CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2013-2014 SUPPLEMENT

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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 non-purple 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* accession PAU 14087 {11002}. The mutations likely affected cellulose synthesis and involved all tissues {11002}.

brc1 {11002}.		1AL {11002}.	**dv:**	*T. monococcum* mutant *brc1* {11002}.
	ma:	*Xwmc470-1A* – 3.9 cM – *Brc1* – 2.1 cM – *Xgwm135-1A* {11002}.		
brc2 {11002}.		3AL {11002}.	**dv:**	*T. monococcum* mutant *brc2* {11002}.
	ma:	*Xcfa2170-3A* – 2.9 cM – *Brc2* – 0.8 cM – *Xcfd62-3A* {11002}.		
brc3 {11002}.		6AS {11002}.	**dv:**	*T. 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, viz. 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}.

<u>Cleistogamous flowering in durums</u>
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 8 QTLs on 7 chromosomes, viz. 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 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*, re-designated 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:**	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 fourfold 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}. 6 varieties {10977}; 25 varieties {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 non-vernalization 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. spelta* Altgold {10995}.
	tv:	*T. 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 – *Xiwa*7593-*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 [{10935}].	*Pm46* {10935}.	5DS {10935}.			
	bin:	5DS1.	**v**	Tabasco {10935}.	
	ma:	*Xgwm205-5D* – 17.6 cM – *Pm48* – 1.3 cM – *Xmp510(BE498794)* – 1.8 cM – *Xcfd81-5D* {10935}.			
Pm49 {10938,[{10937}]}.	*Ml5323* {10937}.	2BS {10937}.			
	bin:	2BS3-0.84-1.00.	**tv:**	*T. 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. dicoccum* M129 {10942}	
	ma:	*Xgwm294-2A* – 2.9 cM – *Pm50* {10942}.			
K2 is a backcross derivative of German winter wheat cv. Alcedeo with *T. 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* – 6 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 introductory 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. 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. 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 (?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}.

NEW: 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* semi-dwarfing allele {10972}.

Baishanyuehuang (R) / Jagger (S): RIL population: Four genes/QTLs 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, viz. *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. 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: QTLs 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. dicoccum* KU112 {11046}; KU120 {11046}; KU1222 {11046}.

RmgTd(t) {10949}.	7BL {10949}.	**tv:**	*T. 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 = 0.0.38 – 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

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. 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 US 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}.	

95. 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} = 2SL-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 *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 7A-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: 4 consistent QTLs 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 F_4-158{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 F2 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 QTLs 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 QTLs on 1AL, 1B, 3A, 3B, 4D, 6A, 7AS and 7AL {10928}.

Claire / Lemhi: DH population: 4 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 QTLs 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} = 2SL-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}.
	v2:	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 hade *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. 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 Lr34* {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 'QTLS' add: However, Thatcher backcross derivatives of CI 13227 appeared to have *Lr3c* and *Lr46* {11021}.
Avocet / Pastor: RIL population: QTLs mapped on 1BL (*Lr46*), 2BS, 5A, 6B and 7BL plus minor QTLs 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 *Xbarc102-3B*$_{219}$ 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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