V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2013–14 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 12Th 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.

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Morphological and Physiological Traits

At the end of the introductory paragraph add:
A summary of trait genotypes and markers used in the Canadian wheat breeding program is given in {11044}.

1. Gross Morphology: Spike characteristics

5. Anthocyanin Pigmentation

5.3. Red/purple coleoptiles.

After the introductory sentence add:
In chromosome substitution lines of wild emmer to common wheat, both the 7AS and 7AL derivatives had red coleoptiles, placing *Rc-A1* in the centromeric region {10974}.

5.5. Purple grain/pericarp

Continue the first paragraph:
A purple line PC was obtained from a cross of the nonpurple Line 821 (a 7S(7B) substitution from *Ae. speltoides*) and Line 102/00, a chromosome 2A introgression from *T. timopheevii* {10946}. Purple-grained accessions are unknown in both *Ae. speltoides* and *T. timopheevii*.

8. Blue Aleurone

NEW Brittle Culm

Three independent mutants with brittle tissues were obtained as EMS-induced mutants in *T. monococcum* subsp. *monococcum* accession PAU 14087 {11002}. The mutations likely affected cellulose synthesis and involved all tissues {11002}.

brc1 {11002}. 1AL {11002}. **dv:** *T. monococcum* subsp. *monococcum* mutant *brc1* {11002}.
ma: *Xwmc470-1A* – 3.9 cM – *brc1* – 2.1 cM – *Xgwm135-1A* {11002}.

brc2 {11002}. 3AL {11002}. **dv:** *T. monococcum* subsp. *monococcum* mutant *brc2* {11002}.
ma: *Xcfa2170-3A* – 2.9 cM – *brc2* – 0.8 cM – *Xcfd62-3A* {11002}.

brc3 {11002}. 6AS {11002}. **dv:** *T. monococcum* subsp. *monococcum* mutant *brc3* {11002}.
ma: *Xbarc37-6A* – 1.9 cM – *brc3* – 10.3 cM – *Xbarc113-6A* {11002}.

9. Brittle Rachis

After the introductory sentence add:
In chromosome substitution lines of wild emmer to common wheat, the 3AS derivative was more brittle than the 3BS derivative {10974}.

11. Cadmium Uptake

11.1. Low cadmium uptake

***Cdu1*.** **tv:** Brigade {11044}; CDC Desire {11044}; CDC Verona {11044}; CDC Vivid {11044}; Enterprise {11044}; Eurostar {11044}; Napoleon {11044}; Transend {11044}; Strongfield {11044}.

13. Cleistogamous Flowering

Delete 'in durums' from the heading and begin the section with the following:
Cleisogamy in barley is controlled by the *Cly1* gene, which encodes an AP2 protein. The *Cly1* and *cly1* alleles differ by a single nucleotide within the miR172 binding site. Three wheat homologues of *Cly1*, *i.e., TaAP-2A*, *TaAp-2B*, and *TaAp-2D*, were located in the terminal bins of chromosomes 2AL, 2BL, and 2DL, respectively, in Chinese Spring and Shinchunaga {11013}.

Cleistogamous flowering in durums
Present data.

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

16.1. Common wheat

Kr1. **ma:** Mapped to a 2.0-cM region flanked by *Xw5145-5B* and *CA1500122*/*Xw9340-5B* {10922}.

A second gene in 5BL distal to the *Ph1* locus and flanked by *Oshypl* and *Os09g36440*, but including *Xgwm371-5B*, affected the temperature sensitivity of seed set in *Kr1* genotypes in wide crosses {10922}.

17. Dormancy (Seed)

17.1. Vivipary

Vp-A1g [[11047}]. *Vp-1Ab* {11047}. **v:** Kayansona {11047}; Sonalika {11047}; Yaqui 50 {11047}; Yecora Rojo 76 {11047}.
c: GenBank Gu385899 {11047}.

Vp-A1h [{11047}]. *Vp-1Ad* {11047}. **v:** Attila {11047}; Glenlea {11047}; Tanori F71 {11047}.
c: GenBank Gu385901 {11047}.

Vp-A1i [{11047}]. *Vp-1Af* {11047}. **v:** Debeira {11047}; Kancahn {11047}; Rayon F89 {11047}.
c: GenBank Gu385903 {11047}.

Vp-1Be {10998}. **v:** Fulingkemai {10999}; Hongmangchun {10998}; Wangshuibai {10999}.

Vp-1Bf {10998}. **v:** Wanxanbaimaizi {10998}.

Vp-B1g {11000}. **v:** HD2939 {11000}; Pavon 76 {11000}; Sonora 64 {11000}.
c: GenBank GU385904 {11000}.

17.2. Pre-harvest sprouting

QTL

Association mapping of 198 winter wheat genotypes detected eight QTL on seven chromosomes, 1BS, 2BS, 2BL, 2DS, 4AL, 6DL, 7BS, and 7DS {10959}.

18. Ear Emergence

19. Earliness per se

Add at end of section:

Cutler / AC Barrie: Three QTL were mapped on chromosomes 1B (*QEps.dms-1B.1* and *QEps.dms-1B.2*) and 5B (*QEps.dms5B*) {11039}.

NEW Flag Leaf Width

Two NILs in the backgrounds of Mianyang 99-323 and PH691 possessing *Fhb5* in a *Xbarc303-5A – Xbarc100-5A* interval from Wangshuibai spanning the centromere had a narrow-leaf phenotype. *QFlw.nau-5A*, redesignated as *TaFLW1*, was mapped to a 0.2-cM region, *Xwmc492-5A – Xwmc752-5A*: bin 5AL12-0.37-0.57, and was separated from *Fhb5*: bin 5AS3-C-0.75 {10934}.

40. Height

40.1. Reduced Height : GA-insensitive

Rht-A1a. 4A {10923}, 4AL {11017}.
ma: *Xwmc48-4AS* – 2 cM – *Xgwm610-4A* – 1 cM – *Rht-A1* – 2 cM – *Xgpw4545-4AL* {11017}.

Add to existing note:

A functional *Rht-A1a* allele is expressed at a similar level to its orthologues {10923}.

Rht-B1c. **ma:** Allele-specific markers were designed from the gene sequence {10923}.
c: The *Rht-B1c* transcript carries a 90-bp, in-frame insertion within the region encoding the conserved N-terminal DELLA domain plus two SNPs upstream of the insertion. A much larger insertion occurs in the g-DNA {10923}.

Rht-B1d. **c:** Has the same point mutations as in *Rht-B1b*, there is likely to be another mutation outside the coding region {10923}.

Rht-B1e. **v:** Karlik 1 PI 504549 {10924}, Polukarlikovaya 49 and 11 derivatives {10924}.
ma: A PCR marker distinguishes this allele from *Rht-B1a* and *Rht-B1b* {10923}.
c: A stop codon occurs three codons upstream of the *Rht-B1b* mutation {10923}.

Rht-D1. **bin:** 4AL10-0.82-1.00 {11017}.

