IV. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2011 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 11Th International Wheat Genetics Symposium held in Brisbane, Australia, and the 2009 and 2010 Supplements (*Annual Wheat Newsletter* 55:256-278, 56:256-278) are available from 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. The Wheat Gene Catalog is not included as part of the IWGS proceedings and, therefore, cannot be cited as part of them.

Section numbers given is this supplement are only approximate.
Add to Designators:

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Morphological and Physiological Traits

Pre-harvest Sprouting

QTL

'Argent (non-dormant, white seeded) / W98616 (dormant, white seeded)': 90 DH lines: Strong QTL on chromosomes 1A, 3A, 4A, and 7A and weaker QTL on 2B, 5B, and 6B, all from W98616 {10740}.

XX. Embryo Lethality

XX.1. Embryo lethality in wheat x rye hybrids

The Chinese Spring (Imperial rye) addition lines 6R and 6RL crossed with different inbred rye lines (R2, R6, and R7) produced hybrid seeds with different proportions of differentiated embyos. R2 with (*Eml-R1a*) gave only undifferentiated embryos; R6 and R7 (with *Eml-R1b*) gave 74–100% differentiated embryos {10748}. Crosses 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}.

39. Height

39.2. reduced Height : GA-sensitive

Rht14. 6AS {10767}. ma: *Rht14* – 11.7 cM – *Xbarc3-6A* {10767}.
Allelic with *Rht16* and *Rht18* {10767}.

Rht16. 6AS {10767}. ma: *Rht16* – 28.0 cM – *Xbarc3-6A* {10767}.
Allelic with *Rht14* and *Rht18* {10767}.

Rht18. 6AS {10767}. ma: *Rht18* – 25.1 cM – *Xbarc3-6A* {10767}.
Allelic with *Rht14* and *Rht16* {10767}.

43. Lack of Ligules

lg1. , 2BS {10767}.

XX. Lesian Mimicry

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

lm {10743}. 1BL {10743}. **bin:** C1BL6-0.32 {10743}.
v: Ning 7840 {10743}. **ma:** Proximal to *Xgwm264.1-1*B {10743}.
Lm was positively associated with *QLr.pser.1BL* {10743}.

XX. Soft Glumes

sog. **bin:** C-2AS5-0.78. **dv:** Tm-9, a mutant of TA4342-96 {10769}.
ma: *Xgwm71-2A* – 3.3 cM – *sog* – 3.5 cM – *Xbcd120-2A* {10769}.

Sog. **dv:** *T. monococcum* subsp. *aegilopoides* TA4342-96 {10769}.
Replace the previous entry regarding the relationship to Tenacious Glumes with: 'The Soft Glume locus is not an orthologue of Tenacious Glumes {10769}'.

69. Stem Solidness

Qsst.msub-3BL. Add following the current entry:
Stem solidness in chromosome 3B of Golden Ball was verified in Langdon-Golden Ball disomic substitution lines {10730}.

71.Tenacious Glumes

Tg1. **bin:** 2BS-3 1.00-0.84.

Tg2. **v:** TA 3419 = Tetra Canthatch / *Ae. tauschii* var. *meyeri* TA1599 {10769}.
ma: *Xgwm261*/*Xwmc503-2D* – 2.3 cM – *Tg2* – 5.9 cM – *Xfba88*/*Xfbc400-2D* {10769}.
Replace the note on the relationship with Soft Glumes with: 'The Tenacious Glume loci are not orthologues of the Soft Glume locus {10769}'.

75.Yield and Yield Components

75.1.2. 1,000-kernel weight

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-kernel 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-kernel weights more than 3 g higher than that of Hap-6A-G {10781}.

75.12. Spike number per plant

QSn.sdau-BL {10784}. **ma:** *Xwmc657-4B* – 4.6 cM – *QSn.sdau-4*B – 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.

Proteins

79.5.6. Waxy Proteins

Wx-A1.

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. At the end of section add:
A dominant PCR marker for identifying heterozygotes at the *Wx-B1* locus is reported in {10732}.

