CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2007 Supplement

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INTRODUCTION

Recommended rules.

9. Laboratory designators

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unlp	Dr. A. M. Castro Genetics Faculty of Agricultural Sciences, UNLP, CC31, 1900-La Plata, Argentina amcastro@isis.unlp.edu.ar
cmw	Chinese wheat eSSR Fu et al. 2006 TAG 112: 1239-1247.
cnl	Cornell University eSSR Yu et al. 2004 Genome 47: 805-818.
hbd	SSR loci from sequences in DDBJ {10330}.
hbe	EST sequence based SSR {10330}.
hbg	Genomic SSR {10330}.

Gene Symbols

Add to gene symbols list:

Symbol	Trait
Almt.	Malate transporter (GeneBank AB081803).
Nam1.	Regulation of senescence and grain maturity. Pleiotropic effects in grain protein and nutrient content (iron and zinc).
Lvl.	Loaf volume.
Vrt-2.	Mads-box (GenBank DQ022679) {10294}.

1. Gross Morphology: Spike characteristics

Insert at the end of the introductory paragraph: In a large study of 6 agronomic traits in a AC Karma / 87E03-S2B1 DH population, 24 QTL were detected in 12 chromosomes {10434}.

5.5. Purple grain/pericarp

Pp1.	7BL {10392}.	**v:**	Novosibirsk 67 {10392}. Note, this cultivar has white pericarp.
		v2:	Purple K49426 *Pp3a* {10392}; Purple Feed *Pp3b* {10392}.
		ma:	*Xgwm983-7B* - 15.2 cM - *Pp1* - 11.3 cM - *Xgwm767-7B* {10392}.
Pp2.	Add note: *Pp2* was renamed *Pp3b.*		
Pp3 {10392}.	2A, not 6A {0066;10392}.		
Pp3a {10392}.		**v2:**	Purple K49426 *Pp1* {10392}.
		ma:	*Xgwm328-2AS* - 2.7 cM - *Pp3a* - 3.2 cM - *Xgwm817-2AL* {10392}.
Pp3b {10392}.		*Pp2.*	
		v2:	Purple Feed {0066,10392}.
		ma:	*Xgwm328-2AS* - 5.2 cM - *Pp3b*/*Xgwm817/Xgwm912-2A* - 3.6 cM - *Xgwm445-2A* {10392}.
pp1pp3.		**v:**	Saratovskaya 29 {10392}. Note, this cultivar has red pericarp.

6.Awnedness

6.1.2. Tipped 1

B1. **ma:** Correct the first entry to: *Xgwm410.2-5A* - 8.2 cM - *B1* - 12.2 cM - *Yr34* {10040}. Add: *Xgwm291-5A.3* - 5.3cM - *B1* {10330}.

9.Brittle Rachis

Br-D1.	***Br***^{61} {10362}.	**v:**	R-61 {10362}.

17.Dormancy (Seed)

QTL: After Zenkoujikomugi/CS add:

Zenkoujikomugi/Spica: White seeded wheats with the dormancy-related QTL, *QPhs-3AS* from Zenkoujikomugi were more resistant to PHS than counterparts with the contrasting allele from Spica {10377}. White seeded wheats with contrasting alleles of *QPhs-4AL* were not different {10377}.

<u>Diploid wheat</u>

QTL: *T. monococcum* KT3-5 (non-dormant) / *T. boeoticum* KT1-1 (dormant): RIL population: QTL on chromosome $5A^mL$, *Xcdo1326c-5A* - *Xabc302-5A*), R^2 = 0.2 - 0.27. Weaker QTL were found on $3A^m$ (*TmAB18* - *Xwmc102-3A* and *Xrz444-3A* - *TmABF*) and $4A^m$ (*Xrz261-4A* - *Xrz141-4A*) {0892}. The $3A^m$ QTL co-located with *TmABF* and *TmAB18* {10417}, derived from othologous ABA signaling genes in *Arabidopsis.* The 5A QTL may be orthologous to the barley dormancy gene *SD1* {10417}.

23.Frost Resistance

QTL: Norstar (tolerant) / Winter Manitou (non-tolerant: DH population: Norstar possessed major and minor QTL for tolerance on chromosomes 5A and 1D. The 5A QTL was 46 cM proximal to the *vrn-A1* locus ($R^2 = 0.4$); its peak co-incided with *Xwmc206-5A and Xcfd2-5A,* and expression of C-repeat Binding Factor genes with strong homology to *Cfb14* and *Cfb15* located at the *Fr-2* locus in *T. monococcum* {10414}.

27.Glume Colour and Awn Colour

Black glumes are now included in the following homoeologous series with red/brown/bronze glumes.

27.1. Red (brown/bronze/black) glumes

The majority of studies report a single dominant gene for red glume colour. A few papers report two factors {1009,1477,1520}. Red glume colour in Swedish land cultivars is apparently associated with hairy glumes {1277} suggesting, because *Hg* is located in chromosome 1A, that a red glume factor different from *Rg1* was involved in the Swedish stocks. Nothing was known of the possible association of such a gene with *Bg,* another glume colour gene on 1A. See {1640} for review. A chromosome 1A gene, *Rg3,* was eventually identified by linkage with *Gli-A1* {1405} and shown to cosegregate with *Hg* {624}.

