V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2009 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 11Th International Wheat Genetics Symposium held in Brisbane, Australia, is 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 proceedings and, therefore, cannot be cited as part of them.

INTRODUCTION

9. Laboratory Designators

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Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

1.1. Squarehead/spelt

Q. **bin:** 5AL-17 {10541}.

1.2. Club/Compact spike

C. Add to chromosome location: , probably 2DL {10578}.
bin: C-2DS1 – C-2DL3, markers flanking *C* were located on either side of the centromere {10578}.
v: Coda {10578}; Corrigin {10578}.
ma: Coda / Brundage: *Xwmc144-2D* – 1 cM – *C* – 8 cM – *Xwmc18-2D*; Corrigin / CS (*Ae. tauschii* 2D) {10578}: *Xwmc245-2D* – 1 cM – *Xcfd116-2D / Xgwm358-2D / C / Xcfd-2D* – 1 cM – *Xbarc145-2D* {10578}.

Add note:
C may be orthologous to gene *Sog* for soft glumes on chromosome $2A^m$ {10578}.
Add at the end of the section:
Tetraploid wheat: A compact spike gene C^{17648} in mutant line MA 17648 was 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

S ***B1b.*** Add: [..., s^{16219} {10541}]. **tv:** MA 16219 {10541}.

1.4. Branched spike

Replace the previous entry with the following:
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 – *Xgwm988-2D* {10637}.

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

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 on chromosomes 2A and 4A that promote the development of supernumerary spikelets and a gene on chromosome 2D that prevents their expression.

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

1.7. Multi-gynoecium

Synonym: three pistils (TP)

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

4. Aluminium Tolerance

QTL:

FSW (Al tolerant) / ND35 (Al sensitive): Three QTL 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}.

Add at end of section:

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}.

6. Awnedness

6.1. Dominant inhibitors.

6.1.2. Tipped 1

B2. **tv:** LD222 {10541}. **matv:** *Xgwm291-5A* **-** 8.0 cM - *B1* {10541}.

ma: *Xcfd71-4A* – 10.3 cM – *Ba* – 16.5 cM – *Xcfa2173-4A* {0802}^{3}.

17. Dormancy (Seed)

Vivipary

Following the present material add:

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

Vp-B1a {10615}. Sequence AJ400713 {10615}.
v: Charger {10616}; Zhongyou 9507 {10615}; 271 accessions {10616}.
Vp-B1b (10615}. 193-bp insertion in third intron relative to *Vp-A1a*.
v: Altria {10616}; Recital; {10616}; Yongchuanbaimai {10615}; 2 accessions {10616}.
Vp-B1c {10615}. 83-bp deletion relative to *Vp-B1a*.
v: Scipion {10616}; Xinong 979 {10615}; 101 others {10616}.
Vp-B1d {10616}. 25-bp deletion relative to *Vp-A1a*.
v: Cezanne {10616}; Jason {10616}; 97 others {10616}.
Vp-B1e {10621}. 83-bp deletion, 4-bp insertion, and 2 SNPs relative to *Vp-B1a* {10621}.
v: Hongheshangtou {10621}.

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}.

Pre-harvest sprouting:
QTL:
Insert as the third line in paragraph 2:
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 color {10626}.
Inset before the last paragraph:
'CN10955 (PHS resistant white seeded) / Annuello (PHS susceptible, white seeded)' F_8 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}.

20. Flowering Time
Insert above the entry for *QFlt.ipk-3A*:
Spring wheat cross: 'Nanda 2419 / Wangshuibai': Seven QTL 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*, $R^2 = 10\%$), *XFtl.nau-2D* (*Xwmc601-2D*, $R^2 = 10\%$), *XFtlnau.4A.1* (*Xcfd2-4A, Xmag1353-4A*, $R^2 = 10\%$), *XFtl.nau-4A.2* (*Xmag3386-4A, Xwmc161-4A*, $R^2 = 18–19\%$), and *XFlt.nau7B* (*Xmag2110-7B, Xmag1231-7B, Xgwm537-7B, Xwmc218-7B*, $R^2 = 18\%$) {10566}.

Following the *QFlt.ipk-3A* entry list the following gene:
QFt.cri-3B.1 {10567}. Nearest marker *Xbarc164-3B*; identified in crosses of substitution lines of Ceska Presivka and Zlatka or Sandra (10567}.

26. Glaucousness (Waxiness/Glossiness)
26.2. Epistatic inhibitors of glaucousness
Iw2 **bin:** 2DS5-0.47-1.00 {10578}.
ma: *Xcfd56-2D* – 6 cM – *Iw2* – 10 cM – *Xcfd51-2D* {10578}.

Add at end of section:
A dominant gene (*Vir*) for nonglaucousness was located in chromosome 2BL of cultivar Shamrock, a derivative of *T. turgidum* subsp. *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 glaucous sibs {10543}.

