

V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2020 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 13th International Wheat Genetics Symposium held in Yokohama, Japan, is available on the Komugi (<http://www.shigen.nig.ac.jp/wheat/komugi/top/top.jsp>) and GrainGenes (<http://wheat.pw.usda.gov/GG2/Triticum/wgc/2008/>) websites. Supplements 2014, 2015, 2016, 2017, 2018, and 2019 also are available at those sites as well as this *Annual Wheat Newsletter*.

Suggestions of information, preferably in suitable format, for listing in the Wheat Gene Catalogue can be submitted to the curators. Publication details on papers listed as ‘Draft Manuscript’ or ‘In press’ also would be helpful.

Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

1.1. Sphaerococcum

S-DI. 3DS: Add ‘11415’ to the references.

S-DIb. Add syn: *Tasg-DI* {11415}.

v: Add: Nongda 4332 {11415}.

ma: Located between markers *Xgwm341-3DS* and *Xgdm72-3DS* {11415}.

c: The sphaerococcum phenotype is caused by a gain of function mutation in serine/threonine kinase glycogen synthase kinase 3 (STKc_GSK3) that in rice affects the brassinosteroid signaling pathway and grain shape {11415}. There is a Lys286Glu substitution in the ninth exon of *TraesCSD01G137200* {11415}.

11. Boron tolerance

Bo1. Add syn: *Bot-B5b* {11432}.

c: Boron transporter-like gene {M2239}. GenBank KF148625.

Bo1 functions as a boron transporter {11432}.

Bo4 {11432}. *BOT(TP4A-B5C)* {11432}. 4AL {11431}.

v: G61450 {11431}.

Bo4 is a dispersed duplication of *Bo1* {11432}.

Add note following the *Bo4* entry: A homoeologous nomenclature based on annotated boron transporters inferred from the IWGS CS sequence is provided in Extended Data Table 1 in {11432}.

18. Dormancy (seed)

18.3. Pre-harvest sprouting

Annon 0711 (res) / Henong 825 (sus): RIL population. Differences in germination index were attributed to a 33-bp insertion in the promoter (possibly the AP2 binding site) of *TaMFT-3A* in Annon 0711 relative to Henong 825. *TaMFT-3A* encodes a phosphatidyl ethanolamine-binding protein {11410}.

Totoumai (res) / Siyong (sus): RIL population: A QTL on chromosome 4AL was delimited to a 2.9-cM interval flanked by GBS109947 and GBS212432; nine and two SNP were associated with minor QTL on chromosomes 5A and 5B, respectively {11408}.

Add at end of section: A GWAS identified 12 QTL for PBS resistance among which those on chromosomes 3AS and 4AL were most commonly detected {11409}.

29. Glaucousness (Waxiness/Glossiness)

29.1. Genes for glaucousness

Add at the beginning: The *W* loci are complexes of closely linked genes involved in beta-diketone synthesis.

- W1.** **v:** Bethlehem {11458}. **tv:** Kofa+*Lr19* {11458}.
w1. **su:** Bethlehem CASL*/*T. turgidum* subsp. *dicoccoides* TTD140 2BS(2B) {11458}.
tv: AUS2499 {11458}.
c: *W1* is a highly duplicated, variable gene cluster containing type-III polyploid synthase, hydrolase and cytochrome P450 genes and is homologous to the *Cer-cqu* cluster in barley {11458}.
- W3** {11456}. 2BS {M22063}. **v:** Bobwhite {11456}
w3. **v:** Bobwhite Mutant #056 {11456}.
ma: *Xwmc764-2B* – 0.6 cM – *Xwmc770/Xgwm148-2B* – 5.5 cM – *W3* {11456}.
- W4** {11457}. 3DL {11457}. **dv:** *Aegilops tauschii* KU-2126 {11457}.
w4. **dv:** *Aegilops tauschii* KU-2104 {11457}; KU-2105 {11457}.
ma: *Xgwm645-3DL* – 8.0 cM – *W4* – 8.9 cM – *Xbarc42-3DL* {11457}.

Add at the end of section: Glaucous synthetics LDN/KU-2104 and LDN/KU-2105 are presumed to have genotype *W1W1W4W4*.

29.2. Epistatic inhibitors of glaucousness

- Iw1.** **c:** *IWI* encodes a long non-coding RNA (LncRNA) that putatively arose from an inverted repeat of a carboxylesterase gene (80% homology) in the *W1* cluster that consists of *WI-COE* (non-annotated carboxylesterase), *WI-PKS* (*Traes_2BS_9E10D26DB*, polyketide synthase), and *WI-CYP* (*Traes_2BS_163390FC4*, cytochrome P450-type hydroxylase) {11459}. GenBank C-DNA sequence, KX823910. The IR region has >94% identity to an IR region in *Ae. tauschii* chromosome 2 that also produces miRNA and a marker-based location similar to that of *Iw2* {11459}.
- Iw3.** **sutv:** Add: Langdon*/*T. turgidum* subsp. *dicoccoides* 1B {11455}.
ma: *XWL1967/Xfcp168-1B* – 0.15 cM – *XWL3096* – 0.015 cM – *Iw3* – 0.12 cM – *Xpsp3000-1B* {11455}.

29.4. Leaf glaucousness

RAC875 (non-glaucous leaf) / Kukri (glaucous leaf): *QW.aww-3A*, nearest marker *Xwmc264-3A*, accounted for 36–40% of the phenotypic variation; other QTL were located on chromosomes 1D, 2B (2 QTL), 4D, 5B, and 2D {11460}.

GWAS of flag leaf glaucousness in a large panel of genotypes identified major QTL on chromosomes 2B (*W1/IW1*) and 3A {11482}.

49.2. Early leaf senescence

- Els2** {11472}. 2BL {11472}. **v:** LF2099 {11472}.
ma: *Xgpw4043-2B* – 8.87 cM – *Els2* – 22.27 cM *Xwmc149-2B* {11472}.

The incompletely dominant *Els2* mutant was found in an EMS-treated M_2 population of H261 {11472}.

44. Height

44.2. Reduced height: GA-sensitive

- ht12.** **i:** N98-2105, Yangmai 5*5 / Karcagi 522M7K {11428}.
ma: The *Rht12* phenotype is due to deletion of a 10.73-Mb terminal deletion of chromosome 5AL {11428}. Reduced plant height might be due to activation of *TaGA2ox-A14* {11428}.

44.3 Reduced height QTL

QHt.nau-2D {11463}. Recessive. Gibberellin-sensitive. 2DS {11463}.
bin: 2DS-0.47-1.00. **v:** EMS-Induced Dwarf Wangshuibai {11463}.
ma: *Xbarc-2D* – 2.6 cM-*2D* – *QHt.nau-2D* – 0.3 cM-*2D* – *Xgpw361-2D* {11463}.

49. Leaf Characteristics

49.1. Leaf erectness Currently: 49. Leaf Erectness
49.2. Leaf tip necrosis Currently: 50. Leaf Tip Necrosis
49.3. Seedling leaf chlorosis Currently: 64. Seedling leaf chlorosis
49.4. Early leaf senescence

Insert after ‘... *Ne2*.’ in the comments section: A similar situation was described in {11423} where a claimed a putatively novel gene was designated as *ylw-1*’.