Rg-A1 {10378}.	*Rg3* {924,562}.	1AS {924,562,9906}.	
Rg-A1a {10378}.	**v:**	TRI 542 {10378}; White glumed genotypes.	
	dv:	DV92 {282}; G2528 {10378}.	
Rg-A1b {10378}.	*Rg3.*	**i:**	Saratovskaya 29*3 // F2 CS mono 1 / Strela {924}.
	v:	CS / Strela Seln {9906}; Iskra {9906}; L'goskaya-4 {1405}; L'govskaya-47 {1405}; Zhnitsa {9906,10378}.	
	v2:	Milturum 553 *RgB1b* {9906}; Milturum 321 *Rg-B1b* {9906}; Strela *Rg-B1b* {9906,924}; Sobko & Sozinov {1405,1406} reported a further group of 30 international wheats which, by inference from their *Gli-A1* alleles, probably carry *Rg-A1b*.	
	ma:	A linkage order of *Glu-A1* - cent - *Hg* - *Rg-A1b* was reported {1405}.	
Rg-A1c {10378}.	*Bg* {282,1304}, *Bg(a)* {282}^{3}].	1A {282,1304}.	
	i:	ANK-22A {10378}; S29BgHg {10378}.	
	s:	CS*7/Indian 1A {1304}.	
	dv:	G1777 {282}; G3116 {282}.	
	ma:	*Rg-A1c(Bg)* and *Nor9* co-segregated in *T. monococcum* {282}^{3}; *Xutv1391-1A* (distal) – 3 cM - *Rg-A1c(Bg)* - 1.6cM - *Hg* - 2.4 cM - *Gli-A1* (proximal) {9959}^{2}. *Xgwm1223-A1* - 0 & 0.6 cM - *Rg-A1c* - 4.7 & 4.6 cM - *Xgwm0136-1A* {10378}. Five of 6 wheats with *Rg-A1c* possessed a 264bp allele at *Xgwm0136-1A* {10378}.	
Rg-A1d.	[*Bg(b)* {282}^{3}].	**dv:**	G3116 {282}.
At the diploid level *Rg-A1c* (*Bga*) and *Rg-A1d* (*Bgb*) were dominant and caused a solid black glume and a black line at the margins of the glume, respectively {282}. A single factor for black glumes was reported in diploid, tetraploid and hexaploid wheats {1347}. Linkage with *Hg* was demonstrated at all levels of ploidy, indicating a common gene on chromosome 1A; *Bg* is epistatic to *Rg*.			
Rg-B1 {10378}.	*Rg1, Rg.*	1B {1517}.1BS {369}.	
Rg-B1a {10378}.	**v:**	TRI 542 {10378}; White glumed genotypes.	
	dv:	*T. turgidum* ssp. *dicoccoides* acc. MG4343 {9959}.	
Rg-B1b {10378}.	*Rg1.*	**s:**	CS*5/Red Egyptian 1B {1304}.
	v:	Diamant I {9906}; Federation 41 {1517}; Highbury {1121}; Red Egyptian {1304}; *T. petrapavlovskyi* {9906}.	
	v2:	Milturum 321 *Rg-A1b* {9906}; Milturum 553 *Rg-A1b* {9906}; Strela *Rg-A1b* {9906}.	
	tv:	Messapia {9959}; Ward {792}.	
	ma:	*Xytv1518-1B* (distal) - 7.7 cM - *RgB1b* - 0.8 cM - *G1i-B1* (proximal) {9959}. *Xgwm1078-1B* - 1.5 cM - *Rg-B1b* - 3.1 cM - *Xgwm0550-B1* {10378}. *Xutv1518-*	

		1B (distal) - 7.7 cM - *Rg-B1b* - 0.8 cM - *Gli-B1* (proximal) {9959}[2].	
Rg-D1 {10378}.	*Rg2.*	1DL {769,1241}.1DS.	
Rg-D1a {10378}.	**v:**	Novosibirskaya 67 {10378}; L301 {10378}; White glumed genotypes.	
Rg-D1b {10378}.	*Rg2.*	Derived from *Aegilops tauschii.*	
	i:	Saratovskaya 29*5 // *T. timopheevii* ssp. *timoppheevii / T. tauschii* {9906}.	
	v:	Synthetic Hexaploid-11 {10128}; (*Triticum turgidumI spp. dicoccoides / Ae. tauschii*) {769}; (*Tetra Canthatch / Ae. tauschii* var. *strangulata* RL 5271), RL 5404 {1240}; (*Tetra Canthatch / Ae. tauschii* var. *meyeri* RL 5289), RL 5406 {648,1240}.	
	dv:	*Aegilops squarrosa* accessions.	
	QTL:	*QRg.ipk.1D* was mapped in the Opata/W-7984 (ITMI) mapping population {0255}; Linkage with *Gli-D1* implied *Rg2.* This QTL coincided with a QTL for awn colour, *QRaw.ipk-1D*{0255}.	
	ma:	*Xpsp2000-1D* - 9.3 cM - *Rg-D1b* - 21.2 cM - *Xgwm106-1D*{10128}.	
Rg-D1c {10378}.		Brown or smokey-grey phenotype {729}.	*Brg* {729}.
	i:	ANK-23 = Novosibirskaya 67*10 / K-28535 {729}.	
	v:	Golubka {10378}; K-28535 {729}; K-40579 {729}; *T. aestivum* botanical varieties cinereum, columbina and albiglaucum {10378}.	
	ma:	*Xgwm1223-1D* - 1.5 cm - *Rg-D1c* - 13.1 cM - *Xbarc152-1D* {10378}. *Xbarc149-1D* - 6.3 cM - *Rg-D1c* - 26.5 cM - *Xbarc152-1D* {10378}.	