27. Glume Colour and Awn Colour
27.1. Red (brown/bronze/black) glumes
Rg-A1b. **ma:** Add: *Xgmw1223-1A*/*Rg-A1*/*Hg* - 2.2 cM - *Xgwm136-1A* - 4.2 cM - *Xgwm33-1A* {10635}.
Rg-A1c. **v:** TRI 14341 {10638}.
v2: Sears Synthetic *Rg-D1c* {10638}.
ma: *Rg-A1c* – 0.7 cM – *Xgwm1223-1A* {10638}.
Rg-B1b. **v:** Golubka {10635}.
ma: Add: *Xgwm1078-1B* – 4.6 cM – *Rg-B1* – 2.0 cM – *MW1B002 (Gli-B1)* – 4.1 cM – *Xgwm550-1B* {10635}.
Rg-D1b. **v:** ITMI Synthetic W7984 {10635}.
v2: Sears Synthetic *Rg-A1c* {10638}.
ma: *Xgwm1223-1D* – 6.6 cM – *Rg-D1*/*Xksud14-1D* – 13.9 cM – *Xgwm33-D1* {10635}; *Rg-A1c* – 3.9 cM – *Xgwm1223-1D* {10638}.

28. Grain Hardness/Endosperm Texture

Add at end of section:

'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}.

29. Grain Quality Parameters

Add at the end of the preamble:

'Neixing 188 / Yanshan 1' RIL population: 75 QTL for five quality-related traits are reported in {10640}.

29.2. Flour, semolina, and pasta colour

Add:

'Huapei 3 / Yumai 57': DH lines: 18 additive QTL and 24 pairs of epistatic QTL affected flour colour parameters; *qa-1B*, closely linked with *Xbarc372-1B* was associated with variation of a*, $R^2 = 0.256$ {10625}.

29.8. Loaf volume

QTL: Add:

A total of 30 QTL were located on 12 chromosomes, each of which explained between 5.85 and 44.69% of the phenotypic variation; the QTL of largest effect were located on chromosomes 6B and 6D {10659}.

29.10. Grain fructan content

Add:

Fructans are nondigestible 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}.

29.11. Water absorption

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

29.12. Chinese dry noodle quality

'Chuan 35050 / Shannong 483' RIL population: three 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 QTL for stickiness and total score also on chromosome 4A came from Shannong 483 {10647}.

40. Height

40.1. Reduced height: GA-insensitive

Rht-D1b. **v:** Biscay {10574}; Pirat {10574}; Rubens {10574}.

40.2. Reduced height: GA-sensitive

Rht12. **bin:** 5AL-23, based on co-segregation with *B1* {1606}.

42. Hybrid Weakness

42.1. Hybrid necrosis

Ne2ms. **v:** Mironovskaya {0995}.

Add references ',10627, 0995' to the genotype list.

46. Leaf Tip Necrosis

Ltn1. **c:** See *Lr34*.

This gene is identical to *Yr18, Pm38*, and *Ltn* and confers stem rust resistance in some genetic backgrounds.

48. Male Sterility

48.1. Chromosomal

ms1g {10546}. **v:** Male sterile line 257A {10546}.

62. Response to Photoperiod

Ppd-A1. The present listing for *Ppd-A1a* should be entered as *Ppd-A1*.

ma: *Xwmc177-2A – Ppd-A1*, 2.2 and 2.8 cM in GS100/GS101 and GS105/GS104, respectively {10612}.

Ppd-A1a {10612}. **tv:** GS100 {10612}; GS105 {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-A1b {10612}. **tv:** GS101 {10612}; GS104 {10612}.

Ppd-B1.

Ppd-B1a. **i:** H(C) = ‘Haruhikari*5 / Fukuwasekomugi’ {10611}, H(D) = ‘Haruhikari*/ 5 / Fukuwasekomugi’ *Ppd-D1a* {10611}.
v2: Fukuwasekomugi *Ppd-D1a* {10611}.

Ppd-B1b [{10611}]. **v2:** Haruhikari *Ppd-D1b*[{10611}].

Ppd-D1.

Ppd-D1a. **i:** H(A) = ‘Haruhikari*5 / Fukuwasekomugi’ {10611}; ‘Haruhikari*5 / Saitama 27’ {10611}, H(D) = ‘Haruhikari*/5 /Fukuwasekomugi’ *Ppd-B1a* {10611}
v: Akagomughi {10622}: Mazhamai {10622}; Youzimai {10622}.
v2: Fukuwasekomugi *Ppd-B1a* {10611}.

Ppd-A1a was present in 39% of Chinese landraces and 97% of improved cultivars{10622}.

Ppd-D1b [{10611}]. **v:** Haruhikari *Ppd-B1b* [{10611}].

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

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}.

65. Response to Vernalization

Add at the end of the *Vrn*_section:
Allelic variations at the *Vrn-1* and *Vrn-B3* loci in Chinese wheat cultivars are summarized in {10617}.

