}. **c:** *Lr10* was cloned - it has a CC-NBS-LRR structure, syn, *T10rga1* GenBank AY270157{10442}; A second CC-NBS-LRR gene, *RGA2*, is required for expression of *Lr10* in tetraploid and hexaploid wheats{10760}. ***Lrk10***. A receptor-like kinase. The locus *Xsfr1(Lrk10)-1A*, detected by the probe Lrk10, is completely linked with *Lr10* in chromosome 1AS {356}. The gene encodes a receptor-like kinase with extracellular and kinase domains {0297}. Using probe pLrk10-A, developed from the extracellular domain, 6 homologues were found in chromosomes 1A (1), 1B (3) and 1D (2) as well as group 1 chromosomes of *T. monococcum*, *Ae. tauschii* and barley {0296,0294}. Probes based on the kinase domain identified further homologues in chromosomes 3AS and 3BS as well as the corresponding regions in rice and maize {0294}. Both orthologous and paralogous evolution were suggested.

Lr11{1409}. 2A{1409}. **i:** Thatcher*6/Hussar{306}; Wichita*4/Hussar{613}. **v:** Bulgaria 88{142}; Hart{1024}; Hazen{049}; Hussar{1409}; Panola{10830}; Pioneer 2850{0523}; Pocahontas{10146}; Saluda{10146,10699}. **v2:** Ck9803 *Lr18*{10595}; FFR 524 *Lr18*{10595}; Jamestown *Lr18*{10830}; Karl 92 *Lr3 Lr10*{02101}; Oasis *Lr9*{143}; Pioneer 2684 *Lr18*{10595}; SS520 *Lr18*{10595}.

Lr12{326}. Adult plant reaction. 4B{312}. **i:** Exchange/6*Thatcher{306}. **v:** Opal{306}. **v2:** AC Domain *Lr10 Lr34*{0228}; Caldwell *Lr14a*{10787}; Chinese Spring *Lr34*{301}; Exchange *Lr10 Lr16*{326}; Sturdy *Lr13*{301}; Unknown accessions{208}.
Possible commonality with *Lr31*.

Lr13{326}. Although originally described as a gene for adult plant reaction {032,326}, *Lr13* can be detected at the seedling stage especially at high temperatures {939,1156}. 2BS{939}. **i:** Tc*7/Frontana = RL4031{306}; fifteen Thatcher lines with 2-gene combinations{711}. **v:** This gene is very widespread{939}; Hereward{0288}; Hustler{608}; Kinsman{608}; Kenya Plume{1370}; Manitou{326}; Mardler{608}; Maris Huntsman{608}; Moulin{0288}; Napayo{070}; Neepawa{143}; Norman{608}; Pastiche{0288}; Polk{143}; Virtue{608}. **v2:** AC Barrie *Lr6* {10178}; Beaver *Lr26*{1032}; BH1146 *Lr34*{0268}; Biggar *Lr14a*{712}; Chris *Lr34*; Columbus *Lr16*{1258}; Cumpas 88 *Lr26*{1373}; Era *Lr10*{143}; Frontana *Lr34*{032,326,1374}; Genesis *Lr14a*{712}; Hartog *Lr1 Lr46*{127}; Hobbit *Lr17a*{608}; Hobbit Sib *Lr17a*{1350}; Inia 66 *Lr14a Lr17*{1373}; Klein Aniversario *Lr3ka*{032}; Kenyon *Lr16*{300}; Lerma Rojo 64 *Lr17a Lr34*{1373}; Oasis 86 *Lr19*{1373}; Parula *Lr34 Lr46*{1374}; Suneca *Lr1*{485}; Yecora *Lr1*{1374}. **ma:** *Xpsr912-2B* - 9.1 cM - *Lr13* - 7.9 cM - *Xbcd1709-2B* - 9.8 cM - Cent.{0088}; *Lr13* - 10.7 and 10.3 cM - *Xgwm630-2BS*{10463}; *Xbarc163-2B* - 5.1 cM - *Lr13* - 8.7 cM - *Xstm773b-2B*{0329}.

Lr14.

Lr14a{319,964}. [*LrLla*{10520}]. 7B{964}.7BL{770}. **i:** Selkirk/6*Thatcher{319}. **s:** CS*6/Hope 7B{964}. **v:** Aotea{964}; Brigand{608}; Gala{964}; Glenwari{964}; Hofed{964}; Hope{964}; H-44{964}; Lawrence{964}; Redman{964}; Regent{964}; Renown{964}; Spica{964}. **v2:** Biggar *Lr13*{712}; Brambling *Lr23 Lr34*{10563}; Caldwell *Lr12*{10787}; Genesis *Lr13*{712}; Inia 66 *Lr13 Lr17a*{939}; Selkirk *Lr10 Lr16*{319}. **tv:** Lloreta INIA{10520}; Somateria{10520}. **ma:** *Xwmc273-7B* - 13 cM - *Lr14a* - 10 cM - *Xgwm344-7B*{10520}.

The *Lr14* region in tetraploid wheat harbours *Qlr.ubo-7B.2*, a gene that confers durable resistance in durums {10734, 10736} and that is present in many Italian, CIMMYT and ICARDA durum cultivars {10736}. The relationship of this gene described as *Lr14c* (reference genotype Creso) in {10735} remains to be determined. Reasons for considering *Lr14c* as a unique allele are given in {10735}. In association mapping the presence of *QLr.ubo-7B.2* was predicted with 96% accuracy based on appropriate alleles of *Xcfa2257.2*, *Xgwm344.2* and *Xwmc10* in the distal region of chromosome 7BL {10736}.

Lr14b{319}. **i:** Maria Escobar/6*Thatcher{319}. **v:** Weebill 1{10571}. **v2:** Bowie *Lr3*{9226}; Maria Escobar *Lr17*{319}; Rafaela *Lr17*{314}.

Lr14ab. **i:** Lr14a/6*Thatcher//Lr14b/6*Thatcher Seln{319}.

Lr15{843}. 2DS{843,942}. **i:** Thatcher*6/Kenya W1483{306}. **v:** Kenya W1483{843}. Probably allelic with *Lr2*.

Lr16{318}. The following chromosome locations are consistant with the finding that the first location was based on the use of a Rescue monosomic series. Rescue differs from CS by a 2B-4B translocation {939}. *Lr16* is always asociated with *Sr23*. [*LrE*{031}]. 4B{312}.2BS{939, 10170}. **i:** Exchange/6*Thatcher{306}; RL6096 = Tc*6/T6{307}. **v:** AC Domain{10170}; AC Foremost{10170}; Arapahoe{02101}; Brule{02101}; Ciano 79{1373}; Etoile de Choisy{074}; Imuris 79{1373}; McKenzie{10170}; Millenium{02101}; Papago 86{1373}; Redland{02101}; Vista{02101}. **v2:** AC Barrie *Lr13*{10178}; Columbus (heterogeneous) *Lr13*{1258}; Exchange *Lr10 Lr12*{031}; Kenyon *Lr13*{300}; Selkirk *Lr10 Lr14a*{031}; T6 *Lr3bg*{307}; Warden *Lr10*{031}. **ma:** Distally located: *Lr16* - *Xwmc764-2*, 1, 9 and 3 cM, respectively, in crosses RL4452/AC Domain, BW278/AC Foremost and HY644/McKenzie{10170,10189}.

Lr17{318}. [*Lr17a*]. **v:** Santa Fe{10830}.

Lr17a{318},{1350}. [*Lr17*]. 2A{314}.2AS{062}. **bin:** 2AS-5{10572}. **i:** Klein Lucero/6*Prelude{318}; Klein Lucero/6*Thatcher{318}; Maria Escobar/4*Thatcher{318}. **v:** EAP 26127{314}; Jagger{0338,10146,10346}; Jupateco{939}; Klein Lucero{318}; Santa Fe{10830}; TAM111{10595}; Trego{10572}. **v2:** Fuller *Lr39*{10699}; Inia 66 *Lr13 Lr14a*{9010}; Lerma Rojo 64 *Lr13 Lr34*{1373}; Maria Escobar *Lr14b*{318}; Rafaela *Lr14b*{314}. **ma:** *Xbarc123-2A* - 4.8 cM - *Xgwm636-2A* - 4.0 cM - *Lr17a*{10571}; *Xgwm614-2A* - 0.7 cM - *Lr17a* - *Xwmc407-2A*{10572}; *Lr17a* - 3.7 cM - *Xbarc212-2a*{10795}.

Lr17b{1350}. [*LrH*{970},*WBR2*{615}]. 2A{1350}. **v:** Brock{0260}; Harrier{1350}; Maris Fundin{1350}; Norin 10-Brevor, 14{1350}; Norman{1350}. **v2:** Contra *Lr13*{10345}; Hobbit Sib = Dwarf A *Lr13*{1350}; Kalasz *Lr13*{10345}; Riband *Lr13*{10345}; Sarka *Lr13*{10345}; Tarso *Lr26*{0229}.

Lr18{318}. Derived from *T. timopheevii*. Independently derived lines with *Lr18* possess a unique N band terminally located in chromosome 5BL {1614}. Low seedling responses conferred by *Lr18* are most effective at 15-18C. With increasing temperatures the response becomes less effective and ineffective at 25-27C {935, see also, 1614}. 5BL {935} = T5BS.5BL-5G#1L{389}. **i:** Africa 43/7*Thatcher{318}; Red Egyptian PI 170925/6*Thatcher{318}. **v:** Africa 43{318}; Red Egyptian PI 170925{318}; Red Egyptian PI 17016-2c{318}; Sabikei 12{935}; Timvera{935}; Timvera Derivative{935}; Certain WYR accessions{935}; FTF{1614}; Several Sabikei lines including Sabikei 12{1614}. **v2:** Ck9803 *Lr11*{10595}; FFR 524 *Lr11*{10595}; Jamestown *Lr11*{10830}; Pioneer 2684 *Lr11*{10595}; SS520 *Lr11*{10595}.

A resistance gene, *LrTt2*, in line 842-2 was located on chromosome 5BL in a similar region to *Lr18*. The claim that *Lr18* and *LrTt2* were different based on low seedling infection types, but the genetic background were different {10752}.

Lr19{140}. Derived from *Th. elongatum*.

7DL = T7DS.7DL-7Ae#1L{291,956,1323,388,657,389}. **i:** Agatha = T4 = TC + *Lr19*{956,1323}; Sears trasfer 7D-7Ag no.1{10255}. **v:** Dobrynya{10821}; Ekada 6{10821}; L503{1346}; L505{10821}; L513{1346}; Mutant 28{598}; Samsar{0108}; Sunnan{684}; Volgouralskaya{10821}; See *Sr25*.

7AL. **v:** Lines I-22 and I-23{10255}. **v2:** Kinelskaya Niva *Lr23*{10821}; Oasis 86 *Lr13*{1373}.

7AL. **tv:** This translocation was transferred to durum wheat and engineered to produce normally inherited secondary recombinants with smaller alien segments, such as R5-2-10, and tertiary recombinants such as R1{10633}. **ma:** Located in the *Xwg420-7Ag* - *Xmwg2062-7Ag* interval{10255}; RAPD, SCAR and SSR markers co-inciding with, or flanking, *Lr19* in a derivative of Knott's Agatha Mutant 28 (C80.1) were reported in{10379}.

c: A candidate sequence, AG15, with a 1,258 amino acid sequence and a CC-NBS-LRR structure was reported in{10575}.

The chromosome with *Lr19* in Indis is probably identical to that in Agatha {1162}.

7DL = T7DS.7DL-7Ae#1-7DL {388}. **v:** Mutant 235 {681}.