Immediately following the *Rht-D1d* entry, and before present footnote, insert:
Rht-D1b, *Rht-D1c*, and *Rht-D1d* are identical across the coding region, but *Rht-D1c* has a four-fold increase in copy number relative to *Rht-D1b*; *Rht-D1d* has a reduced copy number relative to *Rht-D1c* {10923,11016}.

40.2. Reduced Height : GA-sensitive
Rht11 {718}. See *Rht-B1e*.

42. Hybrid Weakness
42.1. Hybrid necrosis
Ne2m. **v:** After Manitou {939}add: 'HD2329 {10985}.'

Genotype lists in: add: '10985.'

65. Response to Vernalization
Vrn-B1b. **v:** Ciano 67 {10991}; Polo {10991}; Yaktana 54 {10991}.

Vrn-B1d [{10977,10978}]. Referred to as *Vrn-B1c* in {10977,10978}, *Vrn-B1*^{S} {10977}.
v: Albidum 43 {10991}; Albidum 29 {10991}. Garnet {10991}; Lutescens 62 {10991}; McMurachy {10991}; Saraovskaya 29 {10977,10991}. Six cultivars {10977}; 25 cultivars {10978}.
c: GeneBank HQ593668 {10977}, HQ130482 {10978}. Relative to *Vrn-B1a* (= *Vrn-B1*^{DM}, *Vrn-B1d* has a deletion of 0.8 kb and duplication of 0.4 kb in intron 1 {10977}.

Vrn-D1
List the current *Vrn-D1a* as a continuation under *Vrn-D1*.
To the following note, change the ending to '….Ushio Komugi relative to Vrn-D1 {10202}.
Add note: Nine, spring-habit *Ae. tauschii* accessions from Pakistan and Afghanistan shared a 5,437-bp deletion in the first intron of *Vrn1-D*^{t}*1*; the deletion resulted in a more abundant WFT transcript {10958}. Wheat lines identified as having genotype *vrn-A1*, *vrn-B1*, *Vrn-D1*, *vrn-2*, *vrn-3* were subdivided into spring and facultative types based on a 110-day, nonvernalization flowering test. Relative to *Vrn-D1a*, *Vrn-D1b* has a SNP located 161 bp upstream from the ATG initiation site; cytidylic acid is replaced by aenylic acid. The SNP is in the CArG box, a recognition site for MADS-box proteins {10996}. In qRT-PCR analyses, expression of *Vrn-D1b* was reduced relative to *Vrn-D1a* {10996}. A molecular marker was developed to distinguish the alleles {10996}.

Vrn-D1a {10996}. *Vrn-D1* {1398}. Spring habit.
v: Shimai 12 {10996}; Yumai 7 {10996}; Yumai 18 {10996}; Yangmai 3 {10996}; Yangmai 18 {10996}.

Vrn-D1b {10996}. *Vrn-D1* {10996}. Facultative habit.
v: Jimai 26 {10996}; Kenong 199 {10996}; Shi 4185 {10996}; Shi-91-5093 {10996}; J5265 {10996}.
c: GenBank JQ406528 {10996}.

vrn-D1. **c:** GenBank AY616457 {10996}.

Following the gene lists continue the paragraph starting 'Allelic variations…..{773}: *Vrn-1*, *Vrn-2*, *Vrn-4*, and *Vrn-4* alleles in Indian wheats based on markers are postulated in {10986}.

Following **69. Segregation Distortion**

NEW. Short Roots

A 'very short root' phenotype was produced by heterozygous genotypes from selected crosses between Chinese Spring and certain synthetics. The *Vsr1* locus was localized to a 3.8-cM interval on chromosome 5DL {11014}.

Vsr1 {11014}. 5DL {11014}.
ma: *Xwmc765-5D* – 7.7 cM – *Vsr1* – 1.1 cm – *Xbarc144-5D* {11014}; *Xwmc765-5D* – 1.9 cM – *XWL938* – 3.3 cM – *XWL2506* – 3.3 cM – *Vsr1* – 0.5 cM – *XWL954* – 0.5 cM – *Xbarc144-5D* {11014}.

Vsr1a. **v:** Chinese Spring {11014}.
Vsr1b. **v:** TA4152-71 {11014}.

Proteins

80. Proteins

80.1. Grain protein content

Move the first paragraph and insert below gene *Pro2*.

Gpc-B1b. Add synonym '... NAM-B1 {10995}.'
i: Yecora Rojo NIL PI 638740 {10138}.
v: As II {10995}; Burnside {11044}; Diamant {10995}; Glencross {11044}; Glupro {10138}; Lilian {11044}; Prins {10995}; Somerset {11044}; Stanley {10995}, *T. aestivum* subsp. *spelta* Altgold {10995}.
tv: *T. turgidum* subsp. *dicoccoides* FA-15 {10138}.

This allele was relatively frequent in Scandinavian and Finnish common wheats, landraces, and spelts {10995}.

80.2. Enzymes

80.2.34. Polyphenol oxidase

Ppo-A1. **ma:** *Xcfa2058-2A* – 0.4 cM – *Ppo-A2* – 0.4 cM – *Xiwa174-2A* – 8.3 cM – *Xiwa7593-2A* – 0.6 cM – *Ppo-A1* – 11.0 cM – *Xwmc181-2A* {10931}.
Ppo-A1f. **v:** Penawawa {10931}.
Ppo-A1h {10931}. **v:** Louise {10931}.
c: GenBank JN632506 {10931}.

Ppo-D1. **ma:** *Xcfd62-2D* – 0.2 cM – *Ppo-D2* – 0.4 cM – *Xcfd168-2D* – 7.7 cM – *Xgwm608-2A* – 2.6 cM – *Ppo-D1* – 0.9 cM – *Xbarc349-2D* {10931}.
Ppo-D1a. **v:** Louise {10931}.

Ppo-A2 {10930}. *PPO-A2* {10931}. 2AL {10930}.
ma: *Xcfa2058-2A* – 0.4 cM – *Ppo-A2* – 0.4 cM – *Xiwa174-2A* – 8.3 cM – *Xiwa7593-2A* – 0.6 cM – *Ppo-A1* – 11.0 cM – *Xwmc181-2A* {10931}.
Ppo-A2a {10930}. **v:** Alpowa {10930}.
c: GenBank HQ228148 {10930}.
Ppo-A2b {10930}. **v:** Panawawa {10931}.
c: GenBank HQ 228149 {10930}.
Ppo-A2c {10931}. **v:** Louise {10931}.
c: JN632507 {10931}.

Ppo-B2 {10930}. *PPO-B2* {10930}. 2B {10930}.
ma: *Xiwa175*/*Xiwa4866-2* – 0.7 cM – *Ppo-B2* – 2.3 cM – *Xiwa7593-2B* {10931}.
Ppo-B2a {10930}. **v:** Penawawa {10931}.
c: GenBank HQ228150 {10930}.
Ppo-B2b {10930}. **v:** Alpowa {10930}.
c: GenBank HQ228151 {10930}.

Ppo-B2c {10931}. **v:** Louise {1211}.
c: GenBank JN632508 {10930}.

Ppo-D2 {10930}. *PPO-D2* {10930}. 2DL {10930}.
ma: *Xcfd62-2D* – 0.2 cM – *Ppo-D2* – 0.4 cM – *Xcfd168-2D* – 7.7 cM – *Xgwm608-2A* – 2.6 cM – *Ppo-D1* – 0.9 cM – *Xbarc349-2D* {10931}.