XX. New section: Soft Glumes

sog {10555}. 2AS {10555}. **dv:** *T. monococcum* subsp. *monococcum* var. *sinskajae* ID69 {10555}.
ma: Co-segregation with AFLP loci *Xe423204I and Xe373311* {10555}.

Sog {10555}. **dv:** *T. monococcum* subsp. *aegilopoides* ID49 {10555}.

sog was considered to be an homologue of *Tg1* and *Tg2*. See Tenaceous glumes.

73. Tenacious Glumes

Add note after *Tg2*
Tg1 and *Tg2* were considered to be homologues of *sog* for soft glumes in *T. monococcum*. See Soft glumes.

77. Yield and Yield Components

77.4. Grain yield

Nonglaucous (virescent) lines from a ‘Shamrock/Shango’ DH population had higher yields than glaucous sibs (10543}; see Glaucousness, subsection Epistatic inhibitors of glaucousness.

Proteins

79. Protein

79.1 Grain protein content

QGpc.ipk.7B {10628}. **su:** Favorit (F26-70 7B) {10628}.
v: F26-70 {10628}. Closely associated with *Ppd-B2* {10628}. See Response to Photoperiod.

79.2. Enzymes

79.2.33.1 Phytoene synthase 1 (EC 2.5.1.32)

This section is completely revised:

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 the 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 {10501}. **v:** Chinese Spring 10501}; CA 9648{10501}; Neixiang 188 {10501}; Chinese common wheats with high pigment content {10501}.
c: GenBank EF600063 {10501}, EU096091 {10530}, Eu649788 {10654}. No 37-bp insertion in intron 2 (194-bp fragment for marker Yp7A {10501}. 676-bp insertion in intron 4 {10530}.
tv: Blackbird {10653}. **c:** EF600063 {10653}.

Psy1-A1b {10501}. **v:** PH82-2 {10501}; Shaan 9314 {10501}; Xinong 336 {10501}. Chinese common wheats with low yellow pigment content {10501}.
c: GenBank EF600064 {10501}. 37-bp insertion in 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. turgidum* subsp. *dicoccum* DM28 {10652}.
c: GenBank EU263018 {10651}; FJ 393515 {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. monococcum* subsp. *aegilopoides* BO1 {10652}; *T.monococcum* subsp. *monococcum* MO5 {10652}.
c: FJ393518 {10652}; FJ393519 {10652}.
Psy1-A1i {10652}. **dv:** *T. monococcum* subsp. *monococcum* MO1 {10652}.
c: FJ393520 {10652}.
Psy1-A1j {10652}. **dv:** *T. monococcum* subsp. *monococcum* MO2 {10652}.
c: FJ393521 {10652}.
Psy1-A1k {10652}. **v:** Spelt 167 {10652}.
tv: *T. turgidum* subsp. *dicoccoides* DS3 {10652}; *T. turgidum* subsp. *dicoccum* DM37 {10652}.
c: FJ293527 {10652}; FJ393522 {10652}; FJ393523 {10652}.
Psy1-A1l {10652}. **tv:** Kofa {10230,10530}; Strongfield {10653}; *T. turgidum* subsp. *dicoccoides* DS6 {10652}.
c: EU096090 {10230,10530}; FJ393524 {10652}.
Psy1-A1m {10652}. **tv:** *T. turgidum* subsp. *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-B1 {10230}. 7BL {10230}. **tv:** Kofa {10230}.
ma: *Xcfa2040-7B* – 12 cM – *Psy-B1* – 5 cM – *Xgwm146-7B* {10230}.
Psy1-B1a {10650}. **v:** Chinese Spring {10530,10650,10654}; Spelt SP9 {10652}.
tv: *T. turgidum* subsp. *dicoccoides* DS4 {10652}; FJ393529 {10652}; FJ393528 {10652}.
c: 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}. **c:** EU263021 {10650}.
tv: DR8 {10650}; *T. turgidum* subsp. *dicoccum* DM28 {10652}.
c: EU263021 {10650}; FJ393541{10652}.
Psy1-B1f {10651}. **tv:** Langdon {10651}. **c:** EU263020 {10651}.
Psy1-B1g {10651}. **tv:** DR1 {10651}; *T. turgidum* subsp. *dicoccoides* DS6 10652}.
c: EU650396 {10651}; FJ393530 {10652}.