7AL = T7A-7Ae#1 {330}. **v:** Sears' 7A-7Ag No.12 {330}

7BL {1163}. **v:** 88M22-149 {1163}; 4 further derivatives of 88M22-149 {0232}

7AgL {1304} = 7Ae#1L. **su:** Agrus. **ma:** Co-seg with 8 RFLP markers {048}; *Ep-D1c* - 0.33 cM - *Lr19* {1587}; cosegregation with *Ep-D1d* {974}; Prins *et al* {1162} studied 29 deletion mutants in Indis and determined the gene order: *Sd-1 - Xpsr105-7D- Xpsr129-7D - Lr19 - Wsp-D1 - Sr25 - Y*; The following gene order for the *Thinopyrum* segment is given in {0101}; Cent - *Sd1 - Xpsr165-7D - Xpsr105-7D -Xpsr129-7D - XcslH81-1 - Xwg380-7D - Xmwg2062-7D - Lr19 - Wsp-D1 - Sr25/Y*; An STS marker closely linked and distal to *Lr19* was developed from an AFLP {0273}.

Lr19 is usually associated with *Sr25*. Sears' transfer 7D-7Ag No. 11 carries neither *Lr19* nor *Sr25*. See *Lr29*.

Knott {681} obtained two mutants (28 and 235) of Agatha possessing *Lr19*, but with reduced levels of yellow pigment in the flour. Marais {890,892} obtained mutants and recombined lines with intermediate levels of, or no, yellow pigment. It was shown that recombinant line 88M22-149 lacked yellow pigment {1163}.

Secondary translocation line I-96 derived from Sears' 7D-7Ag no.1 involved *Lr19* being located in an intercalary segment with low yellow pigment and lacking *Sd1* {10255}.

Lr19 in lines I-22 and I-23 retaining yellow pigment but lacking *Sd1* was transferred to durum chromosome 7BL {10255}. One of the lines with the shortest 7Ag segment, *Lr19*-I49-299, was used in a further cycle of recombination {10278}.

Lr20{140}. 7AL{1305,1554}. **i:** Thatcher+Lr20. **s:** CS*5/Axminster 7A{1293}. **v:** Axminster{348,1175,1305}; Birdproof{1554}; Bonus{1554}; Converse{1554}; Festival{1554}; Kenora{1554}; Kenya W744{1554}; Maris Halberd{608}; Normandie{348,1554}; Sappo{608}; Sicco{310}; Thew{140,1552}; Timmo{608}. **v2:** Norka *Lr1*{1554}; See *Pm1* (Reaction to *Blumeria graminis*) & *Sr15* (Reaction to *Puccinia graminis*) with which *Lr20* is always associated. *Lr20* in Sicco appears to differ from that in Sappo, Timmo and Maris Halberd{310}; *Lr20* in Norka (*Lr1*+*Lr20*) may differ from that in Thew{939}. **ma:** Complete cosegregation of several markers including *Xcdo347-7A, Xpsr121-7A, Xpsr680-7A, Xpsr687-7A, Xbzh232(Tha)-7A, Xrgc607-7A* and *Xsts638-7A* with *Pm1* and *Lr20* was reported in {0323}; *Lr20 - STS638*, 7.1 cM{10263}.

Lr21{1241}. [*Lr40*{1200,10415}]. 1D{650}.1DL{1241}.1DS{448}. **i:** Thatcher*6/Tetra Canthatch/*Ae. tauschii* var. *meyeri* RL 5289{306}. **v:** Tetra Canthatch/*Ae. tauschii* var. *meyeri* RL 5289, RL 5406{648}; Lovitt{10766}; McKenzie{0228,10766}; WGRC2 = TA1649/3* Wichita{0299}; WGRC7 = Wichita/TA1649//2*Wichita{0299}. **v2:** AC Cora *Lr13*{713}; WGRC16 = TAM107*3/*Ae. tauschii* TA 2460 *Lr39*{220,10415}. **dv:** *Ae. tauschii* accessions: RL5289 = TA1599{1241}; *Ae. tauschii* TA2460 *Lr39*{220,10415}; TA1649{0299}; TA1691{0299}; TA2378{0299}; TA2470{0299}; TA2483{0299}; TA2495{0299}; TA2527{0299}; TA2528{0299}. **ma:** All members of the *Lr21* family carry a STS derivative of *XksuD14-1D* that has a resistance gene analogue structure{0299}; *XksuD14-1D* was reported to map 1.8 cM proximal to *Lr21* in{0375}; *Lr21* - 0 cM - *rgaYr10b* - 0.6 cM - *Xgdm33-1D*{0360}; *Xksu-1D* is part of *Lr21*{10420}. **c:** *Lr21* was cloned and shown to have a NBS-LRR structure{10420}.

A reconstituted effective *Lr21* allele (designated *Lr21-b*) was obtained as a rare (1/5,872) recombinant (accession TA4446) between *Lr21* pseudogenes in common wheat cultivars Fielder and Wichita {10620}.

Further haplotype analyses are reported in {10766}.

Lr22. 2DS{1241}.

Lr22a{1241}. Adult plant reaction. **i:** Neepawa*6/RL5404, RL4495{10467}; Thatcher*3//Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271{306}; Thatcher*7//Tetra-Canthatch/RL5271, RL 6044{10467}. **v:** Tetra Canthatch/*Ae. squarrosa* var. *strangulata* RL 5271, RL 5404{311}. **v2:** AC Minto *Lr11 Lr13*{713}. **dv:** *Ae. squarrosa* var. *strangulata* RL 5271. **ma:** *Xgwm296-2DS* - 2.0 cM - *Lr22a*{10446}; *Xgwm455-2D* - 1.5 cM - *Lr22a* - 2.9 cM - *Xgwm296-2D*{10467}.

Lr22b{298}. Adult plant reaction. **v:** Canthatch{298}; Marquis{970}; Thatcher{298}. This gene will be present in near-isogenic lines based on Thatcher.

Lr23{948}. [*LrG*{951}]. 2BS{948}. **i:** Lee FL 310/6*Thatcher{948}. **s:** CS*7/Kenya Farmer 2B{948}; CS*6/Timstein 2B{948}. **v:** Cranbrook{02119}; Crim{1091}; Hope/Timstein{1091}; I 310678{1091}; I 310685{1091}; I 349162{1091}; IWP94{10569}; K 45973{1091}; K 51070{1091}; Rocta{1091}. **v2:** Gamenya *Lr3*{1552}; Gabo *Lr10*{1552}; Kenya Farmer *Lr10*{1552}; Lee *Lr10*{1552}; Timstein *Lr10*{1552}; Brambling *Lr14a Lr34*{10563}. **tv:** Altar 84{1058}. **ma:** associated with *Xksu904(Per2)-2B*{0090}. A QTL, which is likely to correspond to *Lr23*, was identified in the Opata 85/W-7984 (ITMI) RI mapping population. The resistance was contributed by W-7974 {0090}.

Lr24. Derived from *Thin. elongatum*.

Always present with *Sr24* {956}. See *Sr24* (Reaction to *P. graminis*). [*LrAg*{141}]. 3DL{956,1389}. **v:** Cody{1284}; Cutter{10595}; Jagalene{10595}; McCormick{10595}; Ogallala{10595}; Osage{143}; Payne{1390,1024}; SST 23{1324}; SST 44 = T4R{1324}; Timpaw{1255}; Torres{128}; Wanken{1255}; Australian genotypes{0340}. **v2:** Blueboy II *Lr1 Lr10*{141}; Fox *Lr10*{141}; Lockett *Lr9*{10146}; Parker 76 *Lr10*{143,1024}; Siouxland *Lr26*{1283}. **ma:** Co-seg of *Lr24* in Agent with 8 RFLP markers; segment in Sears' 3D-3Ag#1 is shorter than in Agent{048}; Tagged with *Xpsr1203-6B*{1271}; cosegregation with RAPD marker that was converted to a SCAR{231}; Linked with SCAR marker SCS73$_{719}$ earlier thought to tag *Lr19*{10147}.

1BL {185} = T1BL.1BS-3Ae#1L{600}. **v:** Amigo{1463,600,185}; Teewon{600}. **ma:** SCAR markers were developed in {10368}.

A PCR marker, Sr24#12, was confirmed across all sources of *Lr24* {10257}.

Lr25. Derived from *S. cereale* cv. Rosen. 4BS{270,271,380,389}. **i:** Tc+Lr25 *Lr48*{10738}. **v:** Transec{273}; Transfed{269}; Always present with *Pm7*. **ma:** Cosegregation with a RAPD{1165}.

Revised to T4BS.4BL-5RL {543} and later to T4BS.4BL-2R#1L. *Lr25* is closely linked with *Lr48* {10738}.

Lr26. Derived from *S. cereale*. See also Reaction to *P. graminis, Sr31*; Reaction to *P. striiformis, Lr26*. 1R (1B).T1BL.1RS. **i:** MA1 and MA2 four breakpoint double translocation lines 1RS-1BS-1RS-1BS.1BL in Pavon{0084}. **v:** AGS 2000{10595}; Derivatives of Petkus rye - see *Yr9* (Reaction to *P. striifromis*) & *Sr31* (Reaction to *P. graminis*); Bacanora 88{1373}; Cougar{0267}; Pioneer 26R61{10595}; Rawhide (heterogeneous){0267}; GR876{753}; Iris{075}; Sabina{075}. **v2:** Beaver *Lr13*{10687}; Cumpas 88 *Lr13*{1373}; Istra *Lr3*{076}; Siouxland *Lr24*{1283}; Solaris *Lr3*{076}; Many wheats with *Lr26* also carry *Lr3*. Amika {heterogeneous} *Lr3*{076}; See also{310}. **tv:** Cando*2/Veery, KS91WGRC14{381}. **ma:** Several markers tightly linked with *Lr26* were identified in {0377}.

1BS/1RS recombinants 4.4 cM proximal to *Gli-B1/Glu-B3* {0084}. Hanusova *et al.* {492} identified 127 wheats with *Lr26* but only 16 of them were listed.

Lr27{1367}. One of two complementary genes; the second gene, *Lr31*, is located in chromosome 4BS {1367}. The following wheats have both *Lr27* and *Lr31*.

Lr27 is present in wheats with *Sr2*, but is not expressed in the absence of the complementary factor {1366}. [*LrGt*{1366},*A*{1058,1366}]. 3BS{1367}. **s:** CS*6/Ciano 3B{1366}; CS*6/Ciano 5B{1366}; CS*6/Hope 3B{1366}. **v:** Gatcher{1366}; Ocoroni 86{1373}. **v2:** Anhuac *Lr13 Lr17*{1361}; Cocoraque 75 *Lr13 Lr17a Lr34*{1361}; Jupateco 73S

Lr17a{1361}; SUN 27A *Lr1 Lr2a*{1366}; Timgalen *Lr3* {heterogeneous} *Lr10*{1366}. **tv:** Benimichi C2004{10585}; Jupare C2001{10585}. **ma:** Positive association with *XksuG53-3B*{1058}.

Lr28{967}. Derived from *Ae. speltoides*. 4AL {967} = T4AS.4AL-7S#2S{389}. **i:** CS 2A/2M 4/2{967}; CS 2D/2M 3/8{967}. **ma:** *Lr28* was tagged using STS primer OPJ-01_{378}{1052}; A linked RAPD marker, S421_{640} was converted to a TPSCAR, SCS421_{570} {10236}.

Lr29{939}. Derived from *Th. elongatum*. 7DS {939} = T7DL-7Ae#1S{389}. **i:** Sears' CS 7D/*Ag*#11{939,1300}; RL6080 = Tc*6/Sears' 7D/Ag#11{316}. **ma:** Co-segregation with two RAPDs{1165}.

Lr30{315}. Recessive {315}. [*LrT*]. 4AL{315}. **i:** RL 6049 = Thatcher*6/Terenzio{315}. **v2:** Terenzio Lr34{315}.