79.5.8. Puroindolines and grain softness protein

Add note:
Lines possessing the alien-derived genes *Lr57* and *Yr40* lack puroindoline genes and therefore should be hard phenotypes {10770}.

79.5.12. Serine proteinase 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}.

79.3. Endosperm Storage Proteins
79.3.1. Glutenins
79.3.1.1 *Glu-1*
Glu-A1

Restore the following entries erroneously deleted in a previous update:
Glu-A1v {10327}. 2.1* {10327}. **v:** KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.
Glu-A1w {10327}. 2' {10327}. **v:** TRI14165/91 {10327}.

Add:
Glu-A1z {10805}. [*Glu-A1^{m}a* {10805}]. **dv:** PI 191146, *T. monococcum*. subsp. *monococcum* {10805}.
Glu-A1aa {10805}. [*Glu-A1^{m}b* {10805}]. **dv:** PI 190946, *T. monococcum*. subsp. *monococcum* {10805}.
Glu-A1ab {10805}. [*Glu-A1^{m}c* {10805}]. **dv:** PI 191098, *T. monococcum*. subsp. *monococcum* {10805}.

Glu-A1ac {10806}.	[*Glu-A^{u}1-I* {10806}].	**dv:** PI 428319, *T. urartu* {10806}.
Glu-A1ad {10806}.	[*Glu-A^{u}1-II* {10806}].	**dv:** PI 428232, *T. urartu* {10806}.
Glu-A1ae {10806}.	[*Glu-A^{u}1-III* {10806}].	**dv:** PI 428240, *T. urartu* {10806}.
Glu-A1af {10806}.	[*Glu-A^{u}1-IV* {10806}].	**dv:** PI 428335, *T. urartu* {10806}.
Glu-A1ag {10806}.	[*Glu-A^{u}1-V* {10806}].	**dv:** PI 538741, *T. urartu* {10806}.
Glu-A1ah {10806}.	[*Glu-A^{u}1-VI* {10806}].	**dv:** PI 428230, *T. urartu* {10806}.
Glu-A1ai {10806}.	[*Glu-A^{u}1-VII* {10806}].	**dv:** PI 428253, *T. urartu* {10806}.
Glu-A1aj {10806}.	[*Glu-A^{u}1-VIII* {10806}].	**dv:** PI 427328, *T. urartu* {10806}.
Glu-A1ak {10806}.	[*Glu-A^{u}1-IX* {10806}].	**dv:** PI 428327, *T. urartu* {10806}.
Glu-A1al {10806}.	[*Glu-A^{u}1-X* {10806}].	**dv:** PI 428256, *T. urartu* {10806}.
Glu-A1am {10806}.	[*Glu-A^{u}1-XI* {10806}].	**dv:** PI 428224, *T. urartu* {10806}.
Glu-A1an {10806}.	[*Glu-A^{u}1-XII* {10806}].	**dv:** PI 428228, *T. urartu* {10806}.
Glu-A1ao {10806}.	[*Glu-A^{u}1-XIII* {10806}].	**dv:** PI 538724, *T. urartu* {10806}.
Glu-A1ap {10806}.	[*Glu-A^{u}1-XIV* {10806}].	**dv:** TRI 6734, *T. urartu* {10806}.
Glu-A1aq {10806}.	[*Glu-A^{u}1-XV* {10806}].	**dv:** TRI 11494, *T. urartu* {10806}.
Glu-A1ar {10806}.	[*Glu-A^{u}1-XVI* {10806}].	**dv:** TRI 11495, *T. urartu* {10806}.
Glu-A1as {10806}.	[*Glu-A^{u}1-XVII* {10806}].	**dv:** PI 428217, *T. urartu* {10806}.
Glu-A1at {10806}.	[*Glu-A^{u}3-XVIII* {10806}].	**dv:** PI 428225, *T. urartu* {10806}.
Glu-A1au {10806}.	[*Glu-A^{u}3-XIX* {10806}].	**dv:** PI 538733, *T. urartu* {10806}.
Glu-A1av {10806}.	[*Glu-A^{u}3-XX* {10806}].	**dv:** PI 428196, *T. urartu* {10806}.
Glu-A1aw {10806}.	[*Glu-A^{u}3-XXI* {10806}].	**dv:** PI 538724, *T. urartu* {10806}.
Glu-A1ax {10806}.	[*Glu-A^{u}3-XXII* {10806}].	**dv:** PI 428191, *T. urartu* {10806}.
Glu-A1ay {10806}.	[*Glu-A^{u}3-XXIII* {10806}].	**dv:** TRI 6734, *T. urartu* {10806}.
Glu-A1az {10806}.	[*Glu-A^{u}3-XXIV* {10806}].	**dv:** TRI 11496, *T. urartu* {10806}.