Psy1-B1h {10652}. **tv:** *T. turgidum* subsp. *dicoccoides* DS3 {10652}.
c: FJ393531 {10652}.
Psy1-B1i {10652}. **tv:** *T. turgidum* subsp. *dicoccoides* DS8 {10652}.
c: FJ393532 {10652}.
Psy1-B1j {10652}. **tv:** T. *turgidum* subsp. *dicoccum* DM26 {10652}.
c: FJ393533 {10652}.
Psy1-B1k {10652}. **tv:** T. *turgidum* subsp. *dicoccum* DM33 {10652}.
c: FJ393534 {10652}.
Psy1-B1l {10652}. **tv:** T. *turgidum* subsp. *dicoccum* DM37 {10652}.
c: FJ393535 {10652}.
Psy1-B1m {10652}. **v:** Spelt 167 {10652}. **c:** FJ393540 {10652}.
tv: *T. turgidum* subsp. *dicoccum* DM47 {10652}.
c: 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:** Spelt217 {10652}. **c:** FJ393546 {10652}.
Psy1-D1g {10652}. **v:** Zhongliang 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-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}.

79.2.34. Polyphenol oxidase

This section is completely revised:

High PPO activity in kernels and flour leads to a time-dependent discoloration 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 higher 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. turgidum* subsp. *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. monococcum* subsp. *aegilopoides* BO1 {10657}.
c: EU371652 {10657}.
Ppo-A1e {10657}. **tv:** DR8 {10657}. **dv:** *T. monococcum* subsp. *monococcum* MO1 {10657}.
c: EU371653 {10657}.
Ppo-A1f {10657}. **tv:** *T. turgidum* subsp. *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}. **v:** CA 9719 {10386}; CA 9632 {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}.

79.2.36. Polygalacturonase-inhibiting proteins

PGIPs are leucine-rich repeat (LRR) proteins involved in plant defense.
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}.

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* subsp. *dicoccoides* MG4343 {10608}.
This nonexpressed 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}.

Endosperm Storage Proteins
77.3.1. Glutenins
77.3.1.1. *Glu-1*
Glu-A1
Glu-A1y
Correction: The subunit encoded by this allele should be 2 and not 2'' as currently listed.

Add note to the end of the *Glu-A1* section:
Primers were designed that enabled Ax2* to be distinguished from Ax1 or Ax-null {10641}.

Glu-B1
Add:
Glu-B1bp {10643}. 7**+8 {10643}. **v:** XM1368-2 {10643}.
v: XM1404-2 {10643}.
Glu-B1bq {10643}. 7+8** {10643}.

Glu-D1
Glu-D1f
Add note:
Glu-D1f is present at high frequencies in wheats of southern Japan. Its presence may be associated with white salted noodle (Udon) quality {0936}.
Add:
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}.

Add note to the end of the *Glu-D1* section:
Primers were designed that enabled Dx2 to be distinguished from Dx5 and Dy10 from Dy12 {10641}.

Glu-A1-1
Glu-A1-1x
The subunit encoded by this allele should read 2 and not 2'' as currently listed.

Glu-B1-1
Add:
Glu-B1-1ag {10643}. 7** {10643}. **v:** XM1368-2 {10643}.

Glu-B1-2
Add:
Glu-B1-2ag {10643}. 8** {10643}. **v:** XM1404-2 {10643}.

Glu-D1-1
Add:
Glu-D1-1v {10642}. 1.6^t {10642}. **dv:** *Ae. tauschii* TD16 {10642}.

Glu-E1
Add:
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}.
Add note to the end of the *Glu-E1* section:
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 *Aey 10* (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 *Aey4* was a chimeric gene formed by recombination of two other genes {10662}.

79.3.1.3. *Glu-3*

Glu-D3
Add:
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}.

79.3.2. Gliadins

Add note to the end of the text appearing after the *Gli-DT1* locus:
A 1,200-bp *Dra*I RFLP was identified as a gene-specific probe for the T1 omega-gliadin {10645}.
Add:

79.3.2.7 *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}.

79.5.6. Waxy proteins

Wx-A1.
- ***Wx-A1c.*** **v:** Pakistan Zairaishi selection {10629}.
- ***Wx-A1e.*** **tv:** KU 3659 {10629}.
- ***Wx-A1g.*** *Wx-A1*$'$ {10587}. **v:** *T. aestivum* subsp. *spelta* accessions PI 348576 {10587}; PI 348476 {10587}; 2778 Epeautre Noir Velu {10587}.

Wx-B1.
- ***Wx-B1c.*** **v:** Chousen 40 {0094}; Junguk 12 {10629}; Cikotaba {10629}; AF24 {10629}.
- ***Wx-B1d.*** **tv:** KU4213D {10629}.
- ***Wx-B*^{S}*1g*** {10587}. **al:** *Ae. speltoides 33* {10587}.
- ***Wx-B*^{SL}*1h*** {10587}. **al:** *Ae. longissima* 12 {10587}.

Wx-D1.
- ***Wx-D*^{DN}*1g*** {10587}. **al:** *Ae. ventricosa* 12 {10587}.

79.5.8. Puroindolines and grain softness protein

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}.

Pathogenic Disease/Pest Reaction

81. Reaction to *Blumeria graminis* DC.

81.1. Designated genes for resistance

Pm4
- ***Pm4b.*** **ma:** *STS241* – 4.9 cM – *Pm4b* – 7.1 cM – SRAP *Me8/Em7220* – 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}.