Lr31{1367}. One of two complementary genes, the second gene is *Lr27*. [*B*{1058,1366}]. 4BL{1367}. **v:** Ocoroni 86{1373}. **v2:** Chinese Spring *Lr12 Lr34*{1367}; See *Lr27* for list of wheats with *Lr27* +*Lr31*. **tv:** Benimichi C2004{10585}; Jupare C2001{10585}. **ma:** A positive association with *XksuG10-4B*{1058}.
Possible commonality with *Lr12*.

Lr32. 3D{644}.3DS{645}. **i:** RL6086=Tc*7/R15713/Marquis K{10874}; BW196=Katepwa*6/RL5713/2*Marquis K{10874}. **v:** Tetra Canthatch/*Ae. tauschii* RL 5497-1, RL 5713, RL 5713/Marquis-K{644}. **dv:** *Ae. tauschii* RL5497-1{644}. **ma:** *Xbcd1278-3D* - 3.6 cM - *Lr32*{048}; *Xcdo395-3D* - 6.9 cM - *Lr32*{048}; *Xbarc128-3D* - 9.1 cM - *Lr32* - *Xwmc43/Xbarc235-3D*{10874}.

Lr33{325}. 1BL{325}. **i:** RL 6057 = Tc*6/PI 58548{297,325,321}. **v:** PI 268454a{297}; PI 58548{297,325}. **v2:** PI 268316 *Lr2c Lr34*{297}; Others{1322}.

Lr34{297,299}. In addition to conferring seedling and adult plant resistance, *Lr34* responds in a complementary manner when combined with either *Lr33* or *LrT3* {321}. In the Thatcher background, *Lr34* is associated with increased resistance to stem rust {299,321}.
Although the resistance gene in the near-isogenic Thatcher line, RL6077, was considered to be *Lr34* on the basis of disease response, leaf tip necrosis and its association with resistance to stripe rust, a cross with RL6058 segregated for two genes. A translocation to another chromosome was suggested {324}. [*LrT2*{321}]. 7D{299}.7DS{324,1058}. **i:** Arina + Lr34{10648}; Lalbahudar + Lr34{10648}; Line 897{321}; Line 920{321}; Selections Jupateco 73R *Lr17a Lr27* + *Lr31* and Jupateco 73S *Lr17a Lr27* + *Lr31* and Cocoraque 75 *Lr13 Lr17a Lr27* + *Lr31* and Anhuac 75 *Lr13 Lr17a Lr27* + *Lr31*, can be considered near-isogenic for the presence and absence, respectively, of *Lr34*{1361}. **v:** Ardito{10648}; Arina*3/Forno{10380}; Bezostaya{10387,10648}; Condor{10387,10648}; Cook{10387}; Forno{10066,10380,10387}; Fukuho-Komugi{10387,10648}; Kavkaz{10648}; Lantian 12{10682}; Libellula{10682}; Otane{10387}; Pegaso{10648}; Penjamo 62{10648}; RL 6058 = Tc*6/PI 58548{297}; PI 268454{297}; Strampelli{10682}; Westphal 12{0268}; Others{299,321,1322,1376}; See{1362}; 2174{10888}; List of U.S. hard wheats in {10888}; Pedigree charts showing the presence of *Lr34* in various Canadian wheat classes are given in {10889}. **v2:** Anza = WW15 *Lr13* heterogeneous{10648}; Brambling *Lr14a Lr23*{10563}; BH1146 *Lr13*; Chinese Spring *Lr12 Lr31*{301,10648}; Chris *Lr13*{10648}; Frontana *Lr13*{1374}; Glenlea *Lr1*{327,10648}; Jupateco R *Lr17a*, *Lr27* + *Lr31*{10648}; Lageadinho *LrT3*{321}; Laura *Lr1 Lr10*{712}; Mentana *Lr3b*{10493,10648}; Parula *Lr13 Lr46*{1374}; PI 58548 *Lr33*{297,321}; RL 6059 = Tc*6/Terenzio *Lr33*{297}; RL 6069 = Tc*6/Lageadinho *LrT3*{321}; RL 6070 = Tc*5/PI 321999 *LrT3*{321}; RL 6050 = Tc*6/Terenzio *LrT3*{321}; Saar *Lr46*{10481}; Sturdy *Lr12 Lr13*{301}; Terenzio *Lr3 Lr30 LrT3*{321}; Thirteen Thatcher lines with 2-gene combinations{434}. **ma:** Complete linkage with *Ltn* (leaf tip necrosis){1361}, *Yr18* (Reaction to *P. striiformis*){1362,937} and *Bdv1* (Reaction to barley yellow dwarf virus) and *Pm38* (Reaction to *B. graminis*){0090}; association with *Xwg834-7D*{0268}; *Xgwm120-7D* - 0.9 cM - *Lr34* - 2.7 cM - *Xgwm295-7D*{10259};

Lr34 .....*XsfrBF473324* - 0.5 cM - *Xsfr.cdo475-7D* - 0.7 cM - *Xswm10-7D*{10387}; A 150 bp allele (b) of STS *csLV34*, derived from wEST BQ788742 was identified in most wheats with *Lr34; CsLV34a* - 0.4 cM - *Lr34*{10387}; STS marker csLV34 was used to confirm or postulate the presence of *Lr34* in Australian cultivars {10493} and Hungarian materials{10701}; Further markers for *Lr34* and various marker-positive haplotypes that lack leaf rust resistance are described in {10887,10888}. **c:** *Lr34* spanning 11,805 bp and producing a 1,401 aa protein belongs to the drug resistance subfamily of ABC reporters{10648}; contained within FJ436983{10648}; Putative ABC transporter, GenBank FJ436983, in CS{10862}; Further confirmation of the ABC transporter is provided in {10887}.

A QTL, which is likely to correspond to *Lr34*, was identified in the Opata 85/W-7984 (ITMI) RI mapping population. The resistance was contributed by Opata 85 {0090}.

On the basis of leaf tip necrosis and lack of segregation in a diallel, cv. Saar, Simogh, Homa, Parastoo and Cocnoos were considered to have *Lr34*, but each also possessed 2 or 3 additional adult plant resistance factors {10110}.

This gene is identical to *Yr18, Pm38* and *Ltn* and confers stem rust resistance in some genetic backgrounds.

Diagnostic markers based on the gene sequence are reported in {10713}; AC Domain, Cappelle Desprez, H-45, Jagger, Newton, RL 6077, and H-45 do not carry *Lr34* {10713}.

Lr35{651}. Derived from *Ae. speltoides*{651}. Adult plant resistance {651}. 2B{651}. **v:** RL 5711{651}. **ma:** A. SCAR marker was developed{9923}.

Complete cosegregation between *Lr35* and RFLP loci *Xwg996-2B*, *Xpsr540-2B* and *Xbcd260-2B* was observed. The RFLP probe BCD260 was converted to a CAPS and STS marker {0045}. Lines with shortened alien segments are reported in {10741}.

Lr36. Derived from *Ae. speltoides*. 6BS{292}. **v:** Line 2-9-2; Line E84018. **al:** *Ae. speltoides* Popn. 2.

Lr37{062}. Derived from *Ae. ventricosa*. Recessive {667}.

Lr37 can be recognised in seedlings at low temperatures (17^{o}C) and is effective in adult plants under field conditions. See also *Sr38* (Reaction to *P. graminis*) and *Yr17* (Reaction to *P. striiformis*) 2AS{062}.6M^{v} = 2MS-6MS.6ML or 2MS-6ML.6MS{0009}.

<u>VPM1 and derivatives</u>: 2AS{062} = 2AL.2AS-2N^{v}S{0213}. **i:** RL 6081 = Tc*/VPM1{939}; RL6081 = Tc*8/VPM1{316}; various NILs listed in {0213}. **v:** Hyak{021}; Madsen{020}; Rendezvous{062}; VPM1{062}; VPM1 derivatives{939}; see also Reaction to *P. striiformis tritici Yr17*.

<u>Moisson derivatives</u>: *Lr*{113}. 2AS = 2AL.2AS-2N^{v}S{113}. **ad:** Moisson + 6N^{v}=6N^{v}S.6N^{v}L-2N^{v}S or 6N^{v}L.6N^{v}S-2N^{v}S{0009}. **v:** Mx12 {0213}; Mx22{0213}. **ma:** (relevant to both groups of derivatives.) PCR primers designed from marker csVrga1D3 {0183} producing a 383bp product allows detection of the 2N^{v}S segment{0213}; see also: Reaction to *P. striiformis Yr17*.

A resistance gene analog containing an NBS-LRR R gene sequence was isolated from the *Ae. ventricosa* segment carrying *Lr37* {0183}.

The 2NS translocated segment carrying *Lr37* replaced the distal half of chromosome 2A (25-38 cM) from *Xcmwg682-2A* to *XksuH-9-2A*. PCR markers were developed for the 2NS and 2AS alleles of *Xcmwg682*{10073}. SCAR markers SC-372 and SC-385 were developed in {10796}.

Lr38{392}. Derived from *Th. intermedium*.

1DL = T1DS.1DL-7Ai#2L{390,389}. **v:** T25{390}.
2AL = 2AS.2AL-7Ai#2L{392,389}. **v:** W49{392} = T33{390}.
3DS = 3DL.3DS-7Ai#2L{390,389}. **v:** T4{390}.
5AS = 5AL.5AS-7Ai#2L{390,389}. **v:** T24{390}.

6DL = 6DS.6DL-7Ai#2L{390,389}. **i:** RL6097 = Thatcher*6/T7{307}. **v:** T7{390,307}; 7Ai#2(7D){392,389}; 7Ai#2(7A){390}. **su:** W52{390,389}.

Lr39{1200,02100}. Derived from *Ae. tauschii* {02100}. *Lr41* {215}. 2DS{02100,10731}. **v:** Fuller{10595}; KS90WGRC10 = TAM107*3/*Ae. tauschii* TA2460{220}; Overley{10595,10699}; Postrack{10830}; TA4186 = TA1675*2/Wichita{02100}; Thunderbolt{02100}. **v2:** Fuller *Lr17a*{10699}; WGRC16=TAM107*3/*Ae. tauschii* TA 2460{220}. **dv:** *Ae. tauschii* TA 1675{02100}; *Ae. tauschii* TA2460 *Lr21*{220,10415}; *Lr21*{220,10415}. **ma:** 10.7 cM distal to *Xgwm210-2D*{02100}; Four markers, *Xbarc124-2D*, *Xgwm210-2D*, *Xgdm35-2D* and *Xcfd36-2D* were closely linked with the terminally located *Lr39* (formerly *Lr41*), but the gene order was inconsistent and no specific allele was associated with it{10731}.

Lr40{1200,10415}. Deleted, see *Lr21*

Lr41{215}. Deleted, see *Lr39*

Lr42{218}. 1D{218}. **v:** AR93005{10840}; Fannin{10595}. **v2:** KS91WGRC11 *Lr24*{218,10840}. **dv:** TA2450{218}. **ma:** *Lr42* - 0.8 cM - *Xwmc432-1D* - 1.6 cM - *Xcfd-D1*{10840}.

Lr43{218}. Deleted, wrongly based on a gene combination

Lr44{322}. 1B{322}. **i:** RL = 6147 Thatcher*6/*T. spelta* 7831{322}. **v:** *T. spelta* 7831{322}; *T. spelta* 7839{322}.

Lr45{958}. Derived from *Secale cereale*. 2A = T2AS-2R#3S.2R#3L{958,389}. **i:** RL6144 = Thatcher*7/ST-1{958}. **v:** ST-1{958}; Various Australian backcross derivatives{958}.