48. Lack of Ligules

Add note at end of section:

An erect leaf mutant involving *TaSPL8* (SQUAMOSA promoter-binding protein-like transcription factor), a homolog of *LGI* in maize and rice and was located in chromosome 2D. Knockout mutants of *TaSPL8* orthologs led to a fully liguleless phenotype. The gene in 2D was identified as *TraesCS2D01G502900*. *TaSPL8* transcript was highly expressed in the laminar joint region and young spike. *TaSPL8-2D* transcript was produced at much higher levels than *TaAPL-2B*, whereas *TaSPL-2A* was produced at a minimal level {11401}.

53. Male Sterility**53.1. Chromosomal**

***Ms1*.** **c:** *Ms1* is a phospholipid-binding protein {11421}. Sequence: SRP113340. Encodes a 219 amino acid polypeptide with similarity to a large family of GPI-anchored lipid transfer proteins affecting exine development {11422}. *Ms-A1* = *TraesCS4A02G295900*; *Ms-B1* = *TraesCS4B02G017900*).

***ms1a*.** **c:** Terminal deletion {11422}.

***ms1b*.** **c:** Interstitial deletion {11422}.

***ms1c*.** **c:** Terminal deletion {11422}.

***ms1d*.** **v:** Add: Ningchen mutants *msd.1* and *msd.2* {11421}.
c: G329A {11421, 11422}.

***ms1e*.** **c:** G1431A del1432 {11421}; C1435T del {11422}.

***ms1f*.** **c:** G155A {11422}.

***ms1g* {11421}.** **c:** Deletion of entire sequence {11421}.

***ms1h* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: C1762T {11421}.

***ms1i* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: G1603A {11421}.

***ms1j* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: C1775A {11421}.

***ms1k* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: G1397A {11421}.

***ms1l* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: C226T {11421}.

***ms1m* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: C1472T {11421}.

***ms1n* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: T164A {11421}.

***ms1o* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: G281A {11421}.

***ms1p* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: G155A {11421}.

***ms1q* {11421}.** **v:** Ningchun 4 mutant {11421}.
c: C148T {11421}.

MsIr [11422]. *Mlh* {11422}.
v: Tilling mutant in Qual2000 {11422}.
c: G178A {11422}.

Add at end of section: *MsI* orthologs in the A and D genomes were epigenetically silenced {11421}.

Ms5. 3AL {11427}.
c: Encodes a glycosylphosphatidylinositol-anchored lipid transfer protein that is required for pollen exine development {11427}. *TraesCS3A02G217000* {11427}. GenBank MK577897.

ms5. *ms5a* {11427}.
v: H45 {11427}.
c: A G101A {11427}.

Complete sterility conferred by *ms5* is dependent on the homoeologous *ms-D* genotype – Ecalibur, Gladius, and RAC 875 have an *ms-D* allele that restores fertility to *ms5* genotypes {11427}.

Two non-functional *ms-B* alleles (Chinese Spring and Synthetic W7984 types) were identified {11427}.

57. Meiotic Characters

57.5. Unreduced gametes and polyploidization

QTug.sau-3B {11471}. **bin:** 5BS5-0.07-0.03.
ma: *Xgwm285-3B* – 1.0 cM – *Xcfp11012-3B* {11471}.

Identified in *T. turgidum*/*Ae. tauschii* hybrids involving Langdon durum (high unreduced gamete formation) crossed with AS313 and AS2225 (low unreduced gamete formation) topcrossed with *Ae. tauschii* AS60. The QTL was located near *Ttam*, a homologue of the *TAM* (tardy asynchronous meiosis/CYCA1;2) cyclin gene from Arabidopsis {11471}.

XX. Red Seed Colour

Add at end of section: A fourth QTL for red seed colour was detected on chromosome 1B in a GWAS of U.S winter wheat {11409}.

67. Response to Photoperiod

67.1. PPD1

QTL:

Insert at the beginning of section:

QPpd.zafu-4AL {11443}. 4AL {11443}.
s: CASL 4AL {11443}.
tv: *T. turgidum* subsp. *dicoccoides* TTD140 {11443}.
ma: Flanked by *M576* and *Xwmc468-4AL* in a 1.2-cM region {11443}.

Other publications reporting *Ppd* genes/QTL in the same region are reviewed in {11443}.

67.2. CONSTANS

Wheat genes *CONSTANS1* and *CONSTANS2* interact with *PPD1* to regulate photoperiodic response {11495}.

CONSTANS1

Triticum aestivum: *CO-A1* = *TraesCS7A02G211300*; *CO-B1* = *TraesCS7B02G118300*; *CO-D1* = *TraesCS7D02G212900*.
Triticum turgidum subsp. *durum* cv. Kronos: GenBank accession numbers: MT043302 (*CO-A1*); MT043303 (*CO-B1*) {11495}.

CONSTANS2

Triticum aestivum: *CO-A2* = *TraesCS6A02G289400*; *CO-B2* = *TraesCS6B02G319500*; *CO-D2* = *TraesCS-6D02G269500*.

Triticum turgidum subsp. *durum* cv. Kronos: GenBank accession numbers MT043304 (*CO-A2*) and MT043305 (*CO-B2*) {11495}.

71. Restorers for Cytoplasmic Male Sterility**71.1 Restorers for *T. timopheevii* cytoplasm**

- Rf3.** v: Add: Primepi {11476}.
 ma: Add: *Xbarc128-1Bs* – 5.3 cM – *IWB14060* – 2.0 cM – *Rf3/IWB72107/IWB73447* – 14.5 cM – *Xwmc406-1B* {11476}.
- Rf7** [{11473}]. *Rf6* {11473}. 5DS {11473}.
 v2: Primepi *Rf3* {11474}.
- Rf8** {11474}. 2DS {11474}. v: PWR4099 {11474}.
 ma: *Xwmc503-2D* – 3.3 cM – *Rf8* – 5.8 cM – *Xgwm296-2D* – 0.9 cM – *Xwmc112-2D* {11474}.
- Rf9** {11475}. 6AS {11475}. v: Gerek 79 {11475}.
 ma: *IWB72413-6A* – 4.3 cM – *Rf9* – 4.7 cM – *IWB1550-6A* {11475}.

71.5. Restorers for multi-species cytoplasm

Restorer of *Ae. kotschyi*, *Ae. uniaristata*, and *Ae. mutica* cytoplasmic male sterility.

- Rf^{multi}** {11477}. 1BS {11477}.
 v: All common wheat genotypes except *T. aestivum* subsp. *spelta* var. *duhamelianum* {11477}.
 ma: Localized to a 2.9 cM region in a 1BS map {11477}.
- r^f^{multi}**. v: *T. aestivum* subsp. *spelta* var. *duhamelianum* {11477}.

Sterility in the same plasmons is also found in lines with the T1BL·1RS translocation. Hohn & Lukaszewski {11478} produced a chromosome 1B_{1.6} translocation with a short rye insert replacing the *Rf^{multi}* region (*r^f^{multi}* equivalent) causing partial sterility that can be restored by most common wheat genotypes.