Pm5.
Pm5a. **v2:** Saar *Pm38 Pm39* {10481}.
Pm5d 7BL, FL 0.86 {10542}. **v:** Dream {10542}.
ma: *Xgwm611-7B* – 2.1 cM – *Pm5d* – 2.0 cM – *Xgwm577-7B* – 1.0 cM – *Xwmc581-7B* {10542}.

Pm6. **i:** Eight Prins derivatives {10576}.
ma: RFLP marker *Xbcd135-2B* was converted to STS markers *NAU/STSBCD135-1* and *NAU/STSBCD135-2,* which showed linkage of 0.8 cM with *Pm6* {10576}.

Pm23. Deleted, see *Pm4c*.

Pm36. **bin:** 5BL6-0.29-0.76 {10356}.
ma: Delete the present entry and replace with:
Xcfd7-5B – 10.7 cM – *Pm36* – 0.8 cM – *EST BJ261636* – 8.9 cM – *Xwmc75-5D* {10356}.

Pm38. **v:** Saar *Pm5a Pm39* {10481}.
c: See *Lr34*.
This gene is identical to *Yr18, Lr34,* and *Ltn* and confers stem rust resistance in some genetic backgrounds.

Pm39. Change **v:** to **v2:** and insert '*Pm5a*' in front of '*Pm38*'

Pm40 {10539}. Derived from *Th. intermedium* {10539}. 7BS {10539}.
v: GRY19 {10539}.
ma: Mapped relative to several SSR markers {10539}.

Pm41 {10551}. Derived from *T. turgidum* subsp. *dicoccoides*. 3BL {10551}.
v: XXX = '87-1*4//Langdon/IW2' {10551}.
tv: **'**Langdon/IW2 Seln. XXX' {10551}; *T. turgidum* subsp. *dicoccoides* IW2 {10551}.
ma: *BE489472* – 0.8 cM – *Pm41* – 1.9 cM – *Xwmc687-3B* {10551}.
Pm41 and associated marker alleles showed strongly distorted inheritance with reduced frequencies relative to Langdon alleles {10551}.

Pm42 {10559}. Derived from *T. turgidum* subsp. *dicoccoides*. Recessive.
2BS {10559}. **bin:** 0.75-0.84.
v: P63 = Yanda 1817/G303-1M//3*Jing 411 {10559}.
tv: *T. turgidum* subsp. *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}.

81.3. Temporarily designated genes for resistance to *Blumeria graminis*

PmLK906. After 'recessive' correct second reference to {10477}.

MlIw72 {0908}. 7AL {0908}. **bin:** FL 0.86 {0908}.
tv: *T. turgidum* subsp. *dicoccoides* IW72 {0908}.
ma: *Xmag1759-7A* – 8.2 cM – *MlIw72* – 3.3 cM – *Xmag2185-7A* – 1.6 cM – *Xgwm344-7A* {0908}.

PmYm66 {10619}. 2AL {10619}. **v:** Yumai 66 {10619}.
ma: *XKsum193-2A* – 2.4 cM & 3.6 cM – *PmYm66* {10619}.

Pm2026 [{10604}]. *pm2026* {10604}. Recessive {10604}. $5A^mL$ {10604}.
bin: 5AL17 – 0.78-1.00 {10604}.
dv: *T. monococcum* subsp. *monococcum* TA2026 {10604}.
ma: *Xcfd39-5A* – 1.8 cM – *Xcfd1493-5A/Xmg2170-5A* – 0.9 cM – *Pm2026* – 2.5 cM – *Xgwm126-5A* {10604}.

81.4. QTL for resistance to *Blumeria graminis*

'Avocet R (S) / Saar (R)' F_6 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}.

86. Reaction to *Fusarium graminearum*

86.1. Disease: Fusarium head blight, Fusarium head scab, scab

Fhb3. Change 7D to 7DS.
ma: Three PCR markers, *Be586744-STS, BE404728-STS,* and *BE586111-STS*, were developed {10529}.

Following the entries 'Wuhan-1 / Maringa' in QTL section and under Resistance to Don Accumulation insert: (corrected to 'Wuhan / Nyubai' {10623}).'

Field resistance
After the present entry insert the following:
'G16-92 (R) / Hussar (S)': Two QTL for resistance to *F. culmorum* were identified on chromosomes 1A (resistance from Hussar) ($R^2 = 0.01$) and 2B (resistance from G16-92) ($R^2 = 0.14$) {10588}.