Lr46{1364}. Completely linked with *Yr29* {0119}. Adult plant resistance. 1B{1346}.1BL{0119}. **s:** Lalbahadur(Pavon 1B) *Lr1*{1364}; Lalbahadur(Parula 1B){10281}. **v:** Attila{10281}. **v2:** Pavon F76 *Lr1 Lr10 Lr13*{1364,0119}; Parula *Lr13 Lr34*{10281}; Saar *Lr34*{10481}. **ma:** An RFLP marker associated with *Lr46* with a recombination value of about 10% was identified in{0119}; *Xwmc44-1B* - 1.4 cM - *Xbac24prot* - 9.5 cM - *Lr46* - 2.9 cM - *Xbac17R.......Xgwm140-1B*{10281}; *Xwmc44-1B* - 3.6 cM - *Lr46* 2.1 cM - *XtG818/Xbac17R......Xgwm140-1B*{10281}; *XSTS1BL2* - 2.2 cM - *Lr46/XSTS1BL9* - 2.2 cM - *XSTS1BL17*{10326}.

Associated with *Ltn2* and *Yr29.*

Lr47{9901}. Derived from *Ae. speltoides* {9901}. 7AS. **v:** Bionta 2004{10737}.
7AS = Ti7AS-7S#1S-7AS.7AL{9901}. **v:** Pavon derivative PI 603918{9901}.
7A = T7AS-7S#1S.7S#1L{389}. **v:** CI 17882, CI 17884, CI 17885, KS, 90H450{9901}.
7AL = Ti7AS.7AL-7S#1L-7AL. **v:** Pavon derivative PI 603919{9901}. **ma:** *Lr47* was located in the distal one-third of 7AS, 2-10 cM from the centromere and within a 20-30 cM segment {9901}. Complete linkage with several RFLP markers {9901} and PCR specific markers {0126}.

Lr48{0085}. Adult plant resistance {0085}. Recessive {0085}.
2BS{0329,10842}.4BS{10738}. **i:** CSP44 / 5*Lal Bahadur{0329}. **v2:** CSP44 *Lr34*{0085}; Dove *Lr34*{0329}. **ma:** *Xgwm429b-2B* - 6.1 cM - *Lr48* - 7.3 cM - *Xbarc7-2B*{0329}; RAPD markers flanking *Lr48* at 2.7 and 8.6 cM are reported in{10738}; *Xwmc175-2B* - 10.3 cM - *Lr48* - 2.5 cM - *Xwmc332-2B*{10842}; Centromere - 27.5 cM - *Lr48*(est.){10842}.

Lr48 is closely linked with *Lr25* {10738}.

Lr49{0085}. Adult plant resistance {0085}. 2AS{0329}.4BL{0329}. **i:** VL404 / 5*Lal Bahadur *Lr34*{0329}. **v2:** Tonichi *Lr34*{0329}; VL404 *Lr34*{0085}. **ma:** *Xbarc163-4B* - 8.1 cM - *Lr49* - 10.1 cM - *Xwmc349-4B*{0329}.

Lr50{0221}. Based on linkage with SSR markers. 2BL{0221}. **v:** KS96WGRC36 = TAM*3/TA870/{0221}; U2657 = Karl 92*4/TA674{0221}; U3067 = TAM107*4/TA874{0221}; U3193 = TAM107*4/TA874{0221}. **tv:** *T. armeniacum* TA870{0221}; *T. armeniacum* TA145; TA874{0221}; TA870{0221}; TA895{0221}. **ma:** Linked with *Xgwm382-2B* (6.7 cM) and *Xgdm87-2B* (9.4 cM){0221}.

Lr51{0308}. 1BL{0308}. **i:** Express*7/T1{0308}; Koln*7/T1{0308}; UC1037*7/T2{0308}. **v:** Neepawa*6/*Ae. speltoides* F-7, selections 3 and 12{0306}; Interstitial translocations T1AS.1AL-1S#F7-12L-1AL {0308} = T1; T1BS.1BL-1S#F7L-1BL{0306}. **al:** *Ae. speltoides* F-7 selections 3 and 12{0306}. **ma:** Linked with RFLP markers *Xmwg710-1B* and *Xaga7-1B*{0308}; A CAPS marker was developed from *XAga7-1B*{0308}.

Lr52{10035}. [*LrW*{309}]. 5BS{10035}. **v:** AUS28183=V336{10679}; AUS18187{10679}; Tc-LrW = RL6107{10035}. **v2:** V618 *Lr33*{309}; V336 *Lr33 LrB*{309}. **ma:** *Lr52* - 16.5 cM - *Xgwm443-5B*{10035}; *Xgwm234-5B* - 10.9 cM - *Lr52* - 4.1 cM - *Yr47* - 9.6 cM - *Xcfd309-5B*{10679}; *Xgwm234-5B* - 10.2 cM - *Lr52* - 3.3 cM - *Lr52* - 8.2 cM - *Xcfb309-5B*{10679}.

Lr53{10203}. [*LrS8*{10204}]. 6BS{10203}. **v:** 98M71 = AUS 91388 = *T. dicoccoides* 479/7*CS{10204}. **tv:** *T. dicoccoides* 479 {10204}. **ma:** *Xgwm191-6B* - 18.9 cM - *Yr35* - 3 cM - *Lr53* - 1.1 cM - *Xcfd-6B* - 3.4 cM - *Xgwm50-6B*{10780}.
Lr53 was genetically independent of *Lr36* {10780}

Lr54{10139}. Derived from *Ae. kotschyi*. 2DL{10139}. **v:** Line S14{10139}. **ad:** Line 8078{10139}. **al:** *Ae. kotschyi* 617{10139}.

Lr55{10180}. Derived from *Elymus trachycaulis* {10180}. 1B (1BL.1H^{t}S{10180}. **ad:** CS + 1H^t{10180}. **v:** KS04WGRC45 = Heyne*3/TA5586.

Lr56{10224}. [*LrS12*{10204}]. 6A (6AL-6S^{sh}L.6S^{sh}S){10224}. **v:** Line 0352 = *Ae. sharonensis*-174/9*CS//3*W84-17/3/CS/4/W84-17{10224}; Recombinants with shorter segments - 07M4-39, 07M4-157 and 07M4-175 - are reported in{10691}. **al:** *Ae. sharonensis*-174{10224}.

Lr57{10328}. Derived from *Ae. geniculata*. 5DS (5DL.5DS-T5MS^G{10328}. **v:** TA5602{10328}; TA5603{10328}; Since TA5602 and TA5603 are fourth backcross selections to WL711, they likely also carry *Lr13*. **al:** *Ae. geniculata* (=*ovata*) (U^{S}U^{S}M^{G}M^G TA10437){10328}. **ma:** Completely linked with distinctive alleles of *Gsp*, *Xfbb276* and *Xbcd873*{10328}; Completely linked with *Yr40*{10328}; CAPS marker *XLr57/Yr40-MAS-CAPS16*{10770}.

Lr58{10375}. Derived from *Ae. triuncialis* 2BL{10375}. = T2BS.2BL-2^{t}L(0.95). **v:** TA5605 = WL711*4/*Ae. triuncialis* TA10438 *Lr13*{10375}. **al:** *Ae. triuncialis* TA10438{10375}. **ma:** TA5605 possesses *Ae. triuncialis* alleles of RFLP markers *XksuH16*, *XksuF11* and *Xbg123* and SSR marker *Xcfd50* in the terminal region of chromosome 2BL{10375}; A codominant STS marker *Xncw-Lr58-1* was based on the sequence of *XksuH16*{10819}.

Lr59{10399}. Derived from *Ae. peregrina* 1A probably 1AS alien centric fusion{10399}. **v:** Line 0306 {10399} = *Ae. peregrina*-680/2*CS//5*W84-17{10399}. **al:** *Ae. peregrina* (UUSS, 2n=28) 680{10399}.
Problems in recovering balanced recombinants are reported in {10762}.

Lr60{10400}. [*LrW2*{0305}]. 1DS{10400}. **v:** RL6172{0305} = Thatcher*3/V860. **ma:** *Lr60* - 8.4 cM - *Xbarc149-1D/Lr21*{10400}; *Lr60* - 13 cM - *Lr21*{10400}.

Lr61{10485}. 6BS{10485}. **tv:** Guayacan 2{10485}; Guayacan INIA{10485}. **ma:** *Lr61* - 2.2 cM - *P81/M70*$_{269}$*/P87/M75*$_{131}$ - 4.6 cM - *P87/M76*$_{149}$ - 21.7 cM - *Xwmc487-6B*{10485}.

Lr62{10537}. Derived from *Ae. neglecta* 6A = 6AL-6^{Aen}L.6^{Aen}S{10537}. **v:** Line 03M119-71A{10537}. **al:** *Ae. neglecta* 155{10537}.
Associated with *Yr42* {10537}.

Lr63{10875}. Derived from *T. monococcum* 3AS{10875}. **i:** RL 6137 = Thatcher*6/TMR5-J14-12-24{10646,10875}. **v:** TMR5-J14-12-24{10646}. **dv:** *T. monococcum*{10646}. **ma:** *Xbarc321/Xbarc57-3A* - 2.9 cM - *Lr63*{10875}.

Lr64{10550}. 6AL{10550}. **i:** RL 6149 = Thatcher*6/*T. dicoccoides* 8404{10550}. **tv:** *T. dicoccoides* 8404{10550}. **ma:** *Xbarc104-6A* - 13.9 cM - *Lr64* - 21.9 cM - *Xgwm427-6A*{10550}.

Lr65{10848}. [*LrAlt*{10739}]. 2AS{10739,10848}. **v:** Selection ARK 0;{10848}. **v2:** *T. spelta* Altgold Rotkorn *Lr71*{10739,10848}. **ma:** *Lr65* - 1.8 cM - *Xbarc212-2A/Xwmc382-*

2A - 2 cM - *Xgwm636*{10739}; *XE41M57-165* - 3 cM - *Lr65* - 2 cM - *Xbarc124/Xbarc222/Xgwm614-2A*{10848}; *Lr63* was estimated to be about 10 cM from *Lr17*{10848}.

Some plants of Altgold Rotkorn possess *Lr71* conferring IT 12C {10848}.

Lr66{10591}. *LrS13* {10592}. 3A{10591}.3A=3A-$3S^S$. **v:** Line 07M127-3 = *Ae. speltoides* / 5*CS // 2*CSph1b mutant /3/2* W84-17/4/CSN3AT3B{10591}. **al:** *Ae. speltoides* Accession 691{10591}. **ma:** Most user-friendly marker, SCAR S15-t3{10591}.

Lr67{10675}. Adult plant resistance 4DL{10675}. **bin:** C-0.53{10675}; Distal to 0.56{10678}. **i:** RL6077=Thatcher*6/PI 250413{10675}. **v:** PI 250413{10676}. **ma:** *Xcfd71-4D* - 1.5 cM - *Lr67*{10675}; Pleiotrophic with *Yr46*; Close linkage with *Xcfd71-4D* and *Xbarc98-4D* estimated at 4.4 cM, and *Xcfd23-4D* at 5.2 cM (all on the same side of *Lr67/Yr46*{10678}; *Xgwm165-4D/Xgwm192-4D* - 0.4 cM - *Yr46/Lr67*{10678}.

Lr67 is pleiotropic or closely linked with *Sr55* and *Yr46*

Lr68{10817}. Adult plant resistance 7BL{10817}. **v:** Arula 1 CIMMYT GID 1847450{10817}; Arula 2 CIMMYT GID 1847422{10817}. **v2:** Parula *Lr3b Lr34 Lr46*{10817}. **ma:** Close linkage with several markers in chromosome arm 7BL and *Lr14b* in the Apav x Arula population. Flanking markers are *Xpsy1-1* and *Xgwm146-7BL* at 0.4 and 0.6 cM. Gamma-irradiation induced deletion stocks of Arula 1 that lack *LrP* but have *Lr14b* were identified showing that the two genes are located at different closely linked loci{10817}.

Lr69{10903}. 3DL{10903}. **v:** Toropi-6.3{10903}.

Lr70{10904}. 5DS{10904}. **v:** Yet to be named selection of cross or backcross to Tc{10904}. **v2:** KU3198 *LrXX*{10904}. **ma:** *Lr70 - Xgwm190-5D*{10904}.