81. Tiller Inhibition

Following the *tin1* add note:

A near recessive gene, *ftin*, was located proximal to the *Tin1* locus in putative *Agropyron cristatum* derivative Pub-ing3558{11462}: *Xgwm136-1A* – 4.3 cM – *Xpsp2999-1A* – 0.7 cM – *Xcfa2153-1A* – 1.0 cM – *Ftin* {11462}.

Three QTL were located on chromosomes 2DL (*Qln.siau-2D*), 2BL, and 5AL in a RIL population from ‘H461 (low tillering) / CN16 (high tillering)’, but only the 2DL QTL was confirmed in RIL populations from ‘H461 / cm107’ and ‘H461 / MM37’ {11465}.

84. Yield and Yield Components**84.3.2 1,000-grain weight**

TaCKX6-D1 {11407}. 3D {11407}. Encodes a cytokinin oxidase/dehydrogenase.

- v: Hap a associated with high TKW has an 18-bp deletion relative to hap b: Wenmai 6, Yanzhan 1, Lumai 14 {11407}; Hap b: Bainong 321, Chinese Spring, Hanxuan 10, Neixiang 188 {11407}.
- ma: *Xcfd70-3D* – 3.7 cM – *TaCKX6-D1* – 2.0 cM – *Xwmc533-3D* {11407}.

TaGW2-6A. Insert at end of section: Encodes an E3 RING ligase {11122}.

84.7. Spikelet number/ear

QSns.sau-2DS {11424}. 2DS {11424}.

- v: RIL populations from ‘Line 20828 / Chuanong 16’, ‘Line 20828 / Shumai 51’, and ‘Line 20828 / Sy95-71’; LOD score 3.47–38.24, PV 10–46% in eight environments. Located in a 2-cM interval flanked by *Ax-109836946* (32.8 Mb) and *AX-111956072* (34.43 Mb) {11424}.

QSns.ucw-7AL {11496}. 7AL {11496}.

Underlying gene: *WHEAT ORTHOLOG OF APO1* (*WAPO1*), which is an orthologue of rice gene *ABER RANT PANICLE ORGANIZATION 1* (*APO1*).

WAPO-A1. *TraesCS7A02G481600* {11496}.

WAPO-A1a. Associated with low SNS; has a 115-bp promoter deletion and a D384N amino acid change {11496}.

- v: RAC875, Clark, Lancer, CDC Lanmark, Julius, Arina, Jagger, Cadenza, Robigus, and SY_Mattis {11496}.

tv: Kronos, Ben {11496}. Most frequent allele in durum {11496}.

WAPO-A1b. Associated with high SNS; has a C47F amino acid change and no promoter deletion {11496}.

- v: Berkut, Ning7840, PI 41025, MPV57, Platte {11496}. Most frequent allele in *T. aestivum*.

tv: Rare in durum {11496}.

- WAO-A1c.** Associated with low SNS; has the ancestral C47 and D384 amino acids and no promoter deletion {11496}.
v: AGS2000, LA95135, 26R61 {11496}.
tv: *T. turgidum* subsp. *dicoccoides* PI 471033 and PI 355455; *T. turgidum* subsp. *dicoccum* CIt 14135, PI 94638, and PI 298586; *T. turgidum* subsp. *durum* PI 286539 {11496}.
- WAO-A1d.** Associated with low SNS; has the ancestral C47 and D384 amino acids and no promoter deletion but differs from *WAO-A1c* by a C667 and G764A DNA changes {11496}.
tv: *T. durum* Rusty and Lang; *T. dicoccum* CIt 14919, PI 193877, PI 193882, PI 217640, PI 221400, PI 225332, PI 273980, and PI 94657 {11496}.

86. Proteins

86.3. Endosperm storage proteins

86.3.1. Glutenins

86.3.1.1. *Glu-1*

Glu-B1

Glu-B1d. 6+8. **tv:** Kronos {11497}.

Simultaneous and individual truncation mutations were found *Glu-B1x* and *Glu-B1y* subunits in Kronos mutant lines {11497}. Germplasm was accessioned as PI 692251 (T4-0865, *Bx6* single mutant), PI 692253 (T4-2197, *By8* single mutant), and PI 692252 (T4-1280, *Bx6* + *By8* combined mutant).

Add:

- Glu-B1cf*** {11490}. 20*+33* {11490}. **tv:** *T. turgidum* subsp. *durum* Mexican landrace accession 22 (CWI52215) {11490}.
- Glu-B1cg*** {11490}. 13+16* {11490}. **tv:** *T. turgidum* subsp. *durum* Mexican landrace accession 19 (CWI52200) {11490}.
- Glu-B1ch*** {11490}. 7+22 {11490}. **v:** *T. aestivum* subsp. *aestivum* cv. Wilbur (CW13735) {11490}.
- Glu-B1ci*** {11490}. 7+22* {11490}. **tv:** *T. turgidum* subsp. *durum* Iranian landrace accession 51 (CWI57280) {11490}.
- Glu-B1cj*** {11490}. 13*+15* {11490}. **tv:** *T. turgidum* subsp. *durum* Iranian landrace accession 46 (CWI56913) {11490}.
- Glu-B1ck*** {11491}. 15 {11491}. **v:** *T. aestivum* subsp. *compactum* PI 157920 {11491}.
- Glu-B1cl*** {11491}. 14+8 {11491}. **v:** *T. aestivum* subsp. *macha* PI 272554, PI 278660, PI 290507 {11491}.
- Glu-B1cm*** {11491}. 6+8* {11491}. **v:** *T. aestivum* subsp. *macha* PI 428177 {11491}.
- Glu-B1cn*** {11491}. 17 {11491}. **v:** *T. aestivum* subsp. *sphaerococcum* CIt 4531, PI 272581, PI 282452 {11491}.
- Glu-B1co*** {11493}. 20+22* {11493}. **tv:** *T. turgidum* subsp. *durum* Moroccan landraces MGB-2963, MGB-3152 {11493}.
- Glu-B1cp*** {11493}. 20* {11493}. **tv:** *T. turgidum* subsp. *durum* North American cv. MGB-66023 {11493}.

Glu-B1-1

Add:

- Glu-B1-1ao*** {11490}. 20* {11490}. **tv:** *T. turgidum* ss subsp p. *durum* Mexican landrace accession 22 (CWI52215) {11490}.

Glu-B1-2

Add:

- Glu-B1-2al*** {11490}. 33* {11490}. **tv:** *T. turgidum* s subsp sp. *durum* Mexican landrace accession 22 (CWI52215) {11490}.
- Glu-B1-2am*** {11490}. 22* {11490}. **tv:** *T. turgidum* s subsp sp. *durum* Iranian landrace accession 51 (CWI57280) {11490}.

86.3.1.2 *Glu-2*

Glu-B2

Add:

- Glu-B2d*** {11493}. 12.1 {11493}. **tv:** *T. turgidum* subsp. *durum* Moroccan landrace MGB-3125 {11493}.