Under 'Nanda 2419 (S) / Wangshuiba (R)' and immediately above 'Wanshuibai / Seri 82' add the following:
Type IV resistance (proportion of Fusarium-damaged kernels) was attributed to five QTL, 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 phenotypic 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 QTL 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 QTL occurred on chromosomes 1B (T1B·1R), 4D (*Qfhs.jic-4D.2*), 2A, 3A (each, two QTL), 5A, and 7A. *Xfhs.jic-4d.2* had little effect on Type-2 resistance {10603}.
Add at end of section:
Associations between response to FHB caused by *F. culmorum* and the semidwarfing 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 semidwarf 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. turgidum* subsp. *dicoccoides* Israel A substitution line relative to Langdon was mapped to a 22-cM interval spanned by *Xgwm558-2A* and *Xgwm445-2A* {10613}.

88. Reaction to *Magnaporthe grisea* (Herbert) Barr

List following the note:
Rmg4 {10639}. 4A {10639}. **v:** Norin 4 {10639}; Norin 26 {10639}; Norin 29 {10639}; P168 {10639}; Shin-chunaga {10639}; *T. aestivum* subsp. *compactum* No. 24 {10639}.
Confers resistance to *Digitaria* isolate Dig41 at 26°C {10639}.
Mg5 {10639}. 6D {10639}. **s:** CS (Red Egyptian 6D) {10639}
v: Red Egyptain {10639}.
Confers resistance to *Digitaria* isolate Dig41 at 26°C {10639}.

91. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter

Stb3. After the existing chromosome location, add:
According to {10556} this location is not correct. 7AS {10556}.

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 the section:
'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}.

<u>Tetraploid wheat</u>
'Langdon / Langdon' (*T. turgidum* subsp. *dicoccoides* Israel-A 5B): *QSnb.ndsu-5B* located 8.3 cM proximal to *tsn1* for tan spot resistance; R^2 = 0.38 {10597}.

92.2. Sensitivity to SNB toxins

Australian cultivars with *Tsn1* and *tsn1* are listed in {10540}.

94. Reaction to *Puccinia graminis*

Sr2 **v2:** HD2009 *Sr30* {10632}.
Sr8b. **tv2:** Arrivato *Sr9e Sr13* {10607}.
ma: *Sr8b* – 4.6 cM – *Xgwm334-6A* {10607}.
Sr9e. **tv2:** Arrivato *Sr8b Sr13* {10607}.
ma: *Xgwm191-2B* – 5.5 cM – *Sr9e* – 0.7 cM – *Xgwm47-2B* {10607}.
Sr13. **v2:** Machete *Sr2* {10607}. **tv2:** Arrivato *Sr8b Sr9e* {10607}.
ma: *Xwmc59-6A* – 5.7 cM – *Sr13* {10607}.
Sr17. 7BL {, 10565}. **v:** Forno (10511, 10565}.
ma: *Xwmc273-7B* – 15.3 cM – *Sr17* {10565}.
Sr30. **v2:** HD2009 *Sr2* {10632}.
Sr36 **v:** Others, add reference 10609, i.e., {572, 10609}.
ma: *Xgm429-2B* – 0.8 cM – *Sr36/Xstm773-2-2B/Xgwm31-2B/Xwmc477-2B* {10609}; *Xgwm319-2B* – 0.9 cM – *Sr36/Xstm773-2-2B/Xwmc477-2B* {10609}.
Sr47 {10549}. Derived from *Ae. speltoides*. 2B = T2BL-2SL·2SS {10549}.
tv: DAS15 {10549}. **al:** *Ae. speltoides* PI 369590 {10549}.
Sr48 {10564}. *SrAn1*{10565}. 2AL {10564, 10565}.
bin: 2AL1-0.85-1.00 {10564}. **v:** Arina {10511, 10564, 10565}.
ma: *Yr1* – 16.5 cM – *Sr48* {10564}. *Sr48* is considerably distal to the most distal of published markers, all of which are proximal to *Yr1*.

Add at end of section:

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 QTL gave consistent effects across environments, i.e., *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}.

95. Reaction to *Puccinia striiformis*

95.1. Designated genes for resistance to stripe rust

Yr1. **bin:** 2AL1-0.85-1.00 {10564}.
ma: *Xfba-2A* – 1.3 cM – *Xstm673acag* – 1.1 cM – *Yr1* {10564}.
Yr9. At the end of section add:
Stripe rust resistant wheat–*S. africanum* derivatives G17 (substitution line with 1R^a), L9-15 (T1BL·1RS^a) and L2-20 (putative cryptic translocation) are reported in {10596}.
Yr17. **v:** Apache {10554}; Bill {10554}; Caphorn {10554}; Clever {10554}; Clarus {10554}; Corsaire {10554}; Rapsodia {10554}; To Renan add reference, that is {0044,10554}; Rheia {10554}.
Yr18. **v2:** Saar *Yr29* {10481}.

***Yr26*.** , 1BL {10544}. **Bin:** C-1BL6-0.32 {10544}.
v: Nannong 9918 {10544}; Nei 2938 {10544}; Nei 4221{10544}; Neimai 9 {10544}.
ma: *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 {10544} the markers most closely associated with *Yr26* are actually located in chromosome 1BL.