LrXX is believed to be a known gene for resistance.

Lr71{10911}. [*LrAK12c*{10910}]. 1B centromere region not resolved{10911}. **v:** LrARK12c=*T. spelta* Altgold Rotkorn selection{10910}; Common wheat reference line under increase{10911}. **v2:** *T. speelta* Altgold Rotkorn (heterogeneous) *Lr65*{10910,10911}. **ma:** *Xgwm11-1B* - 3.3 cM - *Xgwm18-1B* - 1.0 cM - *Lr71* - 1.3 cM - *Xbarc187-1B* - 0.5 cM - *Xbarc137-1B*{10911}.

LrKr1{10233}. **v:** Thatcher{10233}. **v2:** Kanred *LrKr2*{10233}.

LrKr2{10233}. **v2:** Kanred *LrKr1*{10233}.

LrMq1{10233}. **v:** Marquis{10233}.

LrTb{820}. Adult plant resistance {820}. **v2:** AC Taber *Lr13 Lr14a*{820}.

LrTm{0277}. **dv:** *T. monococcum.* **ma:** Linked to microsatellite locus *Xgwm136*{0277}.

LrTr{0227}. **v:** *Ae. triuncialis* derivatives{0227}. **ad:** WL711 BC2F5 addition lines{0227}. **al:** *Ae. triuncalis* Acc. 3549{0227}. **ma:** Lines with *LtTr* possessed a homologue of *Xgwm368-4B*{0227}.

LrTt1{10031}. Reccessive allele {10031} [*lrTt1*{10031}]. 2A{10031}. **v:** Line 842 = Saratovskaya*2/*T. timopheevii* spp. *viticulosum*{10031}. **ma:** *Xgwm812-2A* - 1.5 cM - *LrTt1*{10031}.

LrVPM{1603}. 7DL{1603}.

LrW2{305}. A gene, identified only as *Lr*, was transferred to wheat chromosome 2AS from $6M^v$ {113}: cosegregating markers were *Xpsr933-2A* and *Xpsr150-2A.*

LrWo{10747}. 5B{10747}. **tv:** Wollaroi AUS99174{10747}. **ma:** *Xgwm234-5B* - 7.2 cM - *LrWo* - 20.3 cM - *wPT-1420*{10747}.

The relationship of *LrWo* to *Lr52* was not established.

LrZH84{10581}. 1BL{10581}. **v:** Zhoumai 11{10682}. **v2:** Predgornaia 2 *Lr26*{10581}; Zhou 8425B *Lr26*{10581}. **ma:** *Xbarc8-1B* (cent) - 5.2 cM - *LrZh84* - 3.9 cM - *Xgwm582-1B*{10581}.

A series of temporary designations for seedling and adult plant resistance genes in six durums is given in {1648}.

A potentially novel resistance gene was located in chromosome 5BS of Iranian landrace PI 289824. *Xgwm234-5B* - 8.9 cM - *Lr* - 2.3 cM - STS *Xtxw*$_{200}$ {10253}.

Complex genotypes:

AC Domain: *Lr10 Lr16 Lr34* {820}.
AC Splendor: *Lr1 Lr16 Lr34* {10179}
AC Teal: *Lr1 Lr13 Lr16* {821}
Alsen: *Lr2a Lr19 Lr13 Lr23 Lr34* {10152}
Alsen: *Lr2a Lr10 Lr13 Lr23 Lr34* {10223}.
Benito: *Lr1 Lr2a Lr12 Lr13* {1256}.
Buck Manantial: *Lr3 Lr13 Lr16 Lr17 Lr34?* {300}.
Coker 9663 *Lr9 Lr10 Lr14a* {10742}.
Era: *Lr10 Lr13 Lr34* {342}.
Grandin: *Lr2a Lr3 Lr10 Lr13 Lr34* {821}.
Mango: *Lr1 Lr13 Lr26 Lr34* {1374}.
MN7529: *Lr1 Lr2a Lr10 Lr16* {976}.
Norm: *Lr1 Lr10 Lr13 Lr16 Lr23 Lr34* {10152, 10223}
Opata 85: *Lr10 Lr27+Lr31 Lr34* {1058}.
Pasqua: *Lr11 Lr13 Lr14b Lr30 Lr34* {304}.
Pioneer 26R61 *Lr13 Lr14b Lr26* {10742}.
Prospect: *Lr1 Lr2a Lr10 Lr13* {197}.
Roblin: *Lr1 Lr10 Lr13 Lr34* {303,713}.
Trap: *Lr1 Lr3 Lr10 Lr13 Lr34* {1374}.

Genotype lists:Australian cultivars {0288}; Chinese cultivars {0013, 10682}; Combinations with *Lr34*{1361}; Cultivars from the former USSR {1380}; Czechoslovakian cultivars{855,0102}; European cultivars {0229,0260,0288,0337,10345,10794}; Indian cultivars {1365,1345}; Indian Subcontinent{1365}; Mexican cultivars{1373}; U.S.A. cultivars {1219,978,0334,10111,10146,10152}, French cultivars {10792}, see also {970}.

101.2. Suppressor of genes for resistance to *P. triticina*

SuLr23{1058}. Suppressing allele. 2DS{1058}. **v:** Altar 84/*Ae. tauschii* 219{1058}.
suLr23{1058}. Non-suppressing allele **v:** Opata 85{1058}.

See also evidence for specific suppression in {948}.

101.3. QTLs for reaction to *P. triticina*

Two QTLs, located distally on chromosome arm 1BL and on chromosome 7DS, were mapped for leaf rust severity in a Fukuho-komugi/Oligoculm doubled haploid population {10060}. The resistance on 1BL was contributed by Oligoculm and explained 15% of the variation. The 1BL QTL may correspond to *Lr46* and was associated with marker *Xwmc44-1B* {0460}. The resistance on 7DS was contributed by Fukuho-komugi and explained 41% of the variation. The 7DS QTL corresponds to *Lr34* and was associated with marker *Xgwm295-7D* {10060}.

Two major QTL, located on chromosomes 7D and 1BS, for leaf rust resistance were mapped in an Arina/Forno RIL population {10066}. The resistance on 7D was contributed by Forno and explained 32% of the variation. This QTL most likely corresponds to *Lr34* {10066}. The resistance on 1BS (*QLr.sfr-1BS*) was associated with *Xgwm604-1B* and was contributed by Forno {10066}. Additional minor QTLs were identified on chromosome arms 2DL, 3DL, 4BS and 5AL {10066}.

QTLs for leaf rust resistance were identified in {0050} and were named by the catalogue curators as follows:

QLr.pser.1BL{10743}. 1BL{10743}. **bin:** 1BL6-0.32{10743}. **ma:** Proximal to *Xgwm264.1-1BL*{10743}.

Associated with *lm* producing a lesion mimic phenotype in the absence of disease {10743}.

QLr.sfr-1B{0050}. 1BS{0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno{0050}. **ma:** Associated with *Xpsr949-1B* and *Xgwm18-1B*{0050}.

QLr.sfr-2B{0050}. 2B{0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0050}. **ma:** Associated with *Xpsr924-2B* and *Xglk699-2B*{0050}.

QLr.sfr-3A{0050}. 3A{0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno{0050}. **ma:** Associated with *Xpsr570-3A* and *Xpsr543-3A* {0050}.

QLr.sfr-4B{0050}. 4B{0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno{0050}. **ma:** Associated with *Xpsr921-4B* and *Xpsr593-4B*{0050}.

QLr.sfr-4D{0050}. 4DL{0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno{0050}. **ma:** Associated with *Xglk302-4D* and *Xpsr1101-4D*{0050}.

QLr.sfr-5D{0050}. 5DL{0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Oberkulmer{0050}. **ma:** Associated with *Xpsr906-5D* and *Xpsr580-5D*{0050}.

QLr.sfr-7B.1{0050}. 7B {0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno{0050}. **ma:** Associated with *Xpsr593-7B* and *Xpsr129-7B*{0050}.

QLr.sfr-7B.2{0050}. **v:** Forno/*T. spelta* cv. Oberkulmer mapping population; the resistance was contributed by Forno{0050}. **ma:** Associated with *Xglk750-7B* and *Xmwg710-7B*{0050}.

QTLs: Two QTLs for slow leaf rusting, located on chromosomes 2B and 7BL, were mapped for final severity, area under disease progress curve, and infection rate in a CI 13227 (resistant)/Suwon (susceptible) SSD population {10211}. ***QLr.osu-2B*** was associated with microsatellite markers *Xbarc18-2B* and *Xbarc167-2B* (R^2 = 9-18%). ***QLr.osu-7BL*** was associated with microsatellite marker *Xbarc182-7B* (R^2 = 12-15%) {10211}. CI 13227 constributed the resistant alleles for both QTLs. ***QLrid.ocu-2D***, linked to *Xgwm261-2D*, affected the duration of infection {10211}.

Avocet S/Pavon 76: QTL identified included: 1BL (PstAFAMseCAC1&2), 4BL (*Xgwm368*), 6AL (*Xgwm617*), 6BL (PstAGGMseCGA1) {10443}.

Avocet S/Attila: At least two additive genes for slow rusting {10586}. In addition to *Lr46* there were small effects on chromosomes 2BS, 2BL and 7BL {10586}.

Beaver/Soissons DH population: QTL for resistance to Australian pathotypes were located on 4-6 chromosomes over 3 years; the most consistent being 1B(1BL.1RS), 4BS (proximal to *Xbarc20-4B*) and 5AS (*QTLBvr5AS*, proximal to *Xbarc10-5A*) and in the vicinity of *wPt-8756* and *wPt-1931* {10687}.

TA 4152-60 (MR) / ND495 (MR): DH population: Five QTLs for APR were identified in the field, viz *QLr.fcu-3AL* (R^2 = 0.18), *QLr.fcu-3BL* (R^2 = 0.19), *QLr.fcu-5BL* (R = 0.07), and *QLr.fcu-6BL* (R^2 = 0.12) from TA 4152-60 and *QLr.fcu-4DL* (R^2 = 0.13) from ND495 {10757}. The 3AL gene also conferred seedling resistance to some races and the 3BL gene conferred resistance to race MFPS {10757}.

Tetraploid wheat

Colosseo/Lloyd: A major QTL, *QLr.ubo-7B.2*, for seedling and adult plant resistance from Colosseo, was located between *Xgwm344.2-7B* and DART 378059, bin 7BL 10-0.78-1.00 {10600}.

TA4152-60/ND 495 DH population: Four QTLs for APR, *QLr.fcu-3AL*(*Xcfa2183-3AL* - *Xgwm666-3AL*, R^2=0.18), *Qlr.fcu-3BL*(*Xbarc164-3BL* - *Xfcp544-3BL*, R^2=0.19), *Qlr.fcu5BL*, and *Qlr.fcu-6BL*(*Xbarc5-6BL* - *Xgwm469.2-6BL*, R^2=0.12) were from TA4152-60 and *Xlr.fcu-4DL*(*Xgdm61-4DL* - *Xcfa2173-4DL*, R^2=0.13) was from ND495 {10717}. The 3AL QTL conferred seedling resistance to all 3 races, and the 3BL gene gave race-specific seedling resistance to one race. *Xlr.fcu-3BL* was effective only in the presence of an allele associated with *Xgwm359-5DS* {10717}.

Association mapping in durum wheat indicated genomic regions affecting leaf rust response in chromosomes 1A, 1B, 2A, 2B (*Lr13, Lr23* region), 3B, 5A, 5B, 6B, 7A, and 7B (see *Lr14* {10736}.

102. Reaction to *Pyrenophora tritici-repentis* (anomorph: *Drechlera tritici*-repentis)

Disease: Tan spot, yellow leaf spot.