Ppo-D2a {10930}. **v:** Louise {10931}.
c: GenBank HQ228152 {10931}.

Ppo-D2b {10930}. **v:** Penawawa {10930}.
c: HQ228153 {10930}.

80.5.5. Salt soluble globulins

80.5.6. Waxy proteins

Wx-A1

Wx-A1a. **v:** Bao Hua {10989}.
tv: Langdon {10989}.

Wx-A1i {10989}. **v:** KU9259 {10989}.

Wx-A1j {10989}. **v:** M1 {10989}.

After *Wx-A1j* add note:
Functional markers for *Wx-A1c*, *Wx-A1d*, *Wc-A1e*, and *Wx-A1i* were developed from DNA sequences {10990}.

Pathogenic Disease/Pest Reaction

83. Reaction to *Blumeria graminis* DC.

83.1. Designated genes for resistance

Pm24

Pm24a [{571}]. *Pm24* {571}. **bin:** 1DS5-0.70-1.00.
ma: In the present listing modify '– *Pm24* –' to '– *Pm24*/*Xgwm1291-1D* –' and add reference to {10109,10957}.

Pm24b {10994}. 1DS {10994}. **bin:** 1DS1-0.59-1.00.
v: Baihulu {10994}.
ma: *Xgwm789*/*Xgwm603-1D* – 2.4 cM – *Pm24b* – 3.6 cM – *Xbarc229-1D* {10994}.

Pm47. **bin:** Correct to: 7BS1-0.27-1.00.
ma: Change to: *Xgpw2119-7B* – 7.5 cM – *BE606897* – 1.7 cM – *Pm47* – 3.6 cM – *Xgwm46-7A* {M10912}.

Pm48 [{M1215}]. *Pm46* {M1215}. 5DS {M1215}.
bin: 5DS1. **v:** Tobasco {M1215}.
ma: *Xgwm205-5D* – 17.6 cM – *Pm47* – 1.3 cM – *Xmp510* (*BE498794*) – 1.8 cM – *Xcfd81-5D* {M1215}.

Pm49 {10938,[{10937}]}. *Ml5323* {10937}. 2BS {10937}.
bin: 2BS3-0.84-1.00. **tv:** *T. turgidum* subsp. *dicoccum* MG5323 {10937}.
ma: *Xcau516-2B* – 7.2 cM – *Pm48* – 4.1 cM – *XCA695634* {10937}.

Pm50 {10942}. 2AL {10942}. **bin:** C-2AL1-0.85.
v: K2 TRI 29907 {10942}. **tv:** *T. turgidum* subsp. *dicoccum* M129 {10942}
ma: *Xgwm294-2A* – 2.9 cM – *Pm50* {10942}.
K2 is a backcross derivative of German winter wheat cultivar Alcedeo with *T. turgidum* subsp. *dicoccum* accession M129 as donor of mildew resistance {10942}.

Pm51 {11026}. Putative *Th. ponticum* derivative. *PmCH86* {11026}.
2BL {11026}. **bin:** 2BL6-0.89-1.00. **v:** CH7086 {11026}.
ma: *Xwmc332-2B* – 4.7 cM – *Pm51* – 1.4 cM – *BQ246670* {11026}.

Pm52 {11029}. *MlLX99* {11028,11029}. **bin:** 2BL2-0.35-0.50.
v: Liangxing 99 {11028,11029}.
ma: *Xcfd73-2B* – 5.3 cM – *Xwmc441-2B* – 0.2 cM – *XBE604758* – *Pm52* – 2.9 cM – *Xgwm120-2B* {11028}; *XBE604758* – 5.5 cM – *Xics34* – *Pm52* – 0.8 cM – *Xics30* – six additional *ics* markers – *Xgwm120* {11029}.

Pm53 {11045}. Derived from *Ae. speltoides*. *PmNC-S16* {11045}.
5BL {11045}. **v:** NC09BGTS16, PI669386 = 'Saluda*3 / TAU829' {11045}.
al: *Ae. speltoides* TAU829 {11045}.
ma: *Xwmc759*/*Xgwm499-5B*/*IWA6024* – 0.7 cM – *Pm53* – *IWA2454* – 5.9 cM – *Xgwm408-5B* {11045}.

83.2. Suppressors of *Pm*

In the introductort paragraph insert ', and 11025}' following reference 491, that is '{401, and 11025}'.

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

MlIw170 {10921}. 2BS. **bin:** 2BS3-0.84-1.00.
tv: *T. turgidum* subsp. *dicoccoides* IW170 {10921}.
ma: *XcauG2* – 0.6 cM – *MlIw170*/*Xcau516*/*Xcfd238-2B* – 2.15 cM – *XcauG8*/*BF201235*/*Xwmc243-2B* {10921}. *Iw1* – 18.77 cM – *MlIw170* {10921}.
This gene is located in the same region as *Pm26* {M1201}.

MLNCD1 {11004}. 7DS {11004}. **bin:** 7DS4-0.61-1.00 {11004}.
v: NC96BGD1 PI 597348 {11004} = 'Saluda*3 / TA2570' {11004}.
ma: *Xgwm635-7D* – 5.5 & 8.3 cM – *MlNCD1* – 16.2 & 13.6 cM – *Xgpw328-7D* {11004}.

PmAS846 {10926}. 5BL {10926}. **bin:** 5BL14-0.75-0.76.
v: N9134 {10926}; N9738 {10927}.
tv: *T. turdigum* subsp. *dicoccoides* AS846 {10926}.
ma: *XMAG2498-5B* – 1.3 cM – *Pm36*/*XBJ261635* – 1.1 cM – *PmAS846* – 1.3 cM – *XFCP1-5B* {10927}.

PmTm4 {10961}. 7BL {10961}. **bin:** 7BL10-0.78-1.00.
v: Tangmai 4 {10961}.
ma: *Xgwm611-7B* – 7.0 cM – *PmTm4* – 14.6 cM – *Xest92* – 2.9 cM – *Xbarc1073*/*Xbarc82-7B* {10961}.

Pmx {11009}. Recessive. 2AL {11009}. **bin:** 2AL1-0.58-1.00.
v: Xiaohongpi {11009}.
ma: *Xhbg327-2A* – 0.6 cM – *Pmx*/*Xsts-bcd1231* – 8.9 cM – *XresPm4*/*Xgpw4456-2A* {11009}.

This gene and close markers showed distorted segregation ratios and some discrepancy of markers relative to *Pm4* alleles {11009}.

Add at end of section:
A normally inherited resistance to powdery mildew in wheat–*Th. intermedium* translocation line 08-723 (T?B–?S^{t}·6AL) was reported in {11035}.

83.4. QTL for resistance to *Blumeria graminis*

AGS 2000 (*Pm3a+Pm8*) / Pioneer 26R61 (*Pm8*). *QSuSuPm.uga-1AS* (*SuPm8*) with an inhibitory effect on powdery mildew response was located at or near *Pm3a*. *QPm.uga-7AL* from Pioneer 26R61, flanked by *Xcfa2257-7A* and *Xwmc525-7A,* was in the region of the *Pm1* locus, even though the test culture was virulent for known *Pm1* alleles {11025}.