86.3.1.3. *Glu-3****Glu-A3***

Add:

<i>Glu-A3ay</i> {11490}.	6+20 {11492}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> landraces BGE047515 and BGE047516 {11492}; Mexican durum landrace accession 10 (CWI52016) {11490}.
<i>Glu-A3az</i> {11490}.	6+10+11* {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> Mexican landrace accession 3 (CWI51941) {11490}.
<i>Glu-A3ba</i> {11490}.	5+11 {11492}.	tv: <i>T. turgidum</i> subsp. <i>turgidum</i> landrace BGE047535 {11492}; Iranian landrace accession 77 (CWI73342) {11490}.
<i>Glu-A3bb</i> {11493}.	20 {11492}.	tv: <i>T. turgidum</i> subsp. <i>dicoccon</i> landrace BGE047498 {11492}; <i>T. turgidum</i> subsp. <i>turgidum</i> landrace BGE047531 {11492}; <i>T. turgidum</i> subsp. <i>durum</i> Moroccan landrace MGB-16563 {11493}.
<i>Glu-A3bc</i> {11493}.	5** {11493}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> Moroccan cv. MGB-20 {11493}.

Glu-B3

Add:

<i>Glu-B3ae</i> {11490}.	1+3+16 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 56 (CWI57386) {11490}.
<i>Glu-B3af</i> {11490}.	1+3+17 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 74 (CWI71827) {11490}.
<i>Glu-B3ag</i> {11490}.	2+4+16 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 46 (CWI56913) {11490}.
<i>Glu-B3ah</i> {11490}.	8+9+16 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 65 (CWI57719) {11490}.
<i>Glu-B3ai</i> {11490}.	2+4+14+18 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 62 (CWI57615) {11490}.
<i>Glu-B3aj</i> {11490}.	19 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 77 (CWI73342) {11490}.
<i>Glu-B3ak</i> {11490}.	2+4+6*+15+19 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 69 (CWI71627) {11490}.
<i>Glu-B3al</i> {11490}.	2+4+7*+15+16 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 61 (CWI57614) {11490}.
<i>Glu-B3am</i> {11490}.	1+3+6*+13'+17 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 72 (CWI71759) {11490}.
<i>Glu-B3an</i> {11490}.	8+9+13'+17 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 58 (CWI57522) {11490}.
<i>Glu-B3ao</i> {11490}.	1+3+8'+17 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 50 (CWI57256) {11490}.
<i>Glu-B3ap</i> {11490}.	2+4+6*+9'+14+19 {11490}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> accession 78 (CWI73350) {11490}.
<i>Glu-B3aq</i> {11493}.	2+4+8+15+19 {11492}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> landraces BGE045634 {11492}; MGB-2963 {11493}.
<i>Glu-B3ar</i> {11493}.	1+3+7+15+18 {11493}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> landrace MGB-16563 {11493}.
<i>Glu-B3as</i> {11493}.	1+3+8+13+16+19 {11493}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> landrace MGB-3152 {11493}.
<i>Glu-B3at</i> {11493}.	2+4+17 {11493}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> landrace MGB-3125 {11493}.
<i>Glu-B3au</i> {11493}.	2+4+7+15+19 {11493}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> landrace MGB-5963 {11493}.
<i>Glu-B3av</i> {11493}.	9+13+16 {11493}.	tv: <i>T. turgidum</i> subsp. <i>durum</i> landrace MGB-3101 {11493}.

86.3.2. Gliadins

Following the introductory paragraph insert:

A catalogue of common wheat gliadin genes and alleles is provided in {11437}.

86.5.6. Puroindolines and grain softness protein

Toward the end of the section expand on the sentence regarding the transfer to durum:

The soft kernel trait was transferred to durum; firstly, to Langdon durum Selection 1-674 and then by backcrossing to cultivar Svevo {10899}, which was in turn used to develop backcross derivatives in cultivars Alzada, Havasu, Kyle, and Strongfield {11444}. Genetic evidence indicated that ~24.4 Mbp from CS chromosome 5DS replaced ~20 Mbp of 5BS {11444}. Further cytogenetic analysis identified the translocation breakpoint in a 39-bp region within a putative glycosyl-transferase gene {11489}.

Pathogenic Disease/Pest Reaction

89. Reaction to *Bipolaris sorokiniana*90. Reaction to *Blumeria graminis* DC.

90.1. Designated genes for resistance

- Pm3.** Add note: *Pm3* has 92.9% identity with *Pm8* at the protein level {11398}.
- Pm6.** Add to comments: *Pm6* was localized to a 0.9 Mb physical region in chr 2BL {11451}.
- Pm8.** Add notes: *Pm8* has 92.9% identity with *Pm3* at the protein level {11398}. *Pm8* is an allele of *Pm17* in rye and orthologue of *Pm3* {11398}.
- Pm17.** **v:** Embrapa 16 {11398}; Hugenoot {11398}.
al: Insave rye Nr 10458 {11398}.
c: GenBank MH077963 {11398}.

Pm17 is an allele of *Pm8* in rye and orthologue of *Pm3* {11398}.

Pm24. Replace *Pm24a* and *Pm24b* with a new section as follows.

- Pm24** {571, 11414}. *Pm24a* {571}; *Pm24b* {10994}, *MIHLB* {2020}.
- bin:** 1DS-0.54-1.00.
- v:** Baihulu {10994, 11414}; Chicacao {571, 11414}; Hongmangmai {11414}; Hulutou {11413, 11414}.
- ma:** *Xgwm789/Xgwm603-1D* – 2.4 cM – *Pm24* 3.6 cM – *Xbarc229-1D* {10109, 10957, 10994}. Located in a 9.3-cM region flanked by *Xgwm337-1D* and *Xcfd83/Xcfd72-1D* {11413}.
- c:** *Pm24* encodes a tandem kinase protein with putative pseudokinase domains. The gene was designated *Wheat Tandem Kinase 3* (WLK30) – this gain of function mutation was conferred by a 6-bp deletion of lysine/glycine codons (K400G401) in the KIN1 domain {11414}. GenBank MK950855.
- Pm41.** **c:** Encodes a unique CC-NBS-LRR gene {11454}. GenBank MN395289. Orthologs: in *tv*: Zavitan (*TRIDC3BG077810*) and Svevo (*TRITD3Bv1G261150.1*), but not in Chinese Spring {11454}.

Pm60. Add note at end of section: Gene *PmU*, flanked by *Xwmc273-7A* and *Xpsp3003-3A*, was transferred to common wheat from *T. urartu* accession UR206 (JIC 10100015) {11402}. *Xwmc273-7A* was 7.8 cM proximal to *Pm60* {11250}.

- Pm67** {11426}. *Pm1V#5* {11426}. 1D (T1DL-1VS#5) {11426}.
- v:** NAU18105 {11426}.
- s:** NAU18103 (1V(1D)) {11426}.
- al:** *Dasyphyrum villosum* 011140 {11426}.

Lines with *Pm67* showed complete immunity as seedlings but adult plants produced some conidial development on leaves whereas the culms were mildew-free {11426}.