Virulence in the pathogen is mediated by host-specific toxins and host resistance is characterized at least in part by insensitivity to those toxins. Three toxins, Ptr ToxA, Ptr ToxB and Ptr ToxC have been identified (see {10153}). Toxin sensitivity determined by use of toxins extracted from pathogen strains and resistance determined by infection experiments are treated as different traits, although common genes may be involved.

A review is provided in {10690}.

102.1. Insensitivity to tan spot toxin (necrosis)

tsn1{346,10207}. Insensitivity (disease resistance) is recessive {346}. *Tsr1* {10508}, see Resistance to tanspot. 5BL{346}. **v:** AC Barrie{10153}; AC Cadillac{10153}; AC Elsa{10153}; Atlas 66{10458}; BR34{0007,10458}; CEP17{0007}; Chinese Spring{0007,10458}; Erik{0007,10030,10458}; IA807{0007}; IA905{0007}; Laura{10153}; ND688{10458}; Opata 85{10458}; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. squarrosa* C122{346,10207,10458}; Synthetic W-7984 = Altar 84/*Ae. tauschii* CI 18{0007,10458}. **tv:** Altar 84{0007}; D87450{0007}; *T. dicoccoides* Israel A{10506}. **ma:** *Xbcd1030-5B* - 5.7 cM - *tsn1* - 16.5 cM - *Xwg583-5B*{346}; *tsn1* - 3.7 cM - *Xbcd1030-5B*{0007}; *Xfgcg7-5B* - 0.4 cM - *Tsn1/Xfcg17-5B* - 0.2 cM -*Xfcg9-5B*{10207}; *Xfcg17-5B* - 0.2 cM -*Tsn1* - 0.6 cM - *Xfcg9-5B*{10207}; *Xfcp1-5B* and *Xfcp2-5B* delineated *Tsn1* to an interval of about 1 cM{10337}; *Tsn1* was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1/XBE425878/Xfcc1/XBE443610*{10413}.

According to {10376} the same dominant allele, presumably *tsn1*, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN 2137 in crosses with 6B-365.

Tsn1. Sensitive to Ptr ToxA. **v:** Bobwhite{10458}; Cheyenne{0007,10458}; Glenlea{10458}; Grandin{10458}; Hope{0007,10458}; Jagger{0007}; Katepwa{10458}; ND2709{10458}; ND495{0007}; Sumai 3{10458}; Timstein{0007,10458}. **v2:** Kulm *Tsc1*{346,10030,10458}; Trenton *Tsc1*{0315}. **dv:** Two *Ae. speltoides* accessions{10756}. **tv:** Langdon{10458}; Some *T. dicoccoides* accessions{10756}. **c:** *Tsn1* has 8 exons and a

S/TPK-NBS-LRR structure; all three domains are required for function and TSN1 protein does not interact directly with ToxA{10756}.

In Kulm/Erik, toxin response accounted for 24% of the variation in disease response, which was affected by 4-5 genes {10030}.

Ptr ToxA is functionally identical to *S. nodorum* ToxA but has two predicted amino acid differences {10459}. See Reaction to *Phaeosphaeria nodorum*.

Australian cultivars with *tsn1* and *Tsn1* are listed in {10540}.

Tsn2{10344}. Conditions resistance to race 3 {10344} 3BL{10344}. **sutv:** LDN(DIC-3B){10344}. **tv:** *T. turgidum* no. 283, PI 352519{10344}; *T. dicoccoides* Israel-A{10344}. **ma:** Identified as a QTL in region *Xgwm285-3B* - *Xwmc366.2-3B* (R^2=91%){10344}; Also classified as a single gene: *Xgwm285-3B* - 2.1 cM - *tsn2* - 15.2 cM - *Xwmc366.2-3B*{10344}.

102.2. Insensitivity to tan spot toxin (chlorosis)

Tsc1{344}. Sensitivity to Ptr ToxC {344}. 1AS{344}. **v:** 6B365{0315}; Opata 85{344}. **v2:** Kulm *Tsn1*{0315}; Trenton *Tsn1*{0315}. **ma:** *Gli-A1* - 5.7 cM - *Tsc1* - 11.7 cM - *XksuD14-1A*{0315}.

According to {10376} the same allele, presumably *tsc1*, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN2137 in crosses with 6B-365.

tsc1{344}. Insensitivity is recessive. *QTsc.ndsu-1A* {9924}. **v:** Katepwa{0315}; Opata 85{344}; Synthetic W-7984{0315}.

Tsc2. Sensitive to Ptr ToxB {10015}. 2BS {10015}. **bin:** 2BS3 0.84-1.00. **v:** Katepwa{10871}; Synthetic W-7984{10015}.

tsc2. Insensitivity allele {10015} **v:** Opata 85{0315, 10015}; Salamouni{10871}. **tv:** Altar 84{10871}. **ma:** *Xmag681-2B/XTC339813* - 2.7 cM - *Tsc/XBE444541* - 0.6 cM - *XBE517745*{10871}; An XBE444541 EST-STS co-segregating marker for *Tsc2* was developed and lines with *tsc2* produced a 505 bp fragment whereas those with *Tsc2* produced a 340 bp band{10871}.

QTsc.ndsu-1A{9924}. Resistance is likely recessive {344} [*Tsc1*{344}]. 1AS{344}. **v:** Synthetic W7984{344}. **ma:** Association with *Gli-A1*{344,0040,0264}.

QTsc.ndsu-1A, or a closely associated gene, confers insensitivity to Ptr ToxC, see {0315}. Inoculation with purified toxin Ptr ToxC was used to map this locus. *QTsc.ndsu-1A* confers resistance in both seedlings and adult plants.

QTsc.ndsu-4A. 4AL{0090}. **v:** Opata 85/Synthetic W-7984 (ITMI) RI mapping population; resistance was contributed by W-7984{0090}; In W-7976/Trenton resistance was contributed by W-7976{0264}. **ma:** Association with *Xksu916(Oxo2)-4A* and *Xksu915(14-3-3a)-4A*{0090}; In W-7976/Trenton there was association with *Xwg622-4A*{0264}; Minor QTLs in chromosomes 1AL, 7DS, 5AL and 3BL were associated with resistance in adult plants{0264}.

QTLs: 'ITMI population': In addition to *tsc2* which accounted for 69% of the phenotypic variation in response to race 5, a QTL in chromosome 4AL (*Xksu916(Oxo)-4AS*, W-7948) accounted for 20% of the phenotypic variation {10015}.

Salamouni/Katepwa: RIL population: variation at the *Tsc2* locus explained 54% of the variation in response to race DW5 {10871}.

102.3. Resistance to tan spot

Tsr1. [*tsn1* See: Insensitivity to tanspot toxin]. Resistance is recessive. 5BL. **v:** Genetic stocks that do not have *Tsn1* and other genes that respond to toxins produced by the pathogen.

The gene in Erik was allelic with resistance in a diverse set of genotypes including spelt and durum derivatives {10557}.

Tsr2. Resistance is recessive. Confers resistance to race 3 {10344}. [*tsn2*{10344}]. 3BL{10344}. **sutv:** LDN (DIC-3B){10344}. **tv:** *T. dicoccoides* Israel-A{10344}. **tv2:** *T. turgidum* no. 283, PI 352519 *Tsr5*{10344}. **ma:** Identified as a QTL in region *Xgwm285-3B* - *Xwmc366.2-3B* (R^2 = 91%){10344}; also classified as a single gene: *Xgwm285-3B* - 2.1 cM - *tsr2* - 15.2 cM - *Xwmc366.2-3B*{10344}.

Tsr3. [*tsn3*{10394}]. 3D{10394}.3DS{10419}. **v:** XX41 = [Langdon/*Ae. tauschii* CI 00017]{10394}; XX45{10394}; XX110{10394}. **dv:** *Ae. tauschii* CI 00017{10394}. **ma:** *Xgwm2a* - *tsn3*, 15.3 cM, 14.4 cM and 9.5 cM in CS/XX41, CS/XX45 and CS/XX110, respectively{10419}.

Resistances in XX41 and XX110 were recessive whereas that in XX45 was dominant - all three were hemizygous-effective {10394}. The genes were given different temporary designations {10394, 10419}, but all will be considered to have a common gene until they are shown to be different.

Tsr4. Resistance is recessive. Resistance to race 1 (culture ASC1a) {10350}. [*tsn4*{10350}]. 3A{10350}. **v:** Salamouni{10350}.

Tsr5. [*tsn*{10509}]. 3BL{10509}. **tv2:** *T. turgidum* no. 283, PI 352519 *Tsr2*{10509}. **ma:** *Tsr5* - 8.3 cM - *Xgwm285-3B* - 2.7 cM - *Tsr2*{10509}.

Tsr6{10668}. Resistance is recessive. 2BS{10668}. **v:** ND-735{10668}. **ma:** *Xwmc382-2B* - 15.3 cM - *wPt-0289* - 4.6 cM - *Tsr6* - 18.7 cM - *Xwmc-2B*{10668}.

According to {10668} *Tsr6* should be identical to *tsc2* (see Insensitivity to tan spot toxin (chlorosis)).

TsrAri{10765}. Recessive 3A{10765}. **v:** Arina{10765}; Heines VII{10765}; Zenith{10765}.

TsrHar{10590}. 3B{10590}. **v:** Dashen{10590}; HAR 604{10590}; HAR 2562{10590}. Effective against races ASC1a (race 1) and DW-16 {10590}.

Grandin(S)/BR34(R) RILs: QTL in 1BS, *QTs.fcu-1BS*, (13-29% of variation depending on race) and 3BL, (13-41%) were involved in resistance to 4 races. Five other QTL showed race specific responses {10248}.

Introgressions of genes for insensitivity to Ptr ToxA and Ptr ToxB are outlined in {10153}.

Batavia (S) / Ernie (R): DH population tested over three years. Four (1A(Ernie), 7A, 2BS, 3BS(Batavia)), five (2BS, 5BL(E), 3D, 6A, 7D(B)) and four (2BS, 5BL(E), 1A, 6A(B),) QTL accounted for most of the variation in each year. The greatest effect across years was the QTL on chromosome 2BS (R^2=0.382, 0.298 and 0.362, respectively). This QTL was validated in four additional populations {10782}.

TA4152-60(R)/ND495(S)DH population. Five QTLs for resistance, all from TA4152-60 {10580}, viz., *QTs.fcu-2AS* and *QTs.fcu-5BL.1* conferring resistance to all races used, *QTs.fcu-5AL* conferring resistance to races 1, 2 and 5, *QTs.fcu-5B.2* conferring resistance to races 1 and 2, and *QTs.fcu-4AL* conferring resistance to race 3.

WH542(R)/HD29(S) RIL population: SIM indicated QTL on chromosomes 1B, 3AS, 3BL, 5B and 6BS, but only two were confirmed by CIM, *Qts.ksu-3AS* flanked by *Xbarc45-3A* and *Xbarc86-3A* (LOD 5,4, R^2 = 0.23) and *Qts.ksu-5BL* (probably *Tsn1*) flanked by *Xgwm499-5B* and *Xest.stsbe968-5B* (LOD 6,5, R^2 = 0.27) {10552}.

Wangshuibai / Ning 7840: RIL population: Race 1: *QTs.ksu-1AS*, R^2=0.39 (nearest marker *Xcfa2153-1A* and *QTs.ksu-2BS*, R^2=0.04) (nearest marker *Xbarc2-2B* {10753}.

103. Reaction to *Rhizoctonia* spp.

Cause of Rhizoctonia root rot.

Rot1{10761}. **v:** Scarlet-Rz1{10761}.

Scarlet-Rz1 was produced by mutagenesis {10761}.

104. Reaction to *Sitobion avenae*

English grain aphid.

Sa1{10877}. [*RA-1*{10877}]. 6AL{10877}. **tv:** C273{10877}. **ma:** *Xwmc179-6A* - 3.37 cM - *Sa1* - 4.73 cM - *Xwmc580-6A*{10877}.