Glu-B1

Amendment:

Glu-B1al. Replace '7+8*' with '7^{OE}+7^{OE}+8*'. Add {899} after 'Glenlea'.

Add to the existing note:

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}.

Add:

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* subsp. *ferrugineum* {10810}.
Glu-B1by {10808}.	7b*+8 {10808}.	**v:** Eshimashinriki {10808}.
Glu-B1bz {10808}.	7^{OE} {10808}.	**v:** Darius {10808}; Cappelle-Desprez {10808}; Festin {10808}; Petrel {10808}; Attila {10808}.
Glu-B1ca {10808}.	6+8b* {10808}.	**v:** Nidera Baguette 10 {10808}; Apollo {10808}; Brimstone {10808}; Clément {10808}; Ruso {10808}; Pepital {10808}; Thesee {10808}.
Glu-B1cb {10808}.	7^{OE}+8 {10808}.	**v:** Demai 3 {10808}; ACA 303 {10808}; Courtot {10808}; Shinchunaga {10808}.
Glu-B1cc {10808}.	7^{OE}+8a* {10808}.	**v:** Pioneer {10808}; Klein Jabal 1 {10808}; ProINTA Redemón {10808}.
Glu-B1cd {10808}.	7^{OE}+8b* {10808}.	**v:** ACA 601 {10808}.
Glu-B1ce {10808}.	7+8a* {10808}.	**v:** Tasman {10808}; Jing 411 {10808}.

Glu-D1

Add:

Glu-D1bu {10810}.	2'+12 {10810}.	**v:** CWI-64806, *T. aestivum* subsp. *aestivum* {10810}.
Glu-D1bv {10810}.	2"+10 {10810}.	**v:** CWI-65297, *T. aestivum* subsp. *erythroleucon* {10810}.
Glu-D1bw {10810}.	2"+12 {10810}.	**v:** CWI-60509, *T. aestivum* subsp. *graecum* {10810}.

Glu-B1-1

Add:

Glu-B1-1ah {899}.	7^{OE}	**v:** Benkuti 1201 {10196, 10197}; Glenlea; Klein Universal II {10196}; Tezanos Pintos Precoz {10196}; Tobari 66 {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}.	**v:** 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

Add:

Glu-B1-2ai {10809}.	8' {10809}.	**tv:** TGR-244 {10809}.
Glu-B1-2aj {10808}.	8a* {10808}.	**v:** Pioneer {10808}, Jing 411 {10808}, Tasman {10808}.
Glu-B1-2ak {10808}.	b*' {10808}.	**v:** Nidera Baguette 10 {10808} , ACA 601 {10808}.

Glu-A3

Replace:

Glu-A3g {00113, 00114}.	6+10+20 {00114}.	**v:** Glenlea {10185}. **tv:** Claro de Balazote.

with:

Glu-A3g {00113}		**v:** Glenlea {10185}.