- Pm68** {11466}. 2BS {11466}.
- bin:** 2BS-0.84-1.00.
- dv:** *T. turgidum* subsp. *durum* TRI 1796 {11466}.
- ma:** *Xdw04* (TRITD2Bv1G010030, chr2B:21587671-21591163) – 0.22 cM – *Pm68* – 0.22 cM – *Xdw12* (TRITD2Bv1G010880, chr2B:23374401-23375310) – 3.0 Mb – *Pm26/Xcau516-2B* (TRITD2Bv1G012960, chr2B:26398438-26414596) – 36.8 cM – *Pm42* {11466}.

90.3. Temporarily designated gene for resistance to *Blumeria graminis*

- pmDHT** {11447}. Recessive. 7BL {11447}.
- v:** Dahongtuo S761 {11447}.
- ma:** *XBE443877/Xwmc526-7B* – 0.8 cM – *pmDHT* – 0.8 cM – *Xgwm611/Xwmc581-7B* – 0.9 cM – *XBF473539/Xgwm577-7B* – 0.9 cM – *Xgwm577-7B* {11447}.
- PmG3M** {11479}. 6BL {11479}. **bin:** 6BL1-0-70-1.00.
- tv:** *T. turgidum* subsp. *dicoccoides* G-305-3M {11479}.
- ma:** *Xgpw7262-6B* – 6.9 cM – *PmG3M* – 4.5 cM – *Xedm149-6B* {11479}; *Xgpw7262-6B* – 13.6 cM – *PmG3M* – 3.5 cM – *Xuhw213-6B* – 5.7 cM – *Xedm149-6B* {11479}.

PmJM23 {11445}. SDS {11445}.
v: Jimai 23 {11445}.
ma: Xytu3004 – 0.7 cM – PmJM23/Xytu201/Xbwm21/Xcfd81-5D – 1.8 cM – Xswgi068/Xbwm20 {11445}.

PmQ {11461}. Recessive.
v: Hongxinmai {11461}.
ma: Xstars419-2B – 0.6 cM – Xicsq405 2B – 0.8 cM – PmQ – 0.2 cM – XWGGBH913-2B {11461}.

PmQ is very close to *Pm51*, *Pm63*, and *Pm64*.

PmSGD {11453}. Recessive. 7BL {11453}.
v: Shangeda {11453}.
ma: SNP2-58 – 0.4 cM – PmSGD – 0.8 cM – SNP2-46 {11453}.

PmTm4. **ma:** Add: XWGGC6892 – 0.6 cM – PmTm4/XWGGC5746 – 0.03 cM – XWGGC891 {11452}.

MI92145E8-9 {11436}. 2AL {11436}. **bin:** 2AL1-0-0.85.
v: Line 92145E8-9 {11436}.
ma: Xwmc181-2A – 9.3 cM – Xsdauk682-2A – 2.8 cM – MI92145E8-9 – 0.8 cM – Xsdauk-2A – 18.7 cM – Xgwm356-2 {11436}.

96. Reaction to *Fusarium* spp.

96.1. Disease: Add: *Fusarium* head scab, scab

Fhb5. Add note following the gene listing: According to {11487} *Fhb5* might be the same as *Qfhs.ifa-5Ac* but the issue remained ambivalent.

Fhb7. **ma:** Add: Located to a 245-kb region flanked by *Xsdau86* and *Xsdau88* {11483}.
c: Gene Tel7E01T1020600.1 encodes a glutathione S-transferase that detoxifies trichothecene toxin {11483}. Sequence data can be found at <https://www.ncbi.nlm.nih.gov/bioproject/PRJNA540081>.

Fhb7 was considered to be a horizontal gene transfer from an *Epichloe* spp. endophyte {11483}.

Qfhs.ifa-5A. Add: Fine mapping divided this QTL into two components, *Qfhs.ifa-5Ac* located in the centromere region at 245.9 Mbp and a less effective *Qfhs.ifa 5AS* located at 290 Mbp. Both QTL were significantly associated with higher anther extrusion and plant height {11487}.

97. Reaction to *Heterodera* spp.

Cre5. Add syn: *QCre-ma2A* {11394}.
v2: Move Madsen to this group and insert as ‘Madsen *Cre9*’ with same reference.

Add note: *Cre5* conferred resistance to *H. avenae* but not to *H. filipjevi* {11394}.

Cre9 {11394}. *QCre-ma7D* {11394}. 7DL {11394}.
v1: VPM-1/Moisson 951 {11394}.
v2: Madsen *Cre5* {11394}; VPM-1 *Cre5* {11394}.
ma: Flanked by *Xics7D-27-7D* and *BS00129645* {11394}. KASP markers *BS00021745*, *BS00150072*, and *BS00154302* were developed {11394}.

Cre9 conferred resistance to Chinese isolates of *H. filipjevi* but not to *H. avenae*.

99.2. Reaction to *Magnaporthe oryzae*.

Rmg1. **v:** Change to **v1:** Delete Norin 4.
v2: Norin 4 *Rmg6* {302, 11470}.

Rmg1 was present in 87% of surveyed genotypes {11470}.

Rmg6. *Rwt3* {11470}.
v1: Delete Norin 4. Add: IAC-5 {11470}; Transfed {11470}.
v2: Norin 4 *Rmg1* {11470}.

Rmg6 was present in 77% of surveyed genotypes 11470}.

Add at end of section: The wheat blast pathogen became established on wheat cultivar Anahuac (*rmg1 rmg6*) in Brazil in the mid-1980s. It was initially avirulent on cultivars such as IAC-5 with *Rmg6* but later acquired virulence allowing it to attack most wheat genotypes {11470}.

101. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter, *Zymoseptoria tritici*

Stb5. v: Add: Baldus {11446}; Chaucer {11446}; Israel 493 {11446}; Longbow {11446}; Olaf {11446}; Senat {11446}; Veranopolis {11446}.

v2: Gene *Stb10* {11446}; Frontana *Stb10* {11446}; Mentana *Stb10* {11446}.

Stb6. *TaWAKL4* {11434}. v: Add: Cadenza {11434}; Flame {11434}.

ma: *Xgwm369-3A* – 4.3 cM – *Stb6* – 3.8 cM – *Xgwm132-3A* {11434}.

c: Encodes a wall-associated receptor kinase (WAK)-like protein {11434}.

Stb6 is common in *T. turgidum* subsp. *dicoccum* {11434}.

Stb10. v2: Gene *Stb5* {11446}; Frontana *Stb5* {11446}; Mentana *Stb5* {11446}.

Temporary designation

TmStb1 {11446}. Resistance to IPO323.

dv: *T. monococcum* subsp. *monococcum* MDR043 {11446}.

QTL

Spelt HRTI1410 (R) / 3 wheat parents: 135 DH lines: mapped using SNP polymorphisms common to all three S parents: four QTL identified on chromosomes 5AL (74.2–82.4 cM; $r^2 = 0.18$); 4B (52.9–56.9 cM, $r^2 = 0.09$) contributed by the susceptible parents; and 7B.1 (41.2–57.0 cM, $r^2 = 0.09$) and 7B.2 (58.2–67.4 cM, $r^2 = 0.15$) contributed by the susceptible parents {11430}.