With the deletion of section 27.2 and its incorporation into 27.1, the following sections` are renumbered as follows

27.2. Pseudo-black chaff

27.3. Black-striped glumes

27.4. Inhibitor of glume pigment

27.5. Chocolate chaff

27.6. Awn colour

28. Grain Hardness/Endosperm Texture

In the preamble paragraph 2 line 5, correct reference from ‘0380’ to ‘0384’; that is: ‘Friabilin is also referred to by the name ‘Grain Softness Protein’ (GSP) {0384}, and was later shown to be comprised primarily of puroindoline a and puroindoline b {0295}.’

29. Grain Quality Parameters

In a comprehensive study of 46 quality-related traits in a RL4452 / AC Domain RIL population, 99 QTL involving 41 traits were located in 18 chromosomes {10361}; 14 QTL clustered in the *Glu-1B* region (50 cM), 20 QTL occurred in the *Xwmc617-4D - Xwmc48-4D* region (30 cM), 10 QTL mapped to the *Xgwm130-7D - Xwmc405-7D* region (14 cM) and 66 QTL were dispersed {10361}.
In a large study of 11 seed quality traits in a AC Karma / 87E03-S2B1 DH population, 26 QTL were detected in 7 chromosomes {10434}; 6 were clustered in the *Glu-D1* region and 5 were clustered in the *Rht-D1* region.
QTL analyses of 10 milling and baking quality traits (grain hardness, flour yield, grain and flour protein, alkaline water retention capacity (AWRC), sedimentation properties, cookie properties, lactic acid retention, dough strength, extensibility and mixograph properties) in the ITMI population grown in Mexico, France and USA (California) are reported in {10436}.

29.2. Flour, semolina and pasta colour

QTL: W9262-260D3 (low yellow colour) / Kofa (high colour): Four QTL identified on chromosomes 2A (*Xgwm425-2A*), 4B (*Xgwm495-4B*), 6B (*Xgwm193-6B*) and *Psy-B1* (chromosome 7BL) {10230}. See also Enzymes: Phytoene synthase.

31.Grain Weight

Rye Selection 111 (high GW) / CS (low GW) RIL: two definitive QTL *QGw.ccsu-2B.1* and *QGw.ccsu-7A.1* and one tentative QTL, *QGw.ccsu-1A.1*, were detected by CIM analysis{10363}. The chromosome 7A QTL co-located with a QTL for early heading {10363}.

39.Height

39.1. Reduced Height : GA-insensitive

Add at end of section: Genotypes of Indian semi-dwarf wheats based on the Ellis et al. {0378} markers are given in {10404}.

40.Hybrid Lethalities

41.1. Hybrid necrosis

Ne1.		Following the chromosome location insert:
	ma:	*Xbarc216-5B* - 8.3 cM - *Ne1* - 2 cM - *Xbarc74-5B* {10334}.
Ne1s.	**v:**	Add: Synthetics TA4152-19, TA4152-37, TA4152-44, TA4152-60 {10334}.
Ne2.	Following the chromosome location insert:	
	ma:	*Xgwm148-2B* - 6.7 cM - *Ne2* - 3.2 cM - *Xbarc55-2B* {10334}.
Ne2m.	**v:**	Alsen {10334}.

47.Male Sterility

47.1. Chromosomal

ms1g {10355}.	4BS {10354}.	**v:**	Lanzhou Mutant 257A {10354,10355}.

Insert the following after the present entries:

Photoperiod and/or temperature-sensitive male sterility (PTGMS)

wptms1 {10332}.	2B {10332}.	**v:**	BNY-S {10332}.
	ma:	E: AAG/M: CTA_{163} - 6.9 cM - *wtms1* - 4.8 cM - *Xgwm374-2B* {10332}.	
Described as a thermo-sensitive gene (TGMS), giving complete sterility at less than 10C, but fertile at higher temperatures {10332}.			
wptms1 {10333}.	5B {10333}.	**v:**	Line 337S *wptms2* {10333}.
	ma:	*Xgwm335-5B* - 4.2 cM - *wptms1* - 24.4 cM - *Xgwm371-5B* {10333}.	
wptms1 produces sterility only in the presence of *wptms2*.			
wptms2 {10333}.	2B {10333}.	**v:**	Line 337S *wptms1*{10333}.
	ma:	*Xgwms374-2B* - 6.9 cM - *wptms2* - 20.9 cM - *Xgwm120-2B* {10333}.	
wptms2 produces sterility only in the presence of *wptms1*. *wptms1* and *wptms2* were analysed and mapped under long photoperiod/high temperatures, but an earlier study indicated a single gene for male sterility under short photoperiod/low temperatures. Although mapping data are different a possible relationship between *wptms2* and *wptms1* needs to be resolved.			

57.Polyphenol Oxidase (PPO) Activity

Chara (mod high) / WW2449 (low): DH population: PPO activity Associated with *Xgwm294b-2A* (R^2 = 0.82), *Xwmc170-2A*, *Xhwm312-2A* and *Xwmc178-2A* (R^2 > 0.7) {10410}.

A multiplex of markers *PPO33* and *PPO16* was reliable for selecting genotypes with low PPO activity {10418}.