Add:

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* subsp. *monococcum* {10805}.
Glu-A3u {10805}.	*Glu-A3^{m}b* {10805}.	**dv:** PI 190946, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3v {10805}.	*Glu-A3^{m}c* {10805}.	**dv:** BGE-020466, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3w {10805}.	*Glu-A3^{m}d* {10805}.	**dv:** PI 191097, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3x {10805}.	*Glu-A3^{m}e* {10805}.	**dv:** BGE-013624, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3y {10805}.	*Glu-A3^{m}f* {10805}.	**dv:** PI 191094, *T. monococcum* subsp. *monococcum* {10805}.
Glu-A3z {10806}.	*Glu-A^{u}3-I* {10806}.	**dv:** PI 428319, *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-B3

Add:

Glu-B3ab {10804}.	**v:** Hope {10804}; Nanbukomugi {10804}.
Glu-B3ac {10804}.	**v:** Thesee {10804}; ACA 801 {10804}; Klein Proteo {10804}.
Glu-B3ad {10804}.	**v:** AC Vista {10804}; Heilo {10804}; Opata 85 {10804}; Ruso {10804}.

Glu-D3

In the ***Glu-D3d*** entry, add 'Jufy-1 {10813}' to the standard stock list.

Add:

Glu-D3l {10804}.	**v:** Heilo {10804}; Jing 411 {10804}, Pepital {10804}; Thesee {10804}.
Glu-D3m {10804}.	**v:** Darius {10804}.

79.3.2. Gliadins

79.3.2.1. *Gli-1*

Gli-A1

In the appropriate entry, replace:

Gli-A1null with ***Gli-A1w*** and add a column stating 'null allele'.

Add:

Gli-A1x {10805}.	[*Gli-A1^{m}a* {10805}].	**dv:** PI 191146, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1y {10805}.	[*Gli-A1^{m}b* {10805}].	**dv:** PI 190947, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1z {10805}.	[*Gli-A1^{m}c* {10805}].	**dv:** PI 190946, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1aa {10805}.	[Gli-A1^{m}d {10805}].	**dv:** PI 191097, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1ab {10805}.	[Gli-A1^{m}e {10805}].	**dv:** BGE-020466, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A1ac {10805}.	[Gli-A1^{m}f {10805}].	**dv:** BGE-013626, *T. monococcum* subsp. *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
In the appropriate entry, replace:
Gli-B1null with ***Gli-B1x*** and add a column stating 'null allele'.

Gli-D1
In the appropriate entry, replace:
Gli-D1null with ***Gli-D1o*** and add a column stating 'null allele'.

80.3.2.2. Gli-2
Gli-A2
In the appropriate entry, replace:
Gli-A2null with ***Gli-A2aj*** and add a column stating 'null allele'.

Add:

Gli-A2ak {10805}.	[*Gli-A2^{m}a* {10805}].	**dv:** BGE 013630, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2al {10805}.	[*Gli-A2^{m}b* {10805}].	**dv:** PI 094740, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2am {10805}.	[*Gli-A2^{m}c* {10805}].	**dv:** PI 190942, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2an {10805}.	[*Gli-A2^{m}d* {10805}].	**dv:** PI 190947, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2ao {10805}.	[*Gli-A2^{m}e* {10805}].	**dv:** PI 190946, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2ap {10805}.	[Gli-A2^{m}f {10805}].	**dv:** BGE 013626, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2aq {10805}.	[*Gli-A2^{m}g* {10805}].	**dv:** PI 191095, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2ar {10805}.	[*Gli-A2^{m}h* {10805}].	**dv:** BGE 001937, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2as {10805}.	[*Gli-A2^{m}i* {10805}].	**dv:** PI 191096, *T. monococcum* subsp. *monococcum* {10805}.

Gli-A2at {10805}.	[*Gli-A2^{m}j* {10805}].	**dv:** BGE 020466, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2au {10805}.	[*Gli-A2^{m}k* {10805}].	**dv:** BGE 001937, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2av {10805}.	[*Gli-A2^{m}l* {10805}].	**dv:** BGE 029108, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2aw {10805}.	[*Gli-A2^{m}m* {10805}].	**dv:** BGE 013627, *T. monococcum* subsp. *monococcum* {10805}.
Gli-A2ax {10805}.	[*Gli-A2^{m}n* {10805}].	**dv:** BGE 001937, *T. monococcum* subsp. *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
In the appropriate entry, replace:
Gli-B2null with ***Gli-B2au*** and add a column stating 'null allele'.