At the end of section add: For a review of qualitative and quantitative resistance {11439}.

102. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano); *Parastagonospora nodorum***102.2. Sensitivity to SNB toxins (necrotrophic effectors)**

Snn1. ma: *Xfcp618-1B* – 1.9 cM – *Snn1* – 0.16 cM – *Xfcp624-1B* {11433}.

c: *Snn1* is a wall-associated kinase (*TaWAK*) {11433}. GenBank (cDNA) KP091701.

Add note: Lebsock durum carried an intact *Snn1* but it was not expressed {11433}.

snn1. s: CS*/Hope 1B {11433}.

105. Reaction to *Puccinia graminis* Pers.

Sr2. ma: Add: *Bs0006276* – 0.3 cM – *Yr57* – 1.3 cM – *Xgwm389-3B* – 6.1 cM – *csSr2* – 2.6 cM – *Xgwm533-3B* {11480}.

Sr7a. v2: Jagger *Sr38* {11420}.

ma: *Xwmc313-4A* – *SNP1067* – 0.8 cM – *Sr7a* – 2.7 cM – *Xbarc78-4A* – 2.7 cM – *SNP7126* {11420}.

Sr7b. v2: PI 177906 *Sr28 SrTmp* {11419}.

ma: Located at 147–164 in the Wang et al. (2014) consensus map {11419}.

Sr8a. v: Harvest {11418}.

v2: SD4297 *Sr28* {11418}; PI 177906 *Sr7b SrTmp* {11419}.

ma: Terminally located; SNP markers within 2 cM {11416}. *Sr8a* – 2.2 cM – *Xgwm459-6A* {11418}.

Sr9h. *SrWLR* {11485}. v: Matlabas {correct:10058, add: 11486}.

ma: *Xgwm47-2B* – 1.8 cM – *Sr9h (SrWLR)* – 7.0 cM – *Xwmc332-2B* {11485}; *AWA543-HRM* – *Sr9H* – *Xgwm47-2B*.

SR13.

Sr13a. c: GenBank KY924305 for Langdon and ST464 (Haplotype R1); KY825225 for Kronos and Khapstein (Haplotype R3) {11217}.

Sr13b. c: GenBank KY225226 (Haplotype R3) {11217}.

Sr22. c: *Sr22* encodes a CC-NBS-LRR protein with 941 aa {11404}. EBI LN883743, GenBank CUM44200.1.

Sr28. v2: SD4297 *Sr8a* {11419}.

The *Sr28* allele in SD4297 was originally reported as *Sr9h* {11418}.

Sr38. v2: Jagger *Sr7a* {11420}.

Sr45. c: *Sr22* encodes a 1,230 aa CC-NBS-LRR protein {11404}. EBI LN883757.

Add to existing note: Cloning of *Sr45* showed that *Sr45* and *Sr21* were different genes.

- Sr46.** **madv:** Flanked by *Xgwm1099-2D* and *Xbarc297-2D* {11405}.
c: Cloned by AgRenSeq and map-based methods *Sr46* has a CC-NBS-LRR structure {11405}. GenBank MG851023.
- Sr50.** **c:** *Sr50* was shown to encode a CC-NBS-LRR protein homologous to the barley *Mla* gene {11403}. GenBank KT725812.
- Sr60.** Reproduced here and updated in full.
- Sr60** {11208}. 5A^mS {11208}.
dv1: PI 277130 {11385}; PI 277131-2 {11385}; PI 277135 {11385}; PI 306540 {11385}; PI 306545 {11385}; PI 306547 {11385}; PI 428158 {11385}; PI 435001 {11385}.
dv2: PI 306540 *Sr21 SrTm4 SrTm5* {11208}.
v: PI 689563, PI 306540/Kronos/2/UC1361/4UC12014-36 {11385}.
ma: *Pinb-5A^mS.....GH724575/DK22976/CA5012332* – 0.25 cM – *Sr60/LRRK123.1* – 0.19 cM – *CJ942731/CJ884584* {11208}; *GH724575* – 1.56 cM – *Sr60/LRRK123.1* – 0.52 cM – *FD475316* {11208}. *Sr60F2R2* {11385}.
c: *Sr60* from *T. monococcum* subsp. *monococcum* PI 306540 encodes a protein with two putative kinase domains designated *Wheat Tandem Kinase 2 (WTK2)* {11208,11385}. GenBank MK629715 {11385}. The gene is orthologous to *T. aestivum* gene *TraesCS5A02G005400* {11385}.
- Sr60* in UC12014-36+Sr60 (PI 689563) is linked with puroindoline genes for grain softness that were also introgressed from the diploid parent {11385}.
- Sr61** {11397}. *SrB* {11337}. 6AL (T6AS-6AL-6Ae#1-6Ae#3) {11338, 11397}.
v2: AGG91586WHEA *Sr26* {11397}.
su: W3757 = SA8123 {11337}.
- The recombinant AGG91586WHEA was produced after crossing the shortened 6Ae#1 recombinant WA-5 (AUS91436) carrying *Sr26* with SA8123. A separate line carrying *Sr61* alone is currently being selected for *Ph1* homozygosity.
- SrTA1662.** **v:** KS05HW14 {11405}.
c: An SrTA1662 candidate identified by AgRenSeq encoded a CC-NBS-LRR candidate gene (GenBank MG763911) with 83% homology with *Sr33* {11405}.
- SrTA10276-2V** {11395}. 2V {11395}. **d:** TA7753 {11395}.
al: *D. villosum* TA10276 {11395}.
- SrTmp.** **v2:** PI 177906 *Sr7b Sr28* {11419}.
ma: *SrTmp* – 3.1 cM – *IWB49086* {11419}.

Suppressor of Stem Rust Resistance 1

A suppressor of stem rust resistance in cultivar Canthatch was known from the 1980s based on the response of an extracted tetraploid and aneuploid derivatives of Canthach as well as mutation analysis ({11410, 11411}) and references therein.

- SuSr-DI** {11411}. 7DL {11412, 11417}.
v: Canthatch CTH-K RL5451 {11411}; Columbus {11417}; Katepwa {11417}. Other Canadian Thatcher derivatives {11417}.
ma: Localised to a 1.3 cM genetic interval flanked by *Xkwh239* and *Xkwh281* {11412}.
c: *TraesCS7D01G526100*. Encodes a mutant form of *TaMed15b.D*, a subunit of the Mediator complex {11412}.
- suSr-DI** [{11411}]. **v:** Thatcher {11411}; NS1 RL5863 {11412}; NS2 RL5864 {11412}.
c: *TraesCS7D01G526100* {11412}.

106. Reaction to *Puccinia striiformis* Westend.

106.1. Designated genes for resistance to stripe rust

Yr15. Add synonyms: *YrH52* {0003}, *YrG303* {11429}, *Wtk1* {11392}.

Chromosome location add reference: {0003}.