Tetraploid wheat

Messopia / *T. dicoccoides*: RILs: Associated with RFLP *Xutv1427-2A* {10411}.

Jennah (high) / Cham 1 (low): Associated with *Xgwm312-2AL* {10411}.

60.Response to Photoperiod

QTL: Trident (early) / Molineux (late): In addition to an effect associated with chromosome 2B, three QTL were designated as follows: *QPpd.agt-1AL* (*Xwmc304 - Xgwm497*), *QPpd.agt-7AS* (*Xbarc154 - Xbarc108*) and *XPpd.agt-7BS* (*Xgwm46 - Xgwm333*) {10382}. The QTL in chromosome 1A is possibly orthologous to *Ppd-H2* in barley.

61.Response to Salinity

61.2. Salt tolerance

QTL: Opata 85 / W7984. 77 QTL effective at different growth stages were mapped to 16 chromosomes {10384}.

63.Response to Vernalization

Replace the existing material in the *Vrn-3* section with the following and eliminate the *Vrn-B4* section:

Vrn3.

Vrn-B3 {10421}.	[Synonymous with *Vrn-B4* {279} and *Vrn5*, *eHi*{769,771} {769,779}].		
	7BS {768,769,771}.	**s:**	CS (Hope 7B) *Vrn-D1a* {768}.
	v2:	Hope *Vrn-A1a* {1424}.	
	ma:	*Vrn-B3* is completely linked to *TaFT* and 1 cM distal to *Xabc158-7B* on the region of 7BS proximal to the translocation with homoeologous group 5 {10421}.	

The dominant *Vrn-B3* allele in Hope has a retrotransposon insertion in the *TaFT* promoter (GenBank DQ890165) {10421}. Transformation of winter wheat Jagger with the dominant *Vrn-B3* significantly accelerated flowering {10421}. Different Hope seed sources were heterogeneous for this insertion {10421}. The retrotransposon insertion in the *TaFT* promoter is present in the CS (Hope 7B) {10421}.

Vrn-H3{10421}.	[Synonymous to *Sh3*].		
	ma:	Completely linked to *HvFT* and 1 cM distal to *Xabc158* on 7HS. Originally mapped incorrectly on 1H based on loose linkage {1455,1316}	
vrn-B3.	**v**:	Chinese Spring *Vrn-D1* (GenBank DQ890162) {10421}.	

In both wheat and barley *Vrn-3* is completely linked with a flowering promoter gene homologous to Arabidopsis *FLOWERING LOCUS T* (*FT*) {10421}.

Vrn-B4. Synonymous with *Vrn3* and will be deleted {10421}.

69.Stem solidness

Insert introductory note: Solid stem confers resistance to wheat stem sawfly. See also Reaction to *Cephus* spp.

Qsst.msub-3DL.	[*Qss.msub-3DL* {10395}].	3DL {10395}.	
Associated with *Xgwm645-3DL* (R^2 = 0.31), *Xwmc656-3DL* (R^2 = 0.1), and *Xcfd9-3DL* (R^2 = 0.13)			

{10395}. This gene acted as an enhancer of *Qsst.msub-3BL* {10395}.

Tetraploid wheat

Qsf.spa.-3B {10351}. Kyle*2 / Biodur (solid stem) // Kofa (hollow) DH population: *Qsf.spa-3BL* was located to a 21.3 cM interval flanked by *Xgwm247-3B* and *Xgwm114-3B* {10351}. Mapped as a single gene, *Xgwm247-3B* - 6.9 cM - *Qsf.spa-3B* - 14.4 cM - *Xgwm114-3B* {10351}. This location was confirmed in two other crosses involving G9580B-FE1C and Golden Ball as the solid stem parents{10351}.

72.Tiller Inhibition

tin3 {10329}.	3A^{m}L {10329}.	**dv:**	*T. monococcum* TA 4443 = TA4342-96 mutant {10329}.
	ma:	*Xbcd131/Xbcd1431*-3A - 9.6 cM - *tin3/Xpsr1205-3A* - 4.7 cM - *Xcfa2076-3A* {10329}.	

Proteins

77.Proteins

77.1. Grain protein content

Gpc-B1a. *QGpc.ndsu.6Ba* {623}.
This allele, fixed in cultivated durum, is a non-functional frame-shift mutation {10438}. A similar non-functional allele, or a complete deletion of *Gpc-B1,* is fixed in hexaploid wheat {10438}.

Gpc-B1b.
Cointinue from 2006 supplement: *Gpc-B1,* the functional allele {10438} in *T. dicoccoides,* affects senescence and maturity in addition to grain protein content, accelerating senescence and maturity {10298}. *Gpc-B1* is a NAC transcription factor designated *Nam-B1* {10438}. A paralogous copy of this gene is present in homoeologous group 2 (*Nam2*).

Add at end of section: Durum: In 3BIL-85 (high protein introgressed from *T. dicoccoides*) / Latino QTL were detected in chromosomes 2AS (associated with *Xcfa2164-2A*, R^2 = 17%), 6AS (*Xp39M37*$_{250}$*-6A*, R^2 = 17%) and 7BL (*Xgwm577-7B*, R^2 = 9%) {10338}.

77.2. Enzymes

77.2.1. Acid phosphatase

Acph-D2 {10407}.	**tv:**	*Aegilops tauschii* {10407}.