Gli-D2
In the appropriate entry, replace:
Gli-D2null with ***Gli-D2ae*** and add a column stating 'null allele'.

NEW SECTION: Abiotic Stess Responses

Dehydrin-response Element Binding Factors
DREB proteins are a large family of transcription factors induced by abiotic stresses. Using genome-specific primers an othologous *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-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}.

Pathogenic Disease/Pest Reaction

80. Reaction to *Blumeria graminis* DC.
80.1. Designated genes for resistance

Pm4d {10744}. 2AL {10744}. **bin:** 2AL1-0.85-1.00.
dv: *T. monococcum* subsp. *monococcum* Tm27 {10744}.
v: Tm27d2 = WW St 2022 / Tm27 // Amor = TRI 29584 {10744}.
ma: A 218-bp fragment was amplified with STS marker ResPm4 as were other *Pm4* alleles {10744}.

Pm17. **v:** McCormack {10758}; Tribute {10758}; TAM303 {10758}.

Pm41. **bin:** 0.63–1.00.

Pm44 {10790}. 3AS {10790}. **v:** Hombar {10790}.
ma: Flanked by SSR markers 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.

82. Reaction to *Fusarium graminearum*
82.2. Disease: Crown rot cuased by *Fusarium pseudograminearum*, *F. culmorum*, and other *Fusarium* species.

'Cansas / Ritmo': After *QFHS.whs-5BL* add insert: '(remaned *Qfhs.lfl-1BL* in {10768})'. Then continue at end of the paragraph '*Qfhs.lfl-1BL* was verified in $F_{4:7}$ lines and in detected Biscay, History, and Pirat {10768}.

'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}.

'Lang /*T. aestivum* subsp. *spelta* CSCR6': *Qcrs.cpi-3BL* from CSCR6 was flanked by *wPt8438* and *wPt9495*; R^2 up to 0.49, validated in other crosses {10273}. *Qcrs.cpi-4B* from Lang; R^2 up to 0.23 {10273}.

'Soissons (relatively resistant) / Orvantis (susceptible)': Add at end of paragraph: Increased susceptibility associated with the *Rht-D1b* allele was further confirmed in crosses of semi-dwarf cultivars Apachi, History, and Romanus {10793}.

83. Reaction to *Heterodera avenae* Woll.

QCre.pau-1A {10749}. 1AS {10749}. **dv:** *T. monococcum* subsp. *monococcum* Tm 14087 *QCre.pau-2A* {10749}.
ma: *QCre.pau-1A* was mapped in a 3.6 cM interval in a *T. monococcum* subsp. *aegilopoides* 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* subsp. *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}.

90. Reaction to Meloidogyne spp.
Root knot eelworm
Revise to:

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. peregrina* {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. peregrina* translocated to 3BL {10800}.

Add:
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_6F_3 near isogenic lines of Anza (PI 638742), Yecora Rojo, and Express with the 2NS translocation {10801}.

92. Reaction to *Phaeosphaeria nodorum* (E. Muller) Hedjaroude (anamorph: *Stagonospora nodorum* (Berk.) Castellani & E.G. Germano).

92.1. Genes for resistance

QTL

Add at the end of this section:

A summary of QTL analyses is provided in {10276}.

92.2. Sensitivity to SNB toxin

Insert at the beginning of this section:

A discussion on the origin and role of host-specific toxins is provided in {10276}.

Add:
Tsn1. **v:** Forno {10275}. **tv:** Add: Some *T. turgidum* subsp. *dicoccoides* accessions {10756}.
dv: Two *Ae. speltoides* accessions {10756}.
c: *Tsn1* has eight exons and a S/TPK-NBS-LRR structure; all three domains are required for function and the TSN1 protein does not interact directly with ToxA {10756}.
tsn1. **ma:** Add: This interval was reduced to 0.07 cM between *Xfcp620-5B* and *Xfcp394-5B* {10274}.