- tv:** Add: *T. turgidum* subsp. *dicoccoides* H52 {0003, 11429}; *T. turgidum* subsp. *dicoccodes* G303 {11429}.
ma: *T. turgidum* subsp. *dicoccoides* H52 {0003}.
ma: distal ...*Yr15* – 9.6 cM – *YrH52* – 1.4 cM – *Nor-B1* – 0.8 cM – *Xgwm264a* – 0.6 cM – *Xgwm18*{3}; *Xgwm273a* – 2.7 cM – *YrH52* – 1.3 cM – *Xgwm413/Nor1*...centromere {108}.
c: Add: GenBank MG649384 and MG674157 {11392}, MK188918 (*YrH52*) {11429}, and MG18819 (*YrG303*).

- Yr28.** *YrAS2388* {10822, 11438}. **c:** See *YrAs2388*.
- Yr57.** **ma:** Add: *Bs0006276* – 0.3 cM – *Yr57* – 1.3 cM – *Xgwm389-3B* – 6.1 cM – *csSr2* – 2.6 cM – *Xgwm533-3B* {11480}.
- Yr58.** Add: Adult plant resistance. *QYr.sun-3BS* {10964}.
- Change current listing to: **v2:** Sonora W195 AUS 19292 *Yr46* {10964}.
- Yr81.** **ma:** Replace with: *KASP_3077* – 2.7 cM – *Yr81* – 6.4 cM – *Xgwm459-6A* – 1.0 cM *KASP_11315* {11262}.
- Yr83** {M11396}. 6A (T6AL·6RL {11396}).
- tr:** T6AL·6RL C19.3 {11396}.
- ad:** Wheat + 6R {11396}; Wheat + 6RL {11396}.
- su:** CS + 6R(6D) {11396}.
- al:** Triticale accession T-701 {11396}.
- ma:** Deletion mapping indicated that *Yr83* was located in 6RL bin FL 0.73-1.00 containing PCR markers KU.86, TNAC1823, TNAC1826, TNAC1844) {11396}.

The only previously designated *Yr* gene derived from *Secale cereale* is *Yr9* from chromosome 1RS.

106.2. Temporarily designated genes for resistance to stripe rust

- YrAs2388.** Add: *Yr28* {11438}, *NLR_{4D-1}* {11438}.
- v:** Shumai 1675 {11438}.
- dv:** Add: *Ae. tauschii* Clae9 {11438}; PI5111383 {11438}; PI511384 {11438}.
- c:** *Yr28* has a CC-NBS-LRR structure, alternative splicing in the NBS region and duplicated 3' UTR {11438}. GenBank MK73661 – MK73666 {11438}.

Yr28 was present in all tested accessions of *Ae. tauschii* ssp. *strangulata* and some accessions of ssp. *tauschii* {11438}. Often suppressed in synthetic and derived wheat backgrounds.

YrH52. Delete. Synonymous with *Yr15*; moved to *Yr15* section.

YrH9020 {11450}. Derived from *Psathyrostachys huashanica*.

2DS {11450}.

v: H9020-1-6-8-3 {11450}.

ma: *Xgwm455-2DS* – 5.8 cM – *YrH9020* – 4.4 cM – *Xgwm261-2DS* {11450}.

al: *Psathyrostachys huashanica* 0503383 {11450}.

Yru1 {11494}.

5AL {11494}.

bin: 5AL10-0.57-0.78.

dv: *T. urartu* PI 428309 {11494}.

ma: *Xgwm186-5A* – 30.5 cM – *Yru1* – 10.8 cM – *Xgwm7007-5A*, then fine mapped with 82 additional polymorphic markers {11494}.

c: *TuG1812G0500003718*. *Yru1* has as NBS-LRR structure with N-terminal ankyrin and C-terminal WRKY repeats {11494}. GenBank MT018453.

The *Yru* resistance allele was present in a number of *T. urartu* accessions, but not in G1812 {11494}.

106.3. Stripe rust QTL

Correction: The reference for the listing 'Luke (MR) / 2174' in the 2019 supplement should be renumbered to {11393}.

Capo (R) / Arina (S) and Capo (R) / Furore (S): Four QTL on chromosomes 2AL, 2BL, 2BS, and 3BS were from Capo and one on 5BL was from Arina; the QTL on 2AL, 2BL, and 3BS were co-located with QTL for resistance to stripe rust {11449}.

107. Reaction to *Puccinia triticina*

107.1. Genes for resistance

- Lr13.** *LrZH22* {11467, 11468}; *LrLC10* {11468}.
- bin:** 2BS1-0.35-0.75.
- v:** Liaochen 10 {11468}; Zhoumai 22 {11467, 11468}.
- ma:** *Xbarc55-2B* – 2.4 cM – *LrZH22* – 4.8 cM – *Xgwm374-2B* {11467}; *Xbarc55-2B* – 2.2 cM – *XCAUT163* – 1.10 cM – *LrLC10* – 0.55 cM – *Lseq22* – 6.05 cM – *Xbarc18-2B* {11468}.
- Lr39.** **i:** TC*4 / Overley, GSTR 447 {11498}.
- Lr42.** **i:** TC*4 / Century, GSTR 448 {11498}.
- Lr49.** **ma:** Add: *Xgwm251-4B* – 8.6 cM – *XsunKASP_21* – 0.4 cM – *Lr49* – 0.6 cM – *XsunKASP_24* – 8.1 cM – *Xwmc349-4B* {11484}.

- Lr64.** Revise to: **v:** TC/RL6149-RIL13, GSTR 451 {11399, 11498}.
v2: RL6149 *LrX* {10550, 11399}.
ma: Add: *K-IWB38521* – 1.0 cM – *Lr64/K-IWB59855* – 2.9 cM – *K-IWB72197* – 10 cM – *K-IWB73609* {11399}.
 A second recessive gene (*LrX*) in in the previous near-isogenic line RL6149 was located in chromosome 1DS: *K-IWB577* – 11.2 cM – *LrX/IWB38437* {11399}.
- Lr67.** **v:** Chapingo 48 {11070}; Chapingo 53 {11070}; Yaqui 53 {11070}.
v2: NP876 *Lr46* {11441}; Sujata *Lr46* {11440, 11442}.
- Add note: *Lr67* was predicted in 51 accessions mainly collected in the Indian subcontinent {11448} on the basis of the gene-specific marker SNP1-TM4 {11070}.
- Lr68.** **v2:** Sujata *Lr46 Lr67* {11442}.
- Lr77.** **v:** TC*2 / Toropi, GSTR 449 {11498}.
- Lr78.** **v:** TC*2 / Santa Fe, GSTR 450 {11498}.
- Lr80** {11464}. *LrH2* {11464}. 2DS {11464}.
v: FLW6-Selection AGG95499WHEA {11464}.
ma: *Xgdm35-2D* – 7.5 cM – *Xcau96-2D* – 0.4 cM – *Lr80* – 0.2 cM – *Xbarc124-2D* – 13.2 cM – *Xgwm296-2D* {11464}.

107.3. QTL for reaction to *P. triticina*

Immediately above the heading ‘Tetraploid wheat’ insert:
 Review of QTL in hexaploid wheat {11442}.