SHA3/CBRD (S) / Naxos (R): RIL population: A major QTL on chromosome 1AS accounted for 35% of the phenotypic variation; other QTL from Naxos were on 2DL, 2BL and 7AL. Although 'SHA3/CBRD' possessed a *Pm3* haplotype but no known *Pm3* allele, there was no evidence that the *Pm3* allele suppressed *Pm8*, which appeared to be effective in Norway {10934}.

Reaction to *Colletrichum cereale*

Rcc1 {10939}.	5AL {10939}.	
	v:	Chinese Spring {10939}; Norin 4 {10939}; Shinchunaga {10939}.
	ma:	*Xbarc165-5A* – 1.2 cM – *Rcc1* – 12.8 cM – *Xgwm671-5A* – 0.7 cM – *Xwmc415-5A* {10939}.
***rcc1*.**	**v:**	Hope {10939}.

Susceptibility to this non-pathogen of common wheat is rare, with only one susceptible genotype being documented. A few susceptible tetraploid genotypes were identified {10939}.

86. Reaction to *Diuraphis noxia* (Mordvilko)

***Dn6*.**	7D.	
Dn626580 {10981}.	7DS {10981}.	**v:** PI 626580 {10981}.
	ma:	*Dn626580* – 1.8 cM – *Xbarc214-7D* – 3.2 cM – *Xgwm473-7D* – 3.2 cM – *Xgwm473-7D* {10981}.

87. Reaction to *Fusarium* spp.

87.1. Disease: Fusarium head scab, scab

***Fhb5*.**

At end of entry add:

Closely linked in coupling with *Qflw.nau-5A* for narrow leaf width, but recombination is reported in {11041}.

To the alphabetical list of crosses insert:

Alve (S) / Line 685 R: DH population: QTL on chromosomes 4D (*Rht-D1*), 3BS, 5A, and 2BL {10972}. Two resistance QTL were needed to counteract the negative effect of the *Rht-D1b* semidwarfing allele {10972}.

Baishanyuehuang (R) / Jagger (S): RIL population: Four genes/QTL derived from the resistant parent included *Fhb1* (R^2 = 0.16), *Qfhb.hwwg-3BSc* (R^2 = 0.09), *Qfhb.hwwg-3A* (R^2 = 0.05-0.08), and *Qfhb.hwwg-5A* (R^2 = 0.05 in one trial) {10950}.

Sumai 3 (R) / Y1193-6 (S): RIL population: Three resistance QTL on chromosomes 3BS, 6BL, and 2DS with R^2 values of 0.26, 0.11, and 0.19, respectively; the last was derived from Y1193-6 {11001}.

Treho (S) / Heyne (MR): RIL population: Three QTL from Heyne, *Qfhb.hwwwg-3AS* (R^2 up to 0.18), *Qfhb.hwwg-4DL* (R^2 = 0.14-0.23), and *Qfhb.hwwg-4AL* (R^2 up to 0.18) {11005}.

VA00W-38 (mod. R) / Pioneer 26R46 (S): RIL population: Consistent QTL from VA00W-38 detected on chromosomes 1BL, 2A, 2DL, 5B, 6A, and 7A explained 6.5-21.3% of the phenotypic variation; one QTL from 24R46 was identified on chromosome 7A {11022}. Major QTL on 2DL, 6A, and 5B decreased FHB index, Fusarium damaged kernels, and DON, respectively {11022}.

Tetraploid wheat

T. turgidum subsp. *dicoccum* line Td161 crossed to three durum parents: small-effect QTL were detected on chromosomes 3B, 4B, 6A, 6B, and 7B; all except the 6A QTL were located at previously known positions {10993}.

87.2. Disease: Crown rot caused by *Fusarium pseudograminearum*, *F. culmorum*, and other *Fusarium* species.

Sunco / Macon: RIL population: QTL were located in chromosomes 2B, 3B, 4B, and 4D. *Qcrs.wsu-3BL* from Macon and flanked by *Xgwm247-3B* and *Xgwm299-3B* was the most effective {10932}.

Sunco / Otis: RIL population: QTL were located in chromosmes 2B, 3B, 4B, and 7A. *Qcrs.wsu-3BL* from Otis was the most effective {10932}.

88. Reaction to *Heterodera avenae* Woll.

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

Rmg6 {10948}. 1DS {10948}. **v:** Chinese Spring {10948}; Norin 4 {10948}; Shin-Chunaga {10948}.
ma: *Xwmc432-1D* – 9.6 cM – *Rmg6* – 6.6 cM – *Xwmc222-1D* {10948}.
Rmg6 and a second gene with a weaker effect conferred resistance to a selected '*Triticum* x *Lolium*' isolate {10948}.

Rmg7 {11046}. **tv:** *T. turgidum* subsp. *dicoccum* KU112 {11046}; KU120 {11046}; KU1222 {11046}.

RmgTd(t) {10949}. 7BL {10949}. **tv:** *T. turgidum* subsp. *dicoccoides* KU109 {10949}.
ma: *Xhbg338-7B* – 10.5 cM – *Rmg7* {10949}.
RmgTd(t) was detected with a white culture of an *Avena* pathogen isolate backcrossed to a wheat isolate. Avirulence to *RmgTd(t)* was completely associated with white color of the pathogen isolate {10949}. The white color appeared as a mutant variant during backcrossing.

90. Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)

H13. **v:** AGS 2010 {11008}; AGS 2026 PI 658065 {11008}; Oglethorpe PI 657986 {11008}.

H33 {10954}. 3AS {10954}. **v:** Line 97211 {10954}.
tv: PI 134942 {10954}.
ma: *Xgwm218-3A* – 10 &7 cM – *H33* – 28 &25 cM – *Xhbg-3A* {10954}.

H34 {11018}. *Qhf.hwwg-6B* {11018}. 6BS {11018}.
v: Clark {11018}.
ma: Flanked by *Xsnp921-6B* and *Xsnp2745-6B* within a 4.5-cM region, $R^2 = 0.38$-0.42 {11018}.

HR61 {11008}. 6AL {11008}. **bin:** 6AL8-0.90-1.00 {11008}.
v: 26R61 PI 612153 {11008}.
ma: Mapped as a QTL ($R^2 = 0.63$) flanked by *Xgwm427-6A* and *wPt-731936* {11008}.

Insert after temporary designations:

Qhf-hwwg-1A {11018}. 1AS {11018}. **v:** Clark H34 {11018}.
ma: Closely linked to *Xwgm33-1A* {11018}; Located within a 6-cM region flanked by *Xwgm33-1A* and *Xsnp5150-6B*, $R^2 = 0.1$ {11018}.

Add to comment at end of section:

Haplotype analysis was used to postulate *Ae. tauschii*-derived genes *H13*, *H22*, *H23*, *H26*, and *H32* in a set of synthetic wheat lines {10983}.