77.2.32. Phytoene synthase

Psy1-B1.	**ma:**	*Xcfa2040-7B* - 12 cM - *Psy-B1* - 5 cM - *Xgwm146-7B* {10230}.
Psy2-B1.	**ma:**	*Xgwm191-5B* - 17 cM - *Psy-B2* {01230}.

77.2.34. Polyphenol oxidase

Ppo-A1 {10386}.	*PPO-2A* {10385}.	2AL {10385}.
	ma:	Detected with STS markers PPO18 (10385) and PPO33 {10418}. *Xgwm312-2A* - 1.4 cM - *Ppo-A1* - 5.8 cM - *Xgwm294-2A* {10385}.
Ppo-A1a {10386}.	*PPO-2Aa* EF070147{10385}.	
	v:	Zhongyou 9507 {10385,10386}; others {10386}.
	ma:	876bp – wheats with this allele tend to have lower PPO activity {10385,10386}.
Ppo-A1b {10386}.	*PPO-2Ab* EF070148 {10385}.	
	v:	CA 9632 {0758,10386}, others {10386}.
	ma:	685bp (AY596268) – wheats with this allele tend to have lower PPO activity {0758,10386}.
Ppo-D1 {10386}.	2D {10386}.	
	ma:	Detected with primers PPO16 and PPO29. *Xwmc41-2D* – 2.0 cM - *Ppo-D1* {0759,10418}.
Ppo-D1a {0759}.	EF070149 {10384}.	
	v:	Zhonghou 9507 {0759}; others {0759}.
	ma:	713bp with primer PPO16; wheats with this allele tend to have higher PPO activity {0759}.
Ppo-D1b {0759}.	EF070150{0759}.	
	v:	CA 9632 {0759}; others {0759}.
	ma:	490bp with primer PPO29; wheats with this allele tend to have higher PPO activity (0759).

74.2.34. Protein disulfide isomerise (E.C. 5.3.4.1).

Pdi-A1 [{10422}].	4AL {10422}.	**v:**	{10422}.

Pdi-B1 [{10422}].	4DS {10422}.	**v:**	{10422}.

Pdi-D1 [{10422}].	4BS {10422}.	**v:**	{10422}.

The genes for PDI and their promoters were sequenced in {10423}. A related sequence on 1BS was shown to be a partial, non-expressed copy in {10424}, but not detected in {10409}. PCR-RFLP markers for [*TaPDI-4A*] and [*TaPDI-4B*] were designated [*Xvut(PDI)-4A*] and [*Xvut(PDI)-4B*] in {10409}. These were also closely associated with Germin (oxalate oxidase {10441}) genes (10409).

77.3. Endosperm storage proteins
77.3.1. Glutenins
77.3.1.1. Glu-1
Glu-B1

Add:

Glu-B1bn [{10425}].	7+19 {10425}.	**v:**	Triticales: Lasko, Dagno, Tewo, Vision, Dato {10425}.
Glu-B1bo [{10425}].	7+26 {10425}.	**v:**	Triticales: Presto, Modus {10425}.
The number 26 was also used to designate a subunit encoded by *Glu-A1k* and *Glu-A1-1k*.			

Glu-D1

Add:

Glu-D1br [{10426}].	5*t+10.1t {10426}.	**tv:**	*Ae. tauschii* TD 81 {10426}.

Glu-E1

HMW glutenin y-type subunit Ee1.5 encoded by this locus was sequenced {10439} and compared with other y-type subunits, particularly subunit 1Dy10. It has major deletions in its middle region and is one of the smallest known HMW glutenin subunits. It has an additional Cys residue in the middle of the repetitive domain, but lacks one Cys residue commonly found towards the end of this domain. These changes may influence inter- or intra-molecular disulphide bond formation.

Add after the *Glu-V2* section:

Glu-Ta1 {10449}.			**al:**	*Taenitherum crinitum* PI 204577 {10449}.
	Glu-Ta1a [{10449}].		**al:**	*Ta. crinitum* PI 204577 {10449}.
	Glu-Ta1b [{10449}].		**al:**	*Ta. crinitum* PI 205590 {10449}.
	Glu-Ta1c [{10449}].		**al:**	*Ta. crinitum* PI 561094, *Ta. asperum* PI 561091, PI 561092 {10449}.
	Glu-Ta1d [{10449}].		**al:**	*Ta. caput-medusae* PI 598389 {10449}.
	Glu-Ta1e [{10449}].		**al:**	*Ta. caput-medusae* PI 577708 {10449}.
	Glu-Ta1f [{10449}].		**al:**	*Ta. caput-medusae* PI 577710 {10449}.

Each allele identified to date encodes two subunits, an x-type and a y-type. The x-type subunits are slower or equal in mobility to subunit Dx2 of wheat, whereas the y-type subunits are faster than subunit Dx12 {10449}. Phylogenetic analysis based upon the sequence of two genes designated *Tax* and *Tay* isolated from *Ta. crinitum* PI 204577 suggest that the *Tax* subunit was most closely related to Ax1, Cx (*Ae. caudata*), Ux (*Ae. umbellulata*) and Dx5, and the *Tay* subunit to Ay, Cy and Ry (*Secale cereale*) {10449}.

Add at the end of the *Glu-D1* section:
Subunit 10.1t possesses a mobility slightly lower than subunit 10 in SDS-PAGE and its deduced amino acid sequence is similar to subunit 12 (8 amino acid differences) {10426}; the authors used the complete coding sequence to make phylogenetic comparisons with 19 other subunits including both x-type and y-type subunits and concluded that the *Glu-1* gene duplication event probably occurred about 16.83 million years ago.