Capo (R) / Arina (S) and Capo (R) / Furore (S): Four QTL on chromosomes 2AL, 2BL, 2BS, and 3BS were from Capo and one on 5BL was from Arina; the QTL on 2AL, 2BL, and 3BS were co-located with QTL for resistance to stripe rust {11449}.

109. Reaction to *Pyrenophora tritici-repentis*

109.1. Resistance to tan spot

QTL

Add at the end of section: A QTL analysis of 4 durum crosses identified 12 QTL on chromosomes 1B, 2B (2), 3A (3), 5A (5), and 7A {11481}.

XXX. Reaction to *Sitobiplois mosellana* (Gehin)

Henong 215 (R) / Yanyou (S) and 6218 (S) / Jimai 24 (R): selected RIL populations: Several QTL identified: *QSm.hbau-4A.2* with LOD scores 5.58–29.22 and PVE 24.4–44.8% were mapped to a 4.9-Mb interval; nearest markers *AX-109543456*, *AX-108942696* and *AX-110928325* {11425}.

112. Reaction to *Schizaphis graminum*

116. Reaction to *Tilletia caries* (D.C.) Tul., *T. foetida* (Wallr.) Liro, *T. controversa* J.G. Kuhn

- Bt12.** Add syn.: *QBt.ifa-7DS* {11469}. 7DS {11469}.
ma: Associated with 13 markers in a distally located physical region of ~4.3 Mbp {11469}. Validated KASP markers were derived from *IWB61302* and *IWB50978* {11469}. Although appearing to be proximal to *QDB.ui-7DS* {11182} the genes were not clearly distinguished.

QTL

Add: IDO835 (R)/Moreland (S): DH population: *Q.DB.ui-6DL* (PVE 0.53, *Bt9* region) and *Q.DB.ui-7AL* (PVE 0.38) {11400}.

XXX. Reaction to Soil-Borne Cereal Mosaic Virus

Insert immediately following the *SBWMVI* entry:

- Sbwm1** {11435}. **v:** Heyne {11435}. 5D {11435}.
ma: *Xgwm272-5D* – 20.2 cM – *Sbwm1* – 2.2 cM – *w SNP_CAP11_c209_198467* – 0.7 cM – *w SNP_JD_c4438_5568170* – 8.7 cM – *Xgwm469* {11435}.

Change the note to: *Sbm1* and *Sbwm1* are likely the same gene.

118. Reaction to *Ustilago tritici**Ut11* {11406}. 7BS {11406}.**v:** DH line TD14XDIA*B0075, CN 120264 {11406}; Sonop, TD-14 {11406}.**ma:** Co-segregation with *BS00022562_51*, *Excabibur_C3489_182* and *Kukri_rep_c71778_644* at 0.43, 1.20 and 1.25 Mbp {11406}.*Ut11* conferred resistance to race T2 but not T9 and T39; resistance to those races (and race T2) was conferred by *QUt.mrc-5B* {11406}.**119. Reaction to Wheat Spindle Streak Mosaic Bymovirus (WSSMV)****WssI.** Add note: A number of secondary translocations were induced, the smallest of which was NAU421 (FL 0.78-1.00) {11488}.**References.****Updates**

10786. Delete the names Simkova H and Dolezel from this reference.

10801. Replace with: Williamson VM, Thomas V, Ferris H and Dubcovsky J 2013 An *Aegilops ventricosa* translocation confers resistance against root-knot nematodes to common wheat. *Crop Science* 53: 14120-14128.11060. Change title to: High-density mapping of the major FHB resistance gene *Fhb7* derived from *Thinopyrum ponticum* and its pyramiding with *Fhb1* by marker-assisted selection. *Theoretical and Applied Genetics* 128: 2301-2316. DOI: 10.1007/s00122-015-2586-x.11155. Hao M, Liu M, Luo JT, Fan CL, Yi YJ, Zhang LQ, Yuan ZW, Ning SZ, Zheng YL and Liu DC 2018 Introgression of powdery mildew resistance gene *Pm56* on rye chromosome arm 6RS to wheat. *Frontiers in Plant Science* 9, 1040. DOI: 10.3389/fpls.2018.01040.11356. Replace the 2019 reference with: Li GQ, Cowger C, Wang XW, Carver BF and Xu XY 2019 Characterization of *Pm65*, a new powdery mildew resistance gene on chromosome 2AL of a facultative wheat cultivar. *Theoretical and Applied Genetics* 132: 2625-2632. DOI: 10.1007/s00122-019-03377.11364. Update: 2020 *Theoretical and Applied Genetics* 133: 1149-1159. DOI: 10.1007/s00122-020-03538-8.11378. Xu XY, Li GQ, Carver BF and Scott Armstrong JS 2020 *Gb8*, a new gene conferring resistance to economically important greenbug biotypes in wheat. *Theoretical and Applied Genetics* 133: 615-622. DOI: 10.1007/s00122-019-03491-1.11262. Replace with: Gessese M, Bariana H, Wong D, Hayden M and Bansal W 2019 Molecular mapping of stripe rust resistance gene *Yr81* in common wheat landrace AUS27430. *Plant Disease* 103: 1166-1171. DOI: 10.1094/PDIS-06-18-1055-RE.11328. In the 2019 Supplement: *Yr17*: Change reference '19008' to '11328'.11385. Chen S, Rouse MN, Zhang W, Zhang X, Guo Y, Briggs J and Dubcovsky J 2019 Wheat gene *Sr60* encodes a protein with two putative kinase domains that confers resistance to stem rust. *New Phytologist* 225: 948-959. DOI: 10.1111.nph.16169.**New**11393. Liu MY, Lei L, Powers C, Liu ZY, Campbell KG, Chen XM, Bowden RL, Carver BF and Yan LL 2016 *TaXa21-A1* on chromosome 5AL is associated with resistance to multiple pests in wheat. *Theoretical and Applied Genetics* 129: 345-355. DOI: 10.1007/s00122-015-2631-9.11394. Cui L, Qiu D, Sun L, Sun Y, Ren YK, Zhang HJ, Li JT, Zou JW, Wu PP, Hu JH, Xie JZ, Liu HW, Yang L, Zhou Y, Wang Y, Lv Y, Liu ZY, Murray TD and Li HJ 2019 Resistance to *Heterodera filipjevi* and *H. avenae* in winter wheat is conferred by different QTL. *Phytopathology*, in review.11395. Ando K, Krishnan V, Rynearsa S, Rouse MN, Danilova T, Friebe B, See D and Pumphrey M 2019 Introgression of a novel Ug-99-effective stem rust resistance gene into wheat and development of *Dasyphyrum villosum* chromosome-specific markers vis genotyping-by-sequencing (GBS). *Plant Disease* 103: 1068-1074. DOI: 10.1094/PDIS-05-18-0831-RE.11396. Li JB, Dundas I, Dong CM, Li GR, Trethowan R, Yang ZJ, Hoxha S and Zhang P 2020 Identification and characterization of a new stripe rust resistance gene *Yr83* on rye chromosome 6R in wheat. *Theoretical and Applied Genetics* 133: 1095-1107. DOI: 10.1007/s00122-020-03534-y.

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