91. Reaction to *Meloidogyne* spp.

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

Stb2. Add: ', 1BS {10976}'.

ma: Following the present information add: According to {10976} *Stb2* is neither on 3BS nor linked with *Xgwm389-3B*. *Xwmc406-1B* – 6.0 cM – *Stb2* – 5.0 cM – *Xbarc008-1B* {10976}.

QTL:

Solitar (R) / Mazurka (S): DH population: Resistance under field conditions was associated with QTL on chromosomes 5A, 6D and 7D, which accounted for 20% of the genotypic variation; all three were derived from Solitar, but there was no evidence that *Stb6* and *Stb11*, also present in Solitar, were involved {10984}.

Steele-ND (R) / ND735 (S): RIL population: A consistent QTL ($R^2 = 0.1$) for seedling resistance flanked by DArT markers *XwPt-7101* and *X377410* was mapped to chromosome 5BL in the region of *Stb1* {10992}. Two other QTL on chromosomes 1D and 7A were detected in single experiments {10992}.

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

93.1. Genes for resistance

QTL:

93.2. Sensitivity to SNB toxins (necrotrophic effectors)

Snn1. Add: **v:** M-6 {10960}.

Snn3. Add: **v:** BG220 {10960}.

Snn5 {10925}. 4BL {10925}. **bin:** 4BL-6 0.85-1.00.
tv: *T. turgidum* subsp. *carthlicum* PI 94749 {10925}.
ma: *Xbarc163*/*Xcfd-4B* – 13.3 cM – *Snn5* – 2.8 cM – *Xwmc349-4B* {10925}.

snn5. **tv:** LP749-29 {10925}.

Host sensitivity genes in U.S. southern winter wheats are listed in {1241}.

XX. Reaction to *Puccinia coronata* var. *hordei*

Cr1 {10956}. 5DL {10956}. **v:** Chris CItr 14108 {10956}.
ma: *Xwmc41.2-5D* – 11.3 cM – *Cr1* – 16.8 cM – *Xgdm63-5DL* {10956}.

9*5*. Reaction to *Puccinia graminis* Pers.

Sr9. *Sr9h* {11010}. *SrWeb* {10858}. 2BL {10858,11010}.
v: RL6203 {11010}.
v2: Gabo 56 CI 14035 *Sr11* {11010}; Gabo CI 12795 *Sr11* {11010}; Timstein CI 12347 *Sr11* {11010}. Webster RL6201 *Sr30* {10858}.
ma: *Xgwm47-2B* – 1.4 cM – *SrWeb* – 12.5 cM – *Xwmc332-2B* {10858}.

Sr33. **dv:** *Ae. tauschii* PI 603225 {11012}.
ma: *Xwmc432-1D* – 0.3 cM – *Xwmc336-1D* – 1.0 cM – *Sr33* – 4.2 cM – *Xwmc222*/*Xcfa2158-1D* {11012}. Flanked by *BE405778* and *BE499711* within a 1-cM region {10987}.
c: *Sr33* encodes a CC-NBS-LRR protein and is orthologous to *Sr31*, *Sr50*, and the barley powdery mildew locus *Mla* {10987}.

Sr35. **c:** *Sr35* is a CC-NBS-LRR gene {10988}.

Sr39. 2B {651} = T2SL–2SS#2·2SL#2 {11037}.
Add at end of section:
Further lines with shortened segments are described in {11037} along with tightly linked co-dominant STS markers.

Sr42. **ma:** *Xcfd49-6D* – 5.5 cM – *Xbarc183-6D* – 0.5 cM – *Sr42*/*FSD_RSA* – 11.8 cM – *Xbarc301-6D*; *Xcfd6D* – 5.9 cM – *Sr42* – 46.9 cM – *Xcfd13-6D* {10952}.
Add note:
The likelihood that *Sr42* is the same as *SrTmp* and *SrSha7* (see below) is discussed in {11035} where Blouk#1, Coni#1, Niini#1, Phunye#1, Ripper, and Tinkio1 were shown to carry a gene, or closely linked genes, on chromosome 6DS. If they are the same, this list would be enlarged to include Digalu, Gambo, Koshan 09, and Morvarid {11035}. Nearest markers are *Xbarc183-6D* and *Xcfd49-6D* but not in consistent order {11035}.

Sr44 {389}. Changes and new entry as follows:
Derived from *Th. intermedium*.
T7DS–7J#1L·7J#S 7J#1L {389}. **v:** Line 86.187 TA5657 {939}; Several T7A–7J#1L translocations {0089}.
T7DL·7J#1S {11011}. **v:** TA5657 {11011}.
7J#2, 7J#2S. **su:** Group-7 alien substitution lines with 7J#1 and 7J#1S {939}.
ad: TAF2 = L1 {169}.

Sr53. **ma:** Closest markers: *BE443102*/*Mbo1* and *BE442600*/*Mse1* {10789}.

Sr54. **ma:** *Xcfd-283-2D* – 8.1 cM – *Sr54*/linkage block of 18 markers – 15.8 cM – *Xwmc167-2D* {10816}.
The possibility of a large alien linkage block was supported by the fact that many of the associated markers were null {10816}.

Sr58 {10965}. 1BL {10965}. **su:** Lalbahadur (Pavon1B) (GID 519245) {10965}.
v: *Lr46* Deletion Mutant 109 (GID 5349718) {10965}; *Lr46* Deletion Mutant 111 (GID 5349716) {10965}.

SrTA1662 {11012}. 1DS {11012}. **dv:** *Ae. tauschii* TA1662 {11012}.
ma: *Xwmc432-1D* – 4.4 cM – *SrTA1662* – 4.4 cM – *Xwmc222-1D* {11012}.

SrTmp. Add note:
The possibility of this gene being present in a number of South African cultivars, including Betta = Klein Impacto, is discussed in {10941}.

SrWeb. Delete current listing as this gene is now named *Sr9h*.

Sr10171 {10936}. 7DS {10936}. **v:** Genetic stock to be designated {10936}.
dv: *Ae. tauschii* TA10171 {10936}.
ma: *Sr10171* – 0.9 cM – *Xgdm88*/*Xwmc827-7D* – 1.9 cM – *Xcfd30-7D* {10936}.

Sr10187 {10936}. 6DS {10936}. **v:** Genetic stock to be designated {10936}.
dv: *Ae. tauschii* TA10187 {10936}.
ma: *Xcfd49-6D* – 1.9 cM – *Sr10177* – 13.6 cM – *Xbarc173-6D* {10936}.

QTL:
Avocet S / Pavon 76: RIL population of lines lacking *Sr26*: Five QTL, *QSr.cim-3B* (*Sr2*), *QSr.cim-1B* (*Lr46*/*Yr29*/*Pm39* region), and *QSr.cim-3D* ($R^2 = 0.2$) from Pavon 76; *QSr.cim-4B* and *QSr.cim-5A* from Avocet S {10975}.

Carberry (Resistant in Canada) / AC Cadillac (Resistant in Canada and Kenya): DH population: QTL effective in Kenya were located in chromosomes 2B, 5B, 7B, and 7D, those effective in Canada were on 3B (*Sr2*), 5A, and 5B; those effective in Kenya and Canada were on 4B and 6D (*Sr42*); both parents had *Lr34*/*Sr51* {11040}.