Genotype list in {10274}.
Snn1. **bin:** 1BS.sat.18.
ma: *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}.
Snn2. **ma:** *XTC253803* – 3.6 cM – *Snn2* – 0.4 cM – *Xcfd-*2D {10274}.
snn2. **v:** Add: Atlas 66 {10274}; Cheyenne {10274}; Chinese Spring {10274}; Jagger {10274]; Opata 85 {10274}; Salamouni {10274}; TAM 105 {10274}.
Snn3 {10728,10507}. Sensitivity to *SnTox3* is dominant {10728}.
5BS {10728,10507}. **bin:** 5BS-6 {10507}.
v2: Grandin Snn2{10728,10507}.
ma: *Snn3* – 1.4 cM – *Xcfd20-5BS* {10507}.
snn3. **v:** BR34 {10507}.
Snn4 {10275}. Sensitivity to SnTox4 is dominant {10275}. 1AS {10275}.
bin: 1AS3-0.86-1.00 {10275}.
v: Arina {10275}.
ma: *XBG262267/XBG262975* – 0.9 cM – *Snn4* – 1.6 cM – *Xcfd58.1-1AS* {10275}.
snn4. **v:** Forno {10275}.

QTL

'P91193D1 / P92201D5' RIL population: tested in the U.S.A. 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}.

94. Reaction to *Puccinia graminis* Pers.

Sr2. **ma:** Add: Tightly linked CAPS marker csSr2 based on a SNP proved superior to *Xgwm533-3B* as a marker for *Sr2* {10786}.

Sr13. **bin:** 6AL-8. **tv:** Kronos {10777}; Medora {10777}; Sceptre {10777}.
ma: *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*.

Sr22. **bin:** 7AL-0.74-0.86. **v:** Recombinant line reported in {10772, 10773}.
ma: 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}.

Sr38. Add at end of section: SCAR markers SC-372 and SC-385 were developed in {10796}.

Sr39. Add at the beginning of notes:Lines with shortened alien segments are reported in {10741}.

Sr48. **ma:** Replace the first sentence with: *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}.

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 (T3AL·$3S^{S}S$) {10803}. **v:** TA5619 {10803}.
3B (T3BL·$3S^{S}S$) {10803}. **v:** TA5620 {10803}.
3D (T3DL·$3S^{S}S$) {10803}. **v:** TA5621 {10803}.
3D (T3DS-$3S^{S}S$·$3S^{S}L$) {10803}. **v:** TA5622 {10803}.
al: *Ae. searsii* TA2355 {10803}.
ma: $3^{S}S$-specific markers are provided in {10803}.

Sr52 {10774}. 6A (T6AS·6V#3L) {10774}.
v: TA5617 {10775}.
ma: 6V3- specific EST-STS markers are given in {10775}.

The seedling response conferred by *Sr52* is temperature-sensitive.

Sr53 {10789}. Derived from *Ae. geniculata*. 5D {10789}.
Ti5DS·5DL-$5M^{g}L$-5DL {10789}. **v:** TA5630 (U6154-124) {10789}.
T5DL-$5M^{g}L$·$5M^{g}S$ {10789}. **v:** TA5625 (U6200-64) {10789}.
T5DL-$5M^{g}L$·$5M^{g}S$ {10789}. **v:** TA5643 (U6200-117) {10789}.
al: *Ae. geniculata* TA10437 {10789}.

The three translocation lines are re-engineered derivatives of TA5599 (T5DL-$5M^{g}L$·$5M^{g}S$ {10789}).

SrCad {10733}. 6DS {10733}.
v: AC Cadillac {10733}; AC Crystal {10733}; AC Foremost {10733}; AC Karma {10733}; AC Taber {10733}; AC 2000{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* — 8 cM – *Xbarc173-6D* {10733}; *Xcfd49-6D* – 7.2 cM – *SrCad* – 1.8 cM – *FSD-RSA/Bt10* – 14 cM – *Xcfd75-6D* {10733}.

SrR. Delete current listing.

95. Reaction to *Puccinia striiformis* Westend.

95.1. Designated genes for resistance to stripe rust

Yr1. **ma:** Replace the present entry with: *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}.

Yr5. Add note: Allelic with *Yr7* and *YrSp* {10759}.