***Yr27*.** **v2:** Change 'Attila *Lr27*' to 'Attila *Yr27*'.

***Yr29*.** **v2:** Saar *Yr18* {10481}.

***Yr33*.** 7DL {10039}. **ma:** Linkage with *Xgwm111-7D* and *Xgwm437-7D* {10039}.

Yr42 {10537}. Derived from *Ae. neglecta*. 6A = T6AL-6^{Aen}L·6^{Aen}S {10537}.
v: Line 03M119-71A {10537}.
al: *Ae. neglecta* 155 {10537}.

Genotype list: Add:
European wheats {10579}.

95.2. Temporarily designated genes for resistance to stripe rust

YrCN17 {10562}. Derived from *S. cereale*. 1B, T1BL·1RS {10562}.
v: CN12 {10562}; CN17 {10562}; CN18 {10562}.
al: *S. cereale* L155 {10562}.

YrC591 {10606}. 7BL {10606}. **v:** C591 {10606}; Zhongzhi 1 {10606}.
ma: *Xcfa20-40-7B* – 8.0 cM – *YrC591* – 11.7 cM – *SC-P35M48* {10606}.

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}.

YrR212{10562}. Derived from *S. cereale*. 1B, T1BL·1RS {10562}.
v: R185 {10562}**;** R205 {10562}; R212 {10562}.
al: *S. cereale* R212 {10562}.

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}.

95.3. Stripe rust QTL

Add at end of section:

'Luke (R) / Aquileja (R)': Two QTL for high-temperature adult-plant 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': QTL were located on chromosomes 2BS (probably *Yr27*), 2BL (a race-specific effect) and 7BL (*XP32/M59 – Xgwm344-7B* {10586}.

'Guardian / Avocet S': F$_3$ lines. One major QTL, *QPst.jic-1BL* (*Xgwm818-1* **–** *Xgwm259-1B* , R^2 up to 0.45), and two minor resistance QTL on chromosomes 2D and 4B originating from Guardian {10589}. The major QTL was in the region of *Yr29*.

'Stephens / Michigan Ambe'r: Two QTL 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}.

96. Reaction to *Puccinia triticina*

96.1. Genes for resistance

***Lr1*.** **v:** Line 87E03-S2B1 {10561}. **ma:** Co-segegation 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}.

***Lr11*.** **v2:** Ck9803 *Lr18* {10595}; FFR 524 *Lr18* {10595}; Pioneer 2684 *Lr18* {10595}; SS520 *Lr18* {10595}.

Lr13. **ma:** *Xbarc163-2B* – 5.1 cM – *Lr13* – 8.7 cM – *Xstm773b-2B* {0329}.

Lr14a. **v2:** Brambling *Lr23 Lr34* {10563}.

Lr14b **v:** Weebill 1 {10571}.

Lr17a. **bin:** 2AS-5 {10572}. **v:** TAM 111{10595}; Trego {10572}.

ma: *Xbarc123-2A* – 4.8 cM – *Xgwm636-2A* – 4.0 cM – *Lr17a* {10571}; *Xgwm614-2A* – 0.7 cM – *Lr17a* – *Xwmc407-2A* {10572}.

Lr18. **v2:** Ck9803 *Lr11* {10595}; FFR 524 *Lr11* {10595}; Pioneer 2684 *Lr11* {10595}; SS520 *Lr11* {10595}.

Lr19. 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}.

c: A candidate sequence, AG15, with a 1,258 amino-acid sequence and a CC-NBS-LRR structure was reported in {10575}.

Lr21. Add note at end of section:

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}.

Lr23. **v:** IWP94 {10569}. **v2:** Brambling *Lr14a Lr34* {10563}

Lr24. **v:** Cutter {10595}; Jagalene {10595}; McCormick {10595}; Ogallala {10595}.

Lr26. **v:** AGS 2000 {10595}; Pioneer 26R61 {10595}.

Lr27. **tv:** Benimichi C2004 {10585}; Jupare C2001 {10585}.

Lr31. **tv:** Benimichi C2004 {10585}; Jupare C2001 {10585}.

Lr34. **v2:** Brambling *Lr14a Lr23* {10563}; Saar *Lr46* {10481}.

Lr34. **i:** Add: Arina + *Lr34* {10648}; Lalbahudar + Lr34 {10648}.

v: Ardito {10648}; Kavkaz {10648}; Pegaso {10648}; Penjamo 62 {10648}. To the following add reference: Bezostaya {, 10648}; Condor {, 10648}; Fukuko-Komugi {, 10648}.

v2: Anza = WW15 *Lr13* heterogeneous {10648}; Brambling *Lr14a Lr23* {10563}; Chris *Lr13*{10648}; Jupateco R *Lr17a,Lr27+Lr31* {10648}; Saar *Lr46* {10481}. To the following add reference: Chinese Spring *Lr12* {,10648}; Glenlea *Lr1* {,10648}; Mentana *Lr3b* {,10648}.