PBW343 (S) / Muu (I): RIL population: Four consistent QTL were identified, *QSr.cim-2BS, QSr.cim-3BS* (*Sr2*), and *Sr.cim-7AS* from Muu, and *QSr.cim-5BL* from PBW343 {11019}.

96. Reaction to *Puccinia striiformis* Westend.

96.1. Designated genes for resistance to stripe rust

Yr17. **v:** Jagger {10973}.

Yr29. **v:** Quaiu 3 *Yr30* {10943}.

Yr36. **v:** Burnside {11044}; Glencross {11044}; Lilian {11044}; Somerset {11044}.

Yr30. **v:** Quaiu 3 *Yr29* {10943}.

Yr31. **ma:** Add: It is mentioned in {10928} that *Yr31* maps between *Lr13* and *Lr23*.

Yr45. **v:** Add: PI 660056 {11024}.

Yr48 {10705}. Adult-plant resistance. 5AL {10705}.
bin: 5AL23-0.87-1.00.
v: UC1110 (MR) / PI 610750 (MR): RIL4 GSTR 13504 {10705}; RIL 167 GSTR 13618 {10705}.
ma: Co-segregated with *Vrn2*, *Be495011*, *Xcfa2149-5AL*, *Xgpw2181a-5AL*, *Xwmc74-5AL*, and *Xwmc410-5AL* {10705}. *Xwmc727-5AL* – 4.4 cM – *Yr48* – 0.3 cM – *Xwms291-5AL* {10705}.
PI 610750 = 'Synthetic 205 (Croc 1 / *Ae. tauschii*) / Kauz)' {10705}.

Yr50. **ma:** Change the first map value from 6.9 to 8.0.
Add note:
The genetic distance between *Yr50* and *Yr62* was estimated to be 27.1 ± 8.6 cM {11023}.

Yr51. Update by addition of second gene **v2:** AUS 27858 Yr57.

Yr53. **bin:** 2BL3-0-0.35.

Yr54 {10944}. Adult-plant resistance. 2DL {10944}.
v: *Yr54* RIL GID6032209 {10944}; *Yr54* RIL GID6032334 {10944}.
v2: Quaiu 3 *Yr29 Yr30* {10943,10944}.
ma: *Yr54* – 0.4 cM – *Xgwm301-2D* {10944}.
Yr54 could be the same as *Qyr.tam-2D* in Alcedo {10945}.

Yr55 {10953}. 2DL {10953}. **v2:** Frelon *Yr17* AUS 38882 {10953}.
ma: *Xmag4089-2D* – 11.4 cM – *Yr55* – 8.4 cM – *Xmag3385-2D* {10953}.

Yr56 {10955}. *Qyr.sun-2A* {10955}. 2AS {10955}.
bin: Tentatively 2AS5-0.78-1.00 {10955}.
tv: AUS 91575 {10955}; Wollaroi (AUS 99174) {10955}.
ma: *Xbarc212-2A* – 3.7 cM – *Xbarc124-2A* – 2.1 cM – *Xsun167-2A* – 5.7cM – *Yr56* – 7.6 cM – *Xsun168-2A* – 5.0 cM – *Xsun169 2A* – 8.0 cM – *Xgwm512-2A* {10955}.
Wollaroi has additional APR resistance QTL {10955}.

Yr57 {10963}. 3BS {10963}. **bin:** 3BS8-0.78-1.00.
v: AUS 91463 {10963}. **v2:** AUS 27858 *Yr51* {10963}.
ma: *Xsts3B-15* – 4 9 cM – *Yr57* – 2.0 cM – *Xgwm389*/*Xcfp140*/*Xmag2095-3B* {10963}; *Yr57* – *Yr4*, 5.2 ± 1.3 cM {10963}.

Yr58 {10964}. 3BL {10964}. **bin:** 3BL7-0.63-1.00.
v: Sonora W195 AUS 19292 {10964}.
ma: *100016328/123392* – 4.6 cM – *Yr58* – 3.9 cM – *1121669/3023704* {10964}.

Yr59 {10966}. Adult-plant resistance. 7BL {10966}. **bin:** 7BL-0.86-1.00.
v1: PI 660061, 'Avocet S / PI 178759' F4-158{10967}.
v2: PI 178759 {10966}.
ma: *Xwmc557-7B* – 2.2 cM – *Xwgp5175* – 2.1 cM – *Yr59* – 1.1 cM – *Xbarc32* – 0.5 cM – *Xbarc182-7B* {10966}.
Yr59 can be detected in high temperature seedling tests (10966,10967}. *Yr59* is a highly effective HTAP resistance gene. Crosses with lines possessing *Yr39*, *Yr52*, or *YrZH84* previously reported on chromosome 7BL segregated, indicating that they are at different loci. However, the allelism test data are based on F_2 phenotypes only. The linkage order of these genes is (proximal) *Yr39* – 31.2 cM – *Yr52* – 5.4 cM – *YrPI178759* – 6.0 cM – *YrZH84* (distal).

Yr60 {10968}. 4AL {10968}.
v: 'Avocet*3 // Lalbmono1B*4 / Pavon', GID 5934039 {10968}; Lal Bahadur (GID 177343) {10968}.
ma: *Yr60/Xwmc776-4A* – 0.51 cM – *Xwmc313/Xwmc219-4A* {10968}.

Yr61 {10970}. 7AS {10970}. *Yrdp34* {10970}.
v: Pindong 34 {10970}.
ma: *Xwgp5765b* – 3.9 cM – *Yr61*– 1.9 cM – *Xwp5467* – 12.5 cM – *Xcfa2174* {10970}.

Yr62 {11023}. Adult-plant resistance. **bin:** 4BL5-0.86-1.00).
4BL {11023}. **v:** PI 192252 {11023}; PI 660060 = 'Avocet S / PI 192252' F4-103{11024 }.
ma: *IWA3611-4B* – 0.8 cM – *IWA4041-4B* – 0.8 cM – *IWA2171-4B* – 0.7 cM – *IWA99-4B* – 1.0 cM – *IWA1923-4B* – 1.2 cM – *Xgwm251-4B* – 3.3 cM – *Yr62* – 2.0 cM – *Xgwm192-4B* – 0.6 cM – *Xgwm495-4B* – 0.7 cM – *Xgwm513-4B* {11023}.
The genetic distance between *Yr62* and *Yr50* was estimated to be 27.1 ± 8.6 cM {11023}.

Yr63 {11027}. 7BS {11027}. **bin:** 7BS1-0.27-1.00.
v: AUS 27955 {11027}.
ma: *IWB33120* – 0.9 cM – *Yr63* – 1.5 cM – *IWB52844* – 10.5 cM – *Xwmc606-7B* {11027}.

Yr64 {11030}. 1BS {11030}. **bin:** 1BS9-0.84-1.00.
v: PI 660064 = 'Avocet S / PI 331260' {10967}.
tv: PI 331260 {11030}.
ma: *Xbarc8-1B* – 0.6 cM – *Xbarc119-1B* – 6.5 cM – *Xgwm413-1B* – 3.5 cM – *Yr64* – 2.0 cM – *Xgdm33-1B* – 5.0 cM – *Xgwm498-1B* – 3.9 cM – *Xcfd59-1B* – 0.4 cM – *Xgwm273-1B* – 3.9 cM – *Xgwm18-1B* – 2.6 cM – *Xbarc137-1B* – centromere {11030}.