77.5.6. Waxy proteins

Following the formal gene lists, the paragraph ‘Various hard and soft wheats………’ Add: ‘Fifteen percent of Chinese wheats possessed *Wx-B1* null alleles {10357}.’
To the string of references in the following paragraph add: ‘,10437’}.

77.5.8. Puroindolines and grain softness protein

Pina-D1. After CS, add: (GenBank DQ363911) {03108}. Capitole (GenBank X69914) {03110}.

***Pina-D1a*.**	add:	**v:**	Capitole (GenBank X69914) {03110}; Renan (GenBank CR626934) {10440}.
		dv:	*Ae. tauschii* unidentified accession (GenBank AJ249935) {03103}; *Ae. tauschii* CPI 110799 (GenBank CR626926) {10440}.
***Pina-D1b*.**	add:	**i:**	PI 644080 (Alpowa / ID377s // 7*Alpowa) {10429}.
		v:	Glenlea (GenBank AB262660) {10431}.
This allele is now defined as a 15,380 bp deletion versus other possible puroindoline a nulls {10428,10391}.			
Pina-D1c.	add:	**dv:**	*Ae. tauschii* TA10 (GenBank AY649746) {03108}.
***Pina-D1d*.**	add:	**dv:**	*Ae. tauschii* TA1704 (GenBank AY649744) {03108}.
Pina-D1k.	add:	homonym: *Pina-D1b/Pinb-D1h(t)*:	
		v:	Bindokku {10305}; Cheyenne-A {10305}; Chosen 68 {10305}; Gaiyuerui {10316}; KT020-584 {10432}; Saiiku 18 {10305}; Saiiku 44 {10305}; Sifangmai {10316}; Tachun 2 {10316}; ZM2851 {10316}; ZM2855 {10316}.
This allele is currently used to denote a large deletion of undetermined size that involves *Pina-D1, Pinb-D1* and *Gsp-D1* {10077}. The deletion of both puroindolines is associated with harder kernel texture than other known puroindoline hardness alleles {10077,10305,10432}.			
***Pina-D1m*.** Revise ref. {101208} in the 2005 Supplement to 10208}.			
Pina-D1n		**v:**	Hongheshang, add: (GenBank EF620907) {10208}.
		v:	Xianmai, add: (GenBank EF620908) {10208}.
New entries:			
Pina-D1q {10316}.		**v:**	U29 (GenBank AB181238) {10316}; µu-27 (homonym ‘a2’, *Pina-D1p*) {10316}.
Pinb-D1.	Change ‘(GenBank X69914)’ to ‘(GenBank X69912)’.		
***Pinb-D1b*.**	add:	**i:**	PI 644081 (Alpowa / ND2603 // 7*Alpowa) {10429}.
		v:	Cheyenne (GenBank DQ363914) {10315}; Renan (GenBank CR626934) {10440}.
***Pinb-D1c*.**	add:	**i:**	PI 644082 (Alpowa / Red Bobs // 7*Alpowa) {10429}.
***Pinb-D1d*.**	add:	**i:**	PI 644083 (Alpowa / Mjølner // 7*Alpowa) {10429}.
	add:	**v:**	Soissons (homonym ‘b1’) {10433}.