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}.

This gene is identical to *Yr18, Pm38* and *Ltn* and confers stem rust resistance in some genetic backgrounds.

Lr39. **v:** Fuller {10595}; Overley {10595}.

Lr42. **v:** Fannin {10595}.

Lr46. **v2:** Saar *Lr34* {10481}.

Lr48. Correct to 2BS {0329}. **i:** CSP44 / 5*Lal Bahadur {0329}.

ma: *Xgwm429b-2B* – 6.1 cM – *Lr48* – 7.3 cM – *Xbarc7-2B* {0329}.

Lr49. Add: ,4BL {0329}. **i:** VL404 / 5*Lal Bahadur *Lr34* {0329}.

ma: *Xbarc163-4B* – 8.1 cM – *Lr49* – 10.1 cM – *Xwmc349-4B*{0329}.

Lr59. Derived from *Ae. peregrina.* 1A, probably 1AS.alien centric fusion {10399}.

Lr60. **ma:** *Lr60* – 8.4 cM – *Xbarc149-1D/Lr21* {10400}; *Lr60* – 13 cM – *Lr21* {10400}.

Lr61. **ma:** Replace present entry with: *Lr61* – 2.2 cM – *P81/M70269/P87/M75131* – 4.6 cM – *P87/M76149* – 21.7 cM – *Xwmc487-6B* {10485}.

Lr62 {10537}. Derived from *Ae. neglecta*. 6A = T6AL-6^{Aen}L·6^{Aen}S {10537}.

v: Line 03M119-71A {10537}. **al:** *Ae. neglecta* 155 {10537}.

Lr63 {10550}. Derived from *T. monococcum* subsp. *monococcum*. 3AS {10550}.

i: RL 6137 = Thatcher*6/TMR5-J14-12-24 {10646,10550}.

v: TMR5-J14-12-24 {10646}. **dv:** *T. monococcum* subsp. *monococcum* {10646}.

ma: Very closely linked to *Xbarc321-3A* {10550}.

Lr64 {10550}. 6AL {10550}. **i:** RL 6149 = Thatcher*6/ *T. turgidum* subsp. *dicoccoides* 8404 {10550}.

tv: *T. turgidum* subsp. *dicoccoides* 8404 {10550}.

ma: *Xbarc104-6A* – 13.9 cM – *Lr64* – 21.9 cM {10550}.

Lr65. Tentatively approved subject to an allelism test and acceptance by a journal.

Lr66 {10591}. *LrS13* {10592}. 3A {10591}.

v: Line 07M101-127 = *Ae. speltoides* / 5*CS // 2*CS *ph1b* mutant /3/ 2* W84-17 /4/ CSN3AT3B {10591}.

al: *Ae. speltoides* Accession 691 {10591}.

ma: Most user-friendly marker, SCAR S15-t3 {10591}.

List after *LrW2*:

LrZH84 {10581}. 1BL {10581}. **v2:** Predgornaia 2 *Lr26* {10581}; Zhou 8425B *Lr26* {10581}.

ma: *Xbarc8-1B* (cent) – 5.2 cM – *LrZh84* – 3.9 cM – *Xgwm582-1B* {10581}.

96.2. Suppressor of genes for resistance to *P. triticina*

96.3. QTL for reaction to *P. triticina*

Add at end of section:

'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}.

<u>Tetraploid wheat</u>

'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 7BL10-0.78-1.00 {10600}.

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

97.1. Insensitivity to tan spot toxin (necrosis)

Add note following the *Tsn1* section:

Australian cultivars with *tsn1* and *Tsn1* are listed in {0903}.

97.3. Resistance to tanspot

Tsr1. Add note:

The gene in Erik was allelic with resistance in a diverse set of genotypes including spelt and durum derivatives {10557}.

Add after *Tsr5*:

TsrHar {10590}. 3B {10590}. **v:** Dashen {10590}; HAR 604 {10590}; HAR 2562 {10590}.

Effective against races ASC1a (race 1) and DW-16{10590}.

QTL:

TA4152-60 (R) / ND495 (S) DH population. Five QTL for resistance, all from TA4152-60 (10580}, i.e., *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}.

100. Reaction to Soil-Borne Cereal Mosaic Virus

Vectored to the roots by the fungus, *Polymyxa graminis*.

Sbm1 {change reference to 10614}.

5DL {10614}. **v:** 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}.

Delete the paragraph beginning with *QSbv.ksu-5D* because the information duplicates the previous paragraph. Reference {10521} can be deleted because it duplicates {10273}.

Genetic linkages

Chromosome 2A

2AL

Yr1 – *Sr48* 16.5 cM {10564}

Chromosome 2B

2BS

Lr48 – *Lr13* 14.6 cM {0329}

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