Yr65 {11030}. 1BS {11030}. **bin:** 1BS10-0.5-centromere.
v: 'AvS / PI 480016' F_7-12 {11030}. **tv:** PI 480016 {11030}.
ma: *Xbarc119-1B* – 6.5 cM – *Xgwm413-1B* – 5.5 cM – *Xgdm33-1B* – 4.6 cM – *Xgwm498-1B* – 3.5 cM – *Xbarc187-1B* – 2.8 cM – *Xgwm273-1B* – 3.7 cM – *Xgwm18-1B* – 1.2 cM – *Yr65* – 2.1 cM – *Xgwm11-1B* – 2.1 cM – *Xbarc137-1B* – centromere {11030}.

Yr66 {11032}. *YrVL1* {11032}. 3DS {11032}. **bin:** 3DS6-0.55-1.00.
v1: AGG91584WHEA = MSP4543.1 {11032}.
v2: VL892 = AGG91586WHEA *Yr67* {11032}.
ma: *IWB47165* – 3.1 cM – *Yr66* – 2.9 cM – *IWB18087/IWB56281* {11032}.

Yr67 {11032}. *YrVL2* {11032}; *YrC591* {11033}. 7BL {11032,11033}. **bin:** 7BL10-0.78-1.00.
v1: AGG91585WHEA = MSP4543.4 {11032}; C306 {11032}; C591 {11032;11033}.
v2: VL892 = AGG91586WHEA *Yr66* {11032}.
ma: *Xbarc182-7BL* – 5.2 cM – *IWB62475*/*IWB37096* – 1.1 cM – *Yr67* – 0.6 cM – *IWB71995* {11032}; *Xbarc32-7BL* – 2.2 cM – *Xcfa2040-7B* – 8.0 cM – *Yr67* – 11.7 cM – *SC-P35M48* {11033}.

96.2. Temporarily designated genes for resistance to stripe rust

YrAvS {11007}. **v:** Avocet R {11007}; Avocet S {11007}.
This designation was used to describe an assumed resistance gene in both Avocet R and Avocet S, the latter being the genetic background of the Avocet S near-isogenic lines. Av S NILs with *Yr7*, *Yr7*, and *Yr9*, as well as Avocet R, were susceptible to the variant of Pst race 6 E0 {11007}.

YrH9020 {10979}. Derived from *Psathyrostachys huashanica*. 2DS {10979}.
v: H9020-1-6-8-3 {10979}.
ma: *Xgwm102-2D* – 3.8 cM – *Xgwm455-2D* – 5.8 cM – *YrH9020* – 4.4 cM – *Xgwm261-2D* – 2.3 cM – *Xwmc503-2D* – 0.6 cM – *Xcfd53-2D* {10979}.

YrKK {11034}. Adult-plant resistance. 2BS {11034}.
bin: 2BS-1. **v:** Kenya Kuku {11034}.
ma: *Xgwm148-2BS* – 3.2 cM – *YrKK* – 1.8 cM – *Xwmc474-3B* {11034}.
Resistance conferred by *YrKK* at the adult stage approached immunity. A slight effect was observed on seedling response {11034}.

96.3. Stripe rust QTL

In cross 'Avocet / Attila', correct spelling to 'Avocet'

Avocet (S) / Chapio (I): F_6 RIL population: In Mexico, QTL were located in chromosomes 2BS (*Yr31*), 3BS (*Yr30*), and 7DS (*Yr18*); only the last two were effective in 2009. In China, QTL were located in chromosomes 3BS, 5BL, and 7DS. A 3DS QTL was effective in Mexico in 2009 and in China in 2013 {11020}.

Avocet (S) / Pastor (I): RIL population: QTL mapped on 1BL (*Yr29*), 2BS (*Yr31*), 5A, 6B, and 7AL plus minor QTL on 1AL, 1B, 3A, 3B, 4D, 6A, 7AS, and 7AL {10928}.

Claire / Lemhi: DH population: Four QTL for APR: *Qyr.niab-2D.1* (at or near *Yr16*, R^2 = 0.1-0.25), *Qyr.niab2DL.2* (R^2 = 0.14-0.32), *Qyr.niab-2BL*, and *Qyr.niab-7B* (R^2 = 0.11-0.13) {10962}. An unknown seedling resistance gene was located in chromosome 3BL {10962}.

Jagger (MR) / 2174 (MS): RIL population: *Qyr.osu-2A* (*Yr17*) and *QYR.osu-5A* (in *Xgwm156-5A* – centromere region) from Jagger and *Yr18* from 2174 (but only in tests in China) {10973}.

Yr16DH70 (Cappelle Desprez / 2*Palmiet Selection) / Palmiet: DH population: One major-effect QTL, *Qyr.ufs-2A*, and three less effective QTL in 2D (possibly *Yr16*), 5B, and 6D were from Yr16DH70, and a minor effect QTL on 4B was from Palmiet {10933}.

UC1110 (MR) / PI 61070 (MR): RIL population: Four QTL for APR: two, *Qyr.ucw-3BS*, peaking at *Xgwm533.1*, R^2 = 0.22, and *Qyr.ucw-2BS*, R^2=0.05 from UC1110, and *Yr48* and *Qyr.ucw-2AS*, R^2 = 0.02, from PI 61070 {10705}.

92.Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr3a. **v:** Sinvalocho MA {10929}.

Lr3c. **v2:** CI 13227 {11021}.

Lr12. 4BL {10951}.
bin: 4BL5-0.86-1.00.
ma: *Xgwm251-4B* – 0.9 cM – *Lr12* – 1.9 cM – *Xgwm149-4B* {10951}.

Lr14. Lr14a.
bin: 7BL10-0.78-1.00.
tv: Add: Arcangelo {11015}; Bicre {11015}; Creso {11015}; Colosseo {11015}; Italo {11015}; Plinio {11015}.
ma: Add: *Xwmc10*/*Xgwm344*/*wPt1085-7B* – 1.1 cM – *wPt4038-HRM* – 0.1 cM – *Lr14a* – 1.0 cM – *wPt4140-HRM* {11015}.

Lr14b. **v2:** CI 13227 *Lr68* {10817}.

Add note: Most accessions with *Lr14b*, including the Tc NILs probably carry APR gene *Lr68* {10817}, which could be the same as *QLr.osu-7BL* {10817}.

Lr23. **v2:** Pastor *Lr46* {10928}.

Lr35. 2B {651} = T2SL–2SS#2·2SL#2 {11037}.
i: RL 6082 = 'Thatcher*7/RL 5711' {11037}.

Add note: Lines with shortened alien segments bearing *Lr35* are described in {10741}.

Lr42. **v2:** Quaiu 3 *Lr46* {10943}.