105. Reaction to *Sitodiplosis mosellana* (Gehin)

Insect pest: Orange blossum wheat midge, Wheat midge. This pest should not be confused with *Contarinia tritici*, the yellow blossom wheat midge.

Sm1{0218}. 2B{0218}. **v:** Augusta{0218}; Blueboy{0218}; Caldwell{0218}; Clark{0218}; FL302{0218}; Howell{0218}; Knox 62{0218}; Mono{0218}; Seneca{0218}. **ma:** Linked to a SCAR marker{0223}; *Sm1* was mapped to a 2.5 cM interval on chromosome 2BS flanked proximally by AFLP-derived SCAR marker *WM1* and distally by SSR *Xgwm210-2B*{10291}.

QTL:

Reeder I/Conan: RIL population: *QSm.mst-1A*, flanked by *Xwmc59-1A* and *Xbarc1022-1A* was the most effective and constant QTL for reduced larval infection over two years (R^2=0.17 and 0.34) {10841}. RILs with this QTL in three genetic backgrounds had reduced infestations of 42% {10841}.

106. Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)

Insect pest: Greenbug

Gb1{1514}. Recessive. [*gb1*{222}]. **v:** CI 9058{222}; Dickinson Selection 28A{222}.

Gb2{1313,1514}. 1A {554} = T1AL.1R#2S{389}. **v:** Amigo CI 17609{1313}; Century{0008}; TAM107{0008}; TAM200{0008}; TAM202{0008}. **ma:** 2.7 cM proximal to *Sec1* in 1RS, but co-segregated with *Sec-1P*{10167}; Within the 1R segment: *Gb6* - 15.8 cM - *Gb2* - 11.4 cM - *XIA294*{10764}.

Gb3{624,1514}. Resistance in Largo and derivatives was controlled by multiallelic complementary genes {783}. *Gb3* was postulated to be one of the loci concerned. 7D{554}.7DL{0319}. **bin:** 7DL3 0.82-1.00. **v:** Largo CI 17895{622}; TAM110{0319}; TAM112{10764,0194}; TXGBE373{0319}. **al:** Insave rye. **tv:** *Ae. tauschii* PI268210{10907}. **ma:** Completely associated with 2AFLP markers {0319}. These were also present in germplasm line KS89WGRC4, implying the likely presence of *Gb3* or a closely linked resistance gene{0319}; *Xgwm037-7D* - 0.4 cM - *Gb3/Xwmc634-7D* - 0.8 cM - *Xbarc76-7D*{10169}; *H1067J6-R* - 0.7 cM - *Gb3* - 0.4 cM - *H1009B3-F*{10907}.

Gb4{523,1514}. 7DL{10267}. **v:** CI 17959{903}.

Gb4 is either closely linked or allelic to *Gb3* {10267}.

Gb5{1514,1515}. 7S(7A){391}. **su:** CI 17882; CI 17884; CI 17885{1515}.

Gb6. 1A = T1AL.1R#2S{1151}. **v:** GRS1201{1152}; GRS1202{1152}; GRS1203{1152}; GRS1204{1152}; GRS1205{1152}; N96L9970{10764}; see also *Pm17* (Reaction to

Blumeria graminis). **su:** Tx4386{1150}. **ad:** Tx4333{1150}. **al:** Insave rye. **ma:** Within the 1R segment: *Gb6* - 15.8 cM - *Gb2* - 11.4 cM - *XIA294*{10764}.

Gb7{10169}. 7DL{10169}. **v:** Synthetic W7984{10169}. **tv:** *Ae. tauschii* TA1651{10169}. **ma:** *Xwg420-7D* - 2.1 cM - *Gb7* - 13.4 cM - *Xwmc671-7D*{10169}.

Gba{10267}. 7DL{10267}. **v:** TA4152L94 = CETA/*Ae. tauschii* Wx1027{10267}. **ma:** *Xwmc671-7D* - 34.3 cM - *Gba* - 20.7 cM - *Xbarc53-7D*{10267}.

Gbb{10267}. 7DL{10267}. **v:** TA452L24 = CROC 1/*Ae. tauschii* Wx224{10267}. **ma:** *Xwmc671-7D* - 5.4 cM - *Gbb* - 20.2 cM - *Xbarc53-7D*{10267}.

Gbc{10267}. 7DL{10267}. **v:** TA4063.1 = 68111/Rugby//Ward//*Ae. tauschii* TA2477{10289}. **ma:** *Xgwm671-7D* - 13.7 cM - *Gbc* - 17.9 cM - *Xgdm150-7D*{10267}.

Gbd{10267}. **v:** TA4064.1 = Altar 84/*Ae. tauschii* TA2841{10267}. **ma:** *Xgwm671-7D* - 7.9 cM - *Gbd* - 1.9 cM - *Xwmc157-7D*{10267}.

Gbx1{10267}. [*Gbx*{10267}]. 7DL{10267}. **v:** KS89WGRC4 = Wichita/TA1695//2*Wichita{10267}. **dv:** *Ae. tauschii* TA1695{10267}. **ma:** *Xwmc157-7D* - 2.7 cM - *Xgdm150-7D*{10267}.

Gbx2{10267}. [*Gbx*{10267}]. **v:** W7984{10267}. **ma:** *Gbx2* was located 8.8 cM from *Gb3*{10267}.

Gby{10192}. 7A{10192}. **v:** Sando's Selection 4040{10192}. **ma:** *Xpsr119-7A/Xbcd98-7A* - 5.8 cM - *Gby* - 3.8 cM - *Xpr1B-7A*{10192}.

Gbz{10171}. 7DL{10171}. **v:** KSU97-85-3{10171}. **tv:** *Ae. tauschii* TA1675{10171}. **ma:** *Xgdm46-7DL* - 9.5 cM - *Xwmc157-7D/Gb3/Gbz* - 5.1 cM - *Xbarc53-7D*{10171}; *Xwmc671-7D* - 3.9 cM - *Gbz/Xwmc157-7D* - 5.1 cM - *Xbarc53*{10267}.

QTL: Antibiosis was associated with several markers, including *Rc3* (7DS) in chromosome 7D {10167}. ***QGb.unlp.6A***, for antixenosis was associated with *Xgwm1009-6A* and *Xgwm1185-6A* in a CS/CS(Synthetic 6A) DH population {10216}.

107. Reaction to Soil-Borne Cereal Mosaic Virus

Syn.: Soilborne wheat mosaic. Vectored to the roots by the fungus, *Polymyxa graminis*

Sbm1{10614}. [*SbmCz1*{10132}]. 5DL{10614}. **v:** Cadenza{10132}; Tonic{10614}. **ma:** *Xbarc110-5D* - 14.7 cM - *Sbm1* - 2.1 cM - *Xwmc765-5D* - 3.1 cM - *Xbarc144-5D/Xwmc443-5D/RRES01-5D*{10614}; Caps marker RRESO1 was developed from an AFLP fragment{10614}.

Sbm1 was identified in a DH population of Avalon (susceptible)/Cadenza {10132}.

SbmTmr1{10683}. 5D{10683}. **v:** TAM 107-R7{10683}.

SBWMV{10685}. 5D{10685}. **v:** KS96WGRC40{10685}. **dv:** *Ae. tauschii* TA2397{10685}. **ma:** *Xcfd010-5DL* - 9.5 cM - *SBWMV* - 11.1 cM - *Xbarc144-5D*{10685}. The relationship of this gene to *Sbm1* is not known.

A major QTL, ***QSbv.ksu-5D***, (R^2=0.38) was found in Karl 92*2/TA4152-4 {10273}; the resistance was contributed by Karl 92.

108. Reaction to *Tapesia yallundae*. (Anomorph: *Pseudocerosporella herpotrichoides* (Fron) Deighton)

Disease: eyespot, strawbreaker footrot.

Pch1. [*Pch*{261}]. 7D{591,592}.7DL{708,1603}. **s:** Courtot*/Roazon 7D{592}; Hobbit Sib*/VPM1 7D{591}. **v:** *Ae ventricosa* derivative{261}; Coda{10513}; H-93-70{236,1521}; Hyak{021}; Madsen{020}; Rendezvous{1603}; Roazon{591}; 5L 219{1521}.

7A{0224}. **tv:** Five recombinant lines{0224}. **al:** *Ae. ventricosa*{261}. **ma:** *Pch1* was linked to *Ep-D1* and mapped 2 cM from microsatellite marker *XustSSR2001-7D*{10070}; *Ep-*

d1b was a more reliable marker than the STS for selecting *Pch1*{10238}; Leonard et al. {10513} predicted that *Ep-D1* might encode an oligopeptidase B, and by comparative genetics, developed primers to a wheat oligopeptidase B-encoding wheat EST BU1003257. Complete linkage occurred for a derived STS marker *Xorw1* and *Pch1* in a Coda/Brundage RIL population and the marker identified the presence or absence of *Pch1* among 44 wheat accessions{10513}.

Pch1 is closely linked with *Ep-V1* {973}. Delibes *et al.* {236} concluded that *Pch1* was not located in chromosome 7D whereas Law *et al.* {776} found that H-93-70 possessed a unique allele, *Ep-D1b,* in common with VPM1 and its derivatives. Eyespot resistance and *Ep-A1b* in chromosome 7A were genetically associated {704}.

Pch2{228}. 7A{704}.7AL{228,229}. **s:** CS*/Cappelle Desprez 7A{704,228}. **v:** Cappelle Desprez{704,228}. **ma:** *Xcdo347-7A* (distal) - 11 cM - *Pch2* - 18.8 cM - *Xwg380-7A* (proximal){229}.

According to {0380}, this gene is not effective at the adult plant stage. Instead, the adult resistance of Cappelle-Desprez was controlled by a gene on chromosome 5A with the possibility of two less effective genes on 1A and 2B.

Pch3{616}. **ad:** CS + 4V{1050}.

Pch_{Dv}{618}. 4VL{618}. **ad:** Wheat + 4V{618}. **su:** Wheat 4VL(4D), Yangmai 5{618}. **ma:** Distally located; Cent...*Xcdo949-4V* - 16 cM - Pch_{Dv} - 17 cM - *Xbcd588-4V*{618}.

QPch.jic-5A{10771}. **bin:** 5AL-6 0.68-0.78. **ma:** Closely associated with *Xgwm639-5AL*{10771}.

109. Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*

Disease: Bunt, dwarf smut, stinking smut.

Bt1. [*M1*{135}]. 2B{1310}. **s:** CS*7/White Federation 38{1304}. **v:** Albit{129}; Banner Berkeley{129}; Federation 41{137}; Regal{129}; Sherman{137}; White Federation 38{1166}; White Odessa{137}. **v2:** Columbia *Bt6*{1005}; Hussar *Bt2*{135}; Hyslop *Bt4*{733}; Martin *Bt7*{135}; McDermid *Bt4*{734}; Odessa *Bt7*{137}; Tyee *Bt4*{022}.

Bt2. [*H*{129}]. **v:** Canus{137}; Selection PS60-1-1075{551}; Selection 1403{137}. **v2:** Hussar *Bt1*{135}.

Bt3. **v:** Florence{202,203}; Ridit{152,1000,1395}.

Bt4. Since *Bt4* and *Bt6* are very similar, as well as closely linked, only Turkey 3055 should be used as a definite source of *Bt4,* and Rio should be used as the source of *Bt6*. [*T*{136}]. 1B{1005,1274,1285}. **v:** Bison{1285}; Kaw{1285}; Nebred{1285}; Omaha{1285}; Oveson{1235}; Tres {heterogeneous}{023}; Turkey 1558{137}; Turkey 2578{137}. **v2:** Hyslop *Bt1*{733}; McDermid *Bt1*{734}; Oro *Bt7*{137}; Turkey 3055 *Bt7*{137}; Tyee *Bt1*{022}.

Bt5. 1B{1001}. **v:** Hohenheimer{397}; Selection R60-3432{551}.