Pinb-D1e.	add:	**i:**	PI 644084 (Alpowa / Canadian Red // 7*Alpowa) {10429}.
	add:	**v:**	Yunxianxiaomai {10427}.
Pinb-D1f.	add:	**i:**	PI 644085 (Alpowa / Sevier // 7*Alpowa) {10429}.
	add:	**v:**	Abyssinia AV12.4 {10430}.
Pinb-D1g.	add:	**i:**	PI 644086 (Alpowa / Andrews // 7*Alpowa) {10429}.
Pinb-D1h.	add:	**dv:**	TA10 (GenBank AY649748) {03108} CPI110799 (GenBank AY159804) {10037}.
Pinb-D1i.	add:	**dv:**	*Ae. tauschii* TA1704 and TA2381 (GenBank AY649747) {03108, 10315}; *Ae. tauschii* isolate Q03-002 (GenBank DQ257553) (referred to as allele 2) {10314}; *Ae. tauschii* CPI 110799 (GenBank CR626926){10440}.
Q03-002, TA1704, and TA2381 were incorrectly assigned *Pinb-D1w* in the 2006 supplement.			
Pinb-D1j.	add:	**dv:**	*Ae. tauschii* TA1691 (GenBank AY251946) {03108}.
Pinb-D1l.	add:		Note: {10208} reported *Pinb-D1b* in Gaocheng 8901.
Pinb-D1p.	Change reference ‘{10121}’ in 3 places under this heading to ‘{10208}’. add note: The single nucleotide A deletion occurs in the AAAA at position 210-213 and is assigned to the last position at 213.		
	add:	homonym: *Pinb-D1i(t)* {10305}.	
		v:	Qindao landrace 1{10305}; Qitoubai {10305}; Shijiazhuang 34 {10305}; Zigan {10305}.
This homonym sequence (allele) was incorrectly assigned *Pinb-D1v* in the 2006 supplement.			
	add:	homonym: *Pinb-D1z, ‘b3’, Pinb-D1u.*	
		v:	Dahuangpi (GenBank AY581889) {10316}.
Pinb-D1q.		**v:**	Jingdong 11 (GenBank EF620909){10313}.
This allele was used originally (2004 Supplement) in combination with *Pina-D1k* and *Gsp-D1i* to denote the large deletion that encompasses *Pina-D1*, *Pinb-D1* and *Gsp-D1* {10077} (*cf. Pina-D1k*). The haplotype nomenclature of this deletion is under review; *Pinb-D1q* is currently used to denote the C-to-G SNP at position 218 {10313}.			
Pinb-D1t.			add after Guangtouxiamai: (GenBank EF620910).
Pinb-D1u.			add after Tiekemai: (GenBank EF620911).
Pinb-D1v.		**v:**	Tachun 3 {10316}, homonym ‘b5’ {10316}.
The original assignment of this allele in the 2006 supplement was incorrect; the sequence/varieties in {10305} are *Pinb-D1p* as listed above for that allele. The following variety/sequence was assigned *Pinb-D1y* in the 2006 supplement; but the original assignment of {10316} is now unchanged.			
Pinb-D1w	add:	**v:**	Jing 771 (GenBank AY640304, AB180737){10316}, homonym ‘b4’ {10316}. This variety/sequence was incorrectly assigned *Pinb-D1x* in the 2006 supplement; the original assignment of {10316} is now unchanged.
Ae. tauschii isolate Q03-002 (GenBank DQ257553) (referred to as allele 2) {10314}; *Ae. tauschii* TA1704 and TA2381 (GenBank AY649747){10315}; *Ae. tauschii* CPI 110799 (GenBank CR626926) {10440} were incorrectly assigned this allele in the 2006 supplement; they are *Pinb-D1i* as listed above.			
Pinb-D1x.			
The original assignment of this allele in the 2006 supplement was incorrect; the sequence for Jing 771 {10305} is *Pinb-D1w* as listed above. Currently there is no assignment for this allele.			
Pinb-D1y.			
The original assignment of this allele in the 2006 supplement was incorrect; the sequence for Tachun 3 in {10305} is *Pinb-D1v* as listed above. The original assignment of {10316} is now unchanged. Currently there is no assignment for this allele.			
Pinb-D1z.			
This allele/sequence is identical to, and listed under *Pinb-D1p*. Currently there is no assignment for this allele.			
New entries:			
Pinb-D1u {10427}.		**v:**	Tiekamai) {10427}; 31 hard Yunnan endemic wheats (*T.*

			aestivum ssp. *yunnanense* King) {10427}.
Possesses a G deletion at position 127 leading to a shift in ORF {10427}.			
Pinb-D1aa {10391}.		**v:**	Changmangtoulongbai (GenBank EF620912) {10391}; Hongtutou 1 {10391}; Hongtutou 2 {10391}.
Pinb-D1ab {10432}.		**v:**	KU3062 {10432}; KU3069 {10432}.

77.5.9. Grain softness protein

***Gsp-D1i*.** Change reference ‘{10120}’ to ‘{03105}’ in 2 places.

77.7.1 Polygalacturonidase-inhibiting proteins

PGIPs are LRR proteins involved in plant defence as inhibitors of fungal polygalacturonases {10390}.

Pgip1 {10390}.	7BS {10390}.	**v:**	CS ditelo 7BL {10390}.
		v2:	Chinese Spring *Pgip2* {10390}.
		tv:	Langdon {10390}.
Pgip2 {10390}.	7DS {10390}.	**v:**	CS ditelo 7DL {10390}.
		v2:	Chinese Spring *Pgip1* {10390}.

Pathogenic Disease/Pest Reaction

79.Reaction to *Blumeria graminis* DC.

79.1. Designated genes for resistance

33 NILs, including 22 resistance genes and 3 genetic backgrounds are listed in {10389}.

Pm2.		**ma:**	*Xcfd81-5D* - 2.0 cM - *Pm2* {10366}.
Pm3.			
Add note at beginning of section: Following the cloning and sequencing of *Pm3d* {10064}, 6 other alleles were sequenced {10405}. The Chinese Spring (susceptible) allele, *Pm3CS,* considered to be ancestral and present in many hexaploid and tetraploid wheats was also transcribed {10405,10406}. Other wheats possessed a truncated sequence (e.g., Kavkaz), or were null {10405,10406}. Unique markers were developed for all 8 transcribed alleles, and for individual alleles {10405}.			
Pm3b.	*Pm3j*{10405}.		
Pm3c.	*Pm3i* {10405}.		Sequence DQ251587, DQ517917 {10405}.
Pm3d.	*Pm3h* {10405}.		Sequence DQ251488, DQ517518 {10405}.
Pm3e.			
Pm3g.			Sequence DQ251489, DQ517919 {10405}.
Pm3h.	Delete and add to *Pm3d.*		
Pm3i.	Delete and add to *Pm3c.*		
Pm3j.	Delete and add to *Pm3b.*		
Genotype list for *Pm3*: Add: {’,10405,10406’}			
Pm35 {10342}.	5DL {10342}.	**v:**	NC96BGTD3 = PI 603250 = Saluda*3 / TA2377 {10342}.
		dv:	*Ae. tauschii* ssp. *strangulata* TA2377 {10342}.
		ma:	*Xcfd26-5D* – 11.9 cM – *Pm35* {10342}.
Pm36 {10356}.	5BL {10356}.	**tv:**	MG-FN14999, a durum backcross line 5BIL-29 {10356}: *T. turgidum* ssp. *dicoccoides* MG29896 {10356}.
		ma:	Less than 15 cM linkage with 3 SST and one EST-SSR markers on chromosome 6BL {10356}.
Pm37 {10372}.	7AL {10372,10274}.	**v:**	NC99BGTAG11 = *T. timopheevii* ssp. *ameniacum* {10372}.
		tv:	PI 427315 = *T. timopheevii* ssp. *ameniacum* {10372}.
		ma:	*Pm37* (*PmAG11*) was about 15 cM proximal to a cluster of markers that earlier co-segregated with *Pm1* {10372}. A cross indicated linkage between *Pm37*and *Pm1* {10372}.
Pm38 {10373}.	Adult plant resistance.	7DS {10374}.	