Yr7. Add note: Allelic with *Yr5* and *YrSp* {10759}.

Yr9. **v2:** Brigadier *Yr17* {10785}.

Yr17. **v2:** Brigadier *Yr9* {10785}.
ma: Add: SCAR markers SC-372 and SC-385 were developed in {10796}.

Yr35. **ma:** *Xgwm191-6B* – 18.9 cM – *Yr35* – 3 cM – *Lr53* – 1.1 cM – *Xcfd-6B* – 3.4 cM – *Xgwm50-6B* {10780}.

Yr40. **ma:** Add: CAPS marker *XLr57/Yr40-MAS-CAPS16* {10770}.

Yr42. Add note: Associated with *Lr62* {10537}.

Yr46. Update to: 4DL. **bin:** Distal to 0.56.
ma: Change present entry to: *Xgwm165-4D/Xgwm192-4D* – 0.4 cM – *Yr46/Lr67* {10678}.

Yr49 {10746}. Adult plant resistance. 3DS {10746}.
bin: 3DS-6 (0.55-1.00). **v1:** 'Avocet S*3 / Chuanmai 18' AUS91433 {10746}.
v2: Chuanmai 18 Yr18 {10746}.
ma: *Xgpw7321-3D/Yr49* – 1 cM – *Xgwm161-3D* {10746}.

95.2. Temporarily designated genes for resistance to stripe rust

YrSp. Add note: Allelic with *Yr5* and *Yr7* {10759}.

95.3. Stripe rust QTL

'Alcedo (R) / Brigadier (S)': DH population: Two major QTL *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 QTL 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}.

96. Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr10. **tv:** Altar 82 {10760}; Russello {10760}.
c: Add: A second CC-NBS-LRR gene, *RGA2*, is required for expression of *Lr10* in tetraploid and hexaploid wheats {10760}.

Lr12. **v2:** Caldwell *Lr14a* {10787}.

Lr14.
Lr14a. **v2:** Caldwell *Lr12* {10787}.

Add note at end of section: 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}.

Lr17.
Lr17a. **ma:** Add: *Lr17a* – 3.7 cm – *Xbarc212-2a* {10795}.

Lr18. Add note: 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 different low seedling infection types, but the genetic backgrounds were different {10752}.

Lr21. **v:** Lovitt {10766}; McKenzie {10766}
Add to notes: Further haplotype analyses are reported in {10766}.

Lr25. **i:** Tc+Lr25 *Lr48* {10738}.
Add note: *Lr25* is closely linked with *Lr48* {10738}.

Lr35. Add note at the end of section: Lines with shortened alien segments are reported in {10741}.

Lr37. Add at end of section: SCAR markers SC-372 and SC-385 were developed in {10796}.

Lr39. 2DS {add: , 10731}.
ma: 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}.

Lr47. 7AS. **v:** Add: Bionta 2004 {10737}.

Lr48. , 4BS {10738}. **ma:** RAPD markers flanking *Lr48* at 2.7 and 8.6 cM are reported in {10738}.
Lr48 is closely linked with *Lr25* {10738}.

Lr53. **ma:** *Xgwm191-6B* – 18.9 cM – *Yr35* – 3 cM – *Lr53* – 1.1 cM – *Xcfd-6*B – 3.4 cM – *Xgwm50-6B* {10780}.
Lr53 was genetically independent of *Lr36* {10780}.

Lr57. **ma:** Add: CAPS marker *XLr57/Yr40-MAS-CAPS16* {10770}.

Lr59. Add note: Problems in recovering balanced recombinants are reported in {10762}.

Lr62 Add note: Associated with *Yr42* {10537}.

Lr67. **bin:** Distal to 0.56.
ma: add: *Xgwm165-4D/Xgwm192-4D* – 0.4 cM – *Yr46/Lr67* {10678}.

LrAlt {10739}. 2AS {10739}. **v:** *T. aestivum* subsp. *spelta* cv. Altgold {10739}.
ma: *LrAlt* – 1.8 cM – *Xbarc212-2A/Xwmc382-2A* – 2 cM – *Xgwm636-2A* {10739}.