Bt6. Since *Bt4* and *Bt6* are very similar, as well as closely linked, only Turkey 3055 should be used as a definite source of *Bt4,* and Rio should be used as the source of *Bt6*. [*R*{1418}]. 1B{1005}. **v:** Rio{1418}; Turkey 10095 & 10097{053}. **v2:** Columbia *Bt1*{1005}.

Bt7. [*M2*{1275}]. 2D{1000}. **s:** CS*7/Cheyenne 2D{1000}. **v:** Baart{1275}; Cheyenne{1000}; Federation{1275}; Gallipoli{1000}; Onas{1275}; Ranee{1000}; Selection 1833{556}. **v2:** CI 7090 *Bt9*{1000}; Martin *Bt1*{137}; Odessa *Bt1*{137}; Oro *Bt4*{1000}; Turkey 3055 *Bt4*{1000}.

Bt8{1558}. **v:** HY476{10181}; PI 178210{1558}; Yayla 305{1558}.

Bt9{1006}. **v:** PI 166910{1006}; PI 166921{1006}; PI 167822{1006}; Selection M69-2073{551}. **v2:** CI 7090 *Bt7*{1000}; Jeff *Bt10*{1436}; PI 178383 *Bt10*{1006}; Ranger *Bt10*{1438}.

Bt10{1004}. 6DS{10721}. **i:** BW553 = Neepawa*6//Red Bobs/PI 178383{10475}. **v:** AC2000{10181}; AC Cadillac{10181}; AC Carma{10181}; AC Crystal{10181}; AC

Foremost{10181}; AC Taber{10181}; AC Vista{10181}; Fairview{1183}; PI 116301{1004}; PI 116306{1004}; Selection M69-2094{551}; Present in lines with *SrCad*{10733}. **v2:** Jeff *Bt9*{1436}; PI 178383 *Bt9*{1000}; Ranger *Bt9*{1438}; Others{239,0128}. **ma:** *Bt10* was completely linked with a 590 bp fragment produced by UBC primer 196{239}; RAPD - 1.5 cM - *Bt10*{763}; *Bt10/FSD_RSA* - 19.3 cM - *Xgwm469-6D* - 1.8 cM - *Xwmc749-6D.*
The RAPD fragment was sequenced and converted to a diagnostic PCR marker for *Bt10* in {0128}.

QTL: Bizard (R) / 8405-JC3C (S): DH population. Resistance and markers *Xgwm374-1BS, Xgwm364-1BS* and *Xbarc128-1BS* were within a 3.9 cM interval {10783}.

110. Reaction to *Tilletia indica* Mitra

Disease: Karnal bunt.

Kb1{394}. **v:** Chris{394}; CMH77.308 *Kb2*{394}.
Kb2{394}. **v:** PF7 113{394}; CMH77. 308 *Kb1*{394}; Shanghai #8 *Kb4*{394}.
Kb3{394}. **v:** Amsel{394}.
Kb4{394}. **v:** Shanghai #8 *Kb2*{394}.
Kb5{394}. Recessive {394} **v:** Pigeon *Kb6*{394}.
Kb6{394}. Recessive {394} **v:** Pigeon *Kb5*{394}.
Qkb.cnl-3B{9956}. **ma:** Located in the interval *XATPase-3B* - *Xcdo1164-3B.*
Qkb.cnl-5A.1{9956}. **ma:** Located in the interval *Xmwg2112-5A* - *Xcdo20-5A.*
Qkb.cnl-5A.2{9956}. **ma:** Located in the interval *Xabg391-5A* - *Xfba351-5A.*
Qkb.ksu-4BL.1. WL711/HD29 (R) RILs: $R^2 = 0.25$, associated with *Xgwm538-4B* {10498}. WH542/W485 (R) RILs: $R^2 = 0.15$, *Xgwm6-4BL* - *Xwmc349-4BL* interval {10499}.
Qkb.ksu-5BL.1. WH542/HD29 (R) RILs: $R^2 = 0.19$, *Xgdm116-5BL* - *Xwmc235-5BL* {10499}.
Qkb.ksu-6BS.1. WH542/HD29 (R) RILs: $R^2 = 0.13$, *Xwmc105-6BS* - *Xgwm88-6BS* {10499}.

111. Reaction to *Ustilago tritici* (Pers.) Rostrup

Disease: Loose smut.

Ut1{1073}. **v:** Florence/Aurore{1073}; Renfrew{1073}; Red Bobs{1074}.
Ut2{1073}. **v:** Kota{1073}; Little Club{1073}.
Ut3{1074}. **v:** Carma{1074}.
Ut4{1074}. **v:** Thatcher/Regent{1074}.
Utd1{10684}. 5BS{10684}. **tv:** D93213{10684}; P9163-BJ08*B{10684}; VIR 51658{10684}. **ma:** SCAR - 3.2 cM - *Utd1* - 5.9 cM - *Xgwm234-5B*{10684}.
Ut-x{1164}. **v:** Biggar BSR{1164}. **ma:** *Xcrc4-2B* - 14 cM - *Ut-x* - 10 cM - *Xabc153-2B.2*{1164}; *Xcrc4-2B.2* (Syn. *Xcrc4.2*) is a SCAR.
Resistance to race 19 was associated with chromosome 6A of Cadet, Kota, Thatcher and TD18 {0208}. In the case of Cadet, resistance was localized to 6AS {0208}.

112. Reaction to Wheat Spindle Streak Mosaic Bymovirus (WSSMV)

QTL : 79% of the variation between Geneva (resistant) and Augusta (susceptible) was associated with markers *Xbcd1095-2D* and *Xcdo373-2D* located 12.4 cM apart in chromosome 2DL {0131}. WSSMV is soil-borne and vectored by the fungus *Polymxa graminis*. This virus has some sequences similarity to Wheat Yellow Mosaic {10285}.

Wss1{10271}. Derived from *Haynaldia villosa* 4D(4DL.4VS){10271}.T4VS.4DL{10271}. **tr:** NAU413{10271}. **su:** Yangmai#5 4V(4D){10271}.

113. Reaction to Wheat Streak Mosaic Virus

Vectored by wheat curl mites, *Eriophyes tulipae* and *E. tosichella*. See: Resistance to colonization by *Eriophyes tulipae*. According to {10226} WSMV may also be see-borne. At least some sources of resistance to WSMV are also effective against Triticum mosaic virus.

Wsm1{379,440}. Derived from *Th. intermedium*. .

4D = T4DL.4J^{S}S{391,389}. **i:** Karl*4/CI 17884 = PI 583794 = KS93WGRC27{440}.**v:** CI 17766 = B-6-37-1{391,800,1543}; CI 17884{391}; KS90H445{391}; KS90H450{391}; CI 17883{389}.**ad:** CI 17881; CI 17886{391}.**su:** 4J^{S}S(4A):CI 15092{391}; 4J^{S}S(4D):CI 17882 and CI 17885{391}.**ma:** *Wsm1* co-segregated with a STS amplified by the primer set STSJ15{1456}.

4D =T4DL.4DS-4J^{S}S{10788}. **v:** KS08WGGRC50{10788}.

4A {800} = T4AL.4J^{S}S{391}. **:** .

6A=T6AS.4J^{S}L + T6AL-4J^{S}S{389}. **:** .

Wsm1 is located in 4J^{S}S (formerly 4Ai#2S). CI 17882, CI 17884, CI 17885 and KS90H445 also carry a 7S *Ae. speltoides* chromosome substituting for 7A (See Reaction to *Schizaphis graminum*).

Wsm1 also confers resistance to Triticum Mosaic Virus {10788}.

Wsm2{10802,10898}. 3BS{10802}. **v:** CO960293-2{10802}; RonL{10898}; Snowmass{10802}. **ma:** *Wsm2* - 5.2 cM - *XSTS3B-55*{10802}; *Xbarc102-3B* - 1.6 cM - *Wsm2*{10802}; *Xgwm389-3B* - 30.8 cM - *Wsm2* - 45.2 cM - *Xgwm566-3B*{10898}.

Wsm2 confers resistance at temperatures below 19C {10802}.

Wsm3{10775}. 7B(7BS.7S#3L){10775}. **v:** TA5624{10775}.

114. Reaction to *Xanthomonas campestris* pv. *undulosa*

Disease: Bacterial leaf streak

Bls1{244}. **v:** Pavon *Bls2*{244}; Mochis T88 *Bls3 Bls4*{244}; Angostura F88 *Bls5*{244}.

Bls2{244}. **v:** Pavon *Bls1*{244}.

Bls3{244}. **v:** Mochis T88 *Bls1 Bls4*{244}.

Bls4{244}. **v:** Mochis T88 *Bls1 Bls3*{244}.

Bls5{244}. **v:** Turnco F88{244}; Angostura F88 *Bls1*{244}.

bls1 bls2 bls3 bls4 bls5: Alondra {244}.

115. Resistance to Colonization by *Eriophyes tulipae* (*Aceria tulipae*)

Mite pest: Wheat curl mite.

Eriophyes tulipae is the vector of wheat streak mosaic virus (WSMV) and the wheat spot mosaic agent (WSpM).

Cmc1{1467}. 6DS{1576}. **i:** Norsa*5/Cmc1{10166}. **v:** *Ae. squarrosa* CI4/Novamichurinka (= AC PGR 16635){1467}; Norstar derivative{0222}.

Cmc2{1573}. Derived from *Th. elongatum*. 6A = T6AS.6Ae#2S{389}.5B = T5BL.6Ae#2S{389}.6D {1575} = T6DL.6Ae#2S{1575,389}. **i:** Norstar*5/Cmc2{10166}. **v:** 875-94-2{389}. **tr:** Rescue Derivative{1575}. **su:** Cadet 6Ae#2(6A){1575}; Cadet 6Ae#2(6D){1574}; Rescue 6Ae#2(6A){1574}; Rescue 6Ae#2(6B){1574}; Rescue 6Ae#2(6D). **ad:** Cadet + mono-6Ae#2{1574}; Rescue + 6Ae#2{1574}.

Cmc3{0222}. 1A = 1AL.1RS. **i:** Norstar*5/Cmc3 {10166}. Need to confirm relationship of 1RS segment in Amigo and Salmon as this NIL was derived from KS80H4200 a Chinese Spring Salmon line{10166}. **v:** Amigo; TAM107{0222}. **v2:** KS96GRC40 *Cmc4*{0222}. **ma:** Wheat lines with the 1RS segment and hence *Cmc3* can be selected with the rye-specific SSR *Xscm09-1R*{0222}.

Cmc4{0222}. 6DS{0222}. **v2:** KS96WRC40 *Cmc3*{0222}. **dv:** *Ae. tauschii* accession{0222}. **ma:** *XksuG8-6D* - 6.4 cM - *Cmc4* - 4.1 cM - *Xgdm141-6D*{0222}.

116. Reaction to Wheat Yellow Mosaic Virus

WYMV is soil-borne and vectored by the fungus *Polymxa graminis*. This virus has some sequence similarity to Wheat Spindle Streak Mosaic {10258}. another bymovirus.

YmIb{10750}. 2DL{10750}. **v:** Ibis{10750}; Jagger{10750}; KS 831957{10750}; Madsen{10750}; Yumechikara{10750}. **ma:** *Xwmc181-2D* - 12.4 cM - *YmIb* - 2.0 cM - *Xcfd16-2D* - 2.0 cM - *Xwmc41-2D* - 3.1 cM - *Xcfd168-2D*{10750}.

The relationship of *YmIb* to previously mapped gene in 2DL for resistance to WYMC and WSSMV in Yangfu 9311 {10258} and a Geneva derivative {0131} were not established.

YmYF{10258}. 2DL{10258}. **v:** Yangfu 931{10258}. **ma:** *Xpsp3039-2D/Xwmc181-2D* - 0.7 cM - *Xwmc41-3D* - 8.1 cM - *Xgwm349-2D*{10258}.

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