Lr46.
v: Siete Cerros {10817}.
v2: CI 13227 *Lr3c* {M12013}; Quaiu 3 *Lr42* {10943}. Parula *Lr3b Lr13 Lr14b Lr34 Lr68* {10817}. Frontana *Lr13 Lr14b Lr34 Lr68* {10817}.

Lr68 {10817}. Adult-plant resistance. 7BL {10817}.
v2: Parula *Lr3b Lr13 Lr14b Lr34 Lr46* {10817}. Frontana *Lr13 Lr14b Lr34 Lr46* {10817}. Arula 1 *Lr14b* CIMMYT GID 1847450 {10817}; Arula 2 *Lr14b* CIMMYT GID 1847422 {10817}. Rayon F89 *Lr14b* {10817}; Weebill *Lr14b* {10817}.
ma: *Xwmc232-2B* – 0.2 cM – *Xcfa2257-2B* – 1.1 cM – *Cs7BLNLRR* – 0.3 cM – *Psy1-1* – 0.5 cM – *Lr68* – 0.6 cM – *Xgwm146-2B* {10817}. Gamma-irradiation-induced deletion stocks of Arula 1 lacked *Lr68* but had *Lr14b* showing that the two genes are located at different closely linked loci {10817}.

Lr71.
bin: Markers flanking *Lr71* mapped to 1BS10-0.5-cent and 1BL6-cent-0.32.
v2: *T. aestivum* subsp. *spelta* cv. Altgold Rotkorn *Lr65* {10911}.

Lr72 {10947}. 7BS {10947}. **tv:** Altar C84 GID 30374 {10947}; Atil C2000 GID 6719128 {10947}.
ma: *Lr72* – 5.0 cM – *Xwmc606-7B* {10947}.

Lr73 {10969}. 2BS {10969}. 2BS {10969}.
v: Morocco {10969}; Several Australian cultivars {10969}.
ma: *wPt8760* – 4 cM – *Lr73* – 1.4 cM – *wPt8235* {10969}.

Lr74 {11031}. Adult-plant resistance. 3BL {11031}.
bin: 3BL7-0.63-1.00. **v1:** AGG91583WHEA = BT-Schomburgk Selection {11031}.
ma: *GBS2256311* – 3.9 cM – *Lr74* – 2.5 cM – *IWB69699*/*IWB20762* – 2.5 cM – *GBS2325308* {11031}.

LrBi16 {11042}. 7BL {11042}. **v**: Bimai 16 {11042}
ma: *Zcfa2257-7B* – 2.8 cM – *LrBi16* – 2.9 cM – *Xgwm344-7B* {11042}.

Bimai 16 also carries *Lr26* and *LrZH84* {11042}.

LrFun {11038}. 7BL {11038}. **bin:** 7BL-10.
v: Fundulea 90 {11038}. **ma:** *Xgwm344-7B* – 4.4 cM – *LrFun* – 5.7 cM – *Xwmc70-7B* {11038}.

LrGam6 {10929}. 2BL {10929}. **v2:** Sinvalocho MA *Lr3 LrSV1 LrSV2* {10929}.
ma: *Xbarc-2B* – 0.6 cM – *Xgwm382-2B* – 0.6 cM – *LrGam6* – 17.9 cM – *Xgwm528-2B* {10929}.

LrNJ97 {11043 2BL {11043}. **v:** Neijiang 977671 {11043}.
ma: *Xwmc317-2B* – 4.2 cM – *LrNJ97* – 2.2 cM – *Xbarc159-2B* – 2.3 cM – *Xwmc356-2B* {11043}.

LrSV1 {10929}. Adult-plant resistance. 2DS {10929}.
v2: Sinvalocho MA *Lr3 LrGam6 LrSV2* {10929}.
ma: *Xgwm296-2D* – 1.4 cM – *LrSV1* – 7.1 cM – *Xgwm261-2D* {10929}.

LrSV2 {10929}. Adult-plant resistance. 3BS {10929}.
v2: Sinvalocho MA *Lr3 LrGam6 LrSV1* {10929}.
ma: *Xgwm389-3b* – 3.0 cM – *LrSV2*/*Xgwm533-3B* – 4.2 cM – *Xgwm49-3B* {10929}.

LrZh84. **v:** Add: Guizhou 98-18 {11042};Tian 95HF2 {M1215}; Xinong 1183-4 {11042}.

Complex genotypes:
Insert the following alphabetically with the existing file:

Estanzuela Benteveo	*Lr13 Lr26 Lr34* {10980}
Estanzuela Pelon	*Lr1 Lr17a Lr26 Lr34* {10980}
Estanzuela Tarariras	*Lr3bg Lr13 Lr34* {10980}
INIA Boyero	*Lr13 Lr26 Lr3*4 {10980}
INIA Churrinche	*Lr10 Lr24* {10980}
INIA Tero	*Lr17a Lr24* {10980}

97.2. Suppressor of genes for resistance to *P. triticina*
97.3. QTL for reaction to *P. triticina*
To the paragraph beginning with 'QTL' add: However, Thatcher backcross derivatives of CI 13227 appeared to have *Lr3c* and *Lr46* {11021}.
Avocet / Pastor: RIL population: QTL mapped on 1BL (*Lr46*), 2BS, 5A, 6B, and 7BL plus minor QTL on 1B, 2A, and 2D {10928}.

99. Reaction to *Sitodiplosis mosellana* (Gehin)

***Sm1*.** **v:** Glencross {11044}; Goodeye {11044}.

103. Reaction to *Tilletia caries* (D.C.)Tul., *T. foetida* (Wallr.) Liro, *T. controversa*

Bt11 {10997}. **v:** PI 554119, 'Elgin / PI 166910' {10997}.

Bt12 {10997}. **v:** PI 119333 {10997}.

Bt13 {10997}. **v:** Thule III, PI 181463 {10997}.

Bt14 {10997}. **tv:** Doubbi CI 13711 {10997}.

Bt15 {10997}. **tv:** Carleton CI 12064 {10997}.

Btp {10997}. **v:** PI 173437 {10997}.

QTL

Trintella / Piko: DH population: One major gene in the chromosome 1BS centromere region, nearest marker *Xgwm273-1B* {11003}. Smaller QTL effects were detected on chromosomes 7A, 7B, and 5B in different years.

105. Reaction to *Ustilago tritici* (Pers.) Rostrup

Ut5 {10940}. *Ut-Fore* {10940}. **v:** Foremost {10940}. 5BL {10940}.
ma: *Xgpw5029* – 2.8 cM – *Ut5* – 1.3 cM – *Xbarc232-5b* {10940}.
Race T10 was used for analysis {10940}.

107. Reaction to Wheat Streak Mosaic Virus

Wsm1. **v:** CA741 {10971}; KS03HW12 {11006}; Mace {11006}.

Wsm2. **ma:** Add: *Xbarc87-3B* – 4.4 cM – *Wsm2* – 3.9 cM – *Xbarc102-3B* {10982}.
Add note: Allele *Xbarc102-3B219* was the best predictor for *Wsm2* {10982}.

Wsm3. 7B, TBS·7S#3L {10775}. **v:** KS12WGGRC59 TA5624 {10775}.
Wsm3 was also effective against *Triticum* mosaic virus at 18°C {10775}.

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