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.

Add to the list: complex genotypes
Coker 9663 *Lr9 Lr10 Lr14a* {10742}
Pioneer 26R61 *Lr13 Lr14b Lr26* {10742}

Genotype lists: French cultivars {10792}. Add to European cultivars {……., 10794}.

96.3. QTL for reaction to *P. triticina*

Insert above *QLr.sfr-1B*:

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}.

After the entry for 'Avocet / Pavon' add:
'TA 4152-60 (MR) / ND495 (MR)': DH population: Five QTL 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* ($R^2 = 0.07$), 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}.

Add:
<u>Tetraploid wheat</u>
Association mapping 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}.

97. Reaction to *Pyrenophora tritici repentis* (anomorph: *Drechlera tritici-repentis*)

97.1. Insensitivity to tan spot toxin

Tsn. **dv:** Two *Ae. speltoides* accessions {10756}.
tv: Add: Some *T. turgidum* subsp. *dicoccoides* accessions{10756}.
c: *Tsn1* has eight 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}.

93.3. Resistance to tanspot

TsrAri {10765}. Recessive. 3A {10765}.
v: Arina {10765}; Heines VII {10765}; Zenith {10765}.
Add: '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}.

'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}.

XX. Reaction to Rhizoctonia spp.
Cause of Rhizoctonia root rot.
Rot1 {10761}. **v:** Scarlet-Rz1 {10761}.
Scarlet-Rz1 was produced by mutagenesis {10761}.

95. Reaction to *Schizaphis graminum* Rond. (Toxoptera graminum Rond.)
Gb2. **ma:** Within the 1R segment: *Gb6* – 15.8 cM – *Gb2* – 11.4 cM – *XIA294* {10764}.
Gb3. **v:** TAM112 (10764}. **al:** Insave rye.
Gb6. **v:** N96L9970 {10764}.
ma: Within the 1R segment: *Gb6* – 15.8 cM – *Gb2* – 11.4 cM – *XIA294* {10764}.

101. Reaction to *Tapesia* yallunda*e* (Anomorph: *Pseudocerosporella herpotrichoides*)
Add at end of section:
QPch.jic-5A {10771}. **bin:** 5AL-6; 0.68-0.78.
ma: Closely associated with *Xgwm639-5AL* {10771}.

102. Reaction to *Tilletia caries* (D.C.) Tul., *T. foetida* (Wallr.) Liro, *T. controversa*
Bt10. **v:** Present in lines with *SrCad* {10733}.
QTL
'Blizard (R) / 8405-JC3C (S)': DH population: Resistance and markers *Xgwm374-1BS*, *Xgwm364-1BS*, and *Xbarc128-1BS* were within a 3.9 cM interval {10783}.

106. 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 seed-borne. At least some sources of resistance to WSMV are also effective against *Triticum* mosaic virus.

Update:
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* cosegregated 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. 3BS (10802}. **v:** CO960293-2 {10802}; Snowmass {10802}.
ma: *Wsm2* – 5.2 cM – *XSTS3B-55* {10802}; *Xbarc102-3B* – 1.6 cM – *Wsm2* {10802}.
Wsm2 confers resistance at temperatures below 19C {10802}.
Wsm3 {10775}. 7B (T7BS·7S#3L) {10775}. **v:** TA5624 {10775}.

XX. Reaction to Wheat Yellow Mosaic Virus

Vectored by *Polymyxa graminis*. MYMV is closely related to WSSMV, 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 relationships 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.

References

Updates

10375. Correct author name from 'Laur' to 'Kaur' and delete 'Draft manuscript'.

10507. Correct page numbers to 682-693.

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10551. Replace with: Li G, Fang T, Zhang H, Xie C, Li H, Yang T, Nevo E, Fahima T, Sun Q & Liu Z 2009 Molecular identification of a new powdery mildew resistance gene *Pm41* on chromosome 3BL derived from wild emmer (*Triticum turgidum* var. *dicoccoides*). Theoretical and Applied Genetics 119: 531-539.

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