		i:	RL6058 = Tc*6 / PI 58548 {10374}.
	v:	Lines with *Lr34/Yr18* – see Reaction to *Puccinia triticina,* Reaction to *Puccinia striiformis.*	
	ma:	*Xgwm1220-7D* – 0.9 cM – *Lr34/Yr18/Pm38* – 2.7 cM {10374}. See also, Reaction to *Puccinia triticina* and Reaction to *Puccinia striiformis.*	

79.3 Temporarily designated genes for resistance to *Blumeria graminis*

Mlm3033 {10393}.	7AL {10393}.	**dv:**	*T. monococcum* TA2033 {10393}.
		ma:	*Xmag1757/Xmag2185* - 2.7 cM - *Mlm2033/Xmag2185* - 1.3 cM - *Xgwm344-7A* {10393}; *Xmag1757* - 5.9 cM - *Mlm2033/mag2185/Xgwm344/Xgwm146-7A* - 4.7 cM - *Xmag1986* {10393}; *Xmag1757/Xmag1714/Xmag1759* - *Mlm2033* - 0.9 cM - *Xmag2185/Xgwm344-7A* {10393}.
Mlm80 {10393}.	7AL {10393}.	**dv:**	*T. monococcum* ssp. *aegilopoides* M80 {10393}.
		ma:	*Xmag1757/Xmag1759* - 3.6 cM - *Mlm80* - 0.7 cM - *Xmag2166/Xgwm344-7A* {10393}.
Mlm2033 and *Mlm80* appeared to be allelic and their relative locations suggest they are allelic with *Pm1* {10393}.			
PmY39 {10367}.	2U(2B) {10367}.	**su:**	Laizhou 953*4 / Am9 (Am9 = *Ae. umbellulata* Y39 / *T. turgidum* ssp. *carthlicum* PS5) {10367}.
		dv:	*Ae. umbellulata* Y39 {10367}.
		ma:	Associated with 2U markers *Xgwm257, Xgwm296* and *Xgwm319* {10367}.

79.4. QTL for resistance to *Blumeria graminis*

Add at end of section:

Fukuho-Komugi / Oligoculm, DH population. QTL for adult plant resistance located on 1AS (R^2 = 22%, *Pm3* region, *Xgdm33 – Xpsp2999*), 2BL (R^2 = 8%, *Xwmc877.1 – Xwmc435.1*) and 7DS (R^2 = 10%) derived from Fukuho-komugi, and 4BL (R^2 = 6% at one of two sites, *Xgwm373-Xgwm251*) from Oligoculm {10335}. The QTL on 7DS, flanked by *Xgwm295.1-7D* and *Ltn,* is likely to be *Lr34/Yr18.*

CI 13227 (S) / Suwon 92 (R), SSD population: APR (field resistance) was closely associated with *Hg, Xpsp2999-1A* and *Xpm3b.1* and *Xpm3B.2* designed from the *Pm3b* sequence {10340}.

RE9001 (R) / Courtot (S) RIL population: *QPm.inra.2B* (R^2 = 10.3 – 36.6 %), in the vicinity of *Pm6,* was consistent over environments {10360}. Eleven QTL, detected in at least one environment were identified by CIM {10360}.

XX. Reaction to *Cephus* spp.

Pest: Wheat stem sawfly. North American species *C. cinctus*; European species *C. pygmeus*. Resistance to wheat stem sawfly is associated with solid stem (see also: Stem solidness).

<u>Tetraploid wheat</u>

Qsf.spa-3B {10351}. See Stem solidness.

81.Reaction to *Diuraphis noxia* (Mordvilko)

Dn4.	**i:**	Yumar {10397}.
	v:	Ankor {10397}; Prairie Red {10397}.

Dn5. Add ref 10396 to 7DL.
Add note: 'Genetic mapping indicated that *Dn5* is located in chromosome 7DS, but cytological analysis showed it was located in 7DL {10396}. It was also suggested {10396} that the Palmiet Dn5 line {0004} may not have *Dn5* {10396}.'.

82.Reaction to *Fusarium graminearum*

82.1.Disease: Insert: 'Fusarium head blight' as an additional disease name. Fusarium head scab, scab

Fhb1 {add: ',10403'}**.**	**i:**	HC374 / 3*98B69-l47 {10214}; Sumai 3*5 / Thatcher {10214}.	
	v:	HC-l47-126 {10444}.	
	v2:	BW278 *Fhb2* {10225}; Sumai 3 *Fhb2* 10314}.	
	ma:	*XSTS3B-80* - 0.2 cM - *Fhb1* - 1.1 cM - *XSTS3B-142* {10214}. Placed in a 1.2 cM interval flanked by *XSTS3B-189* and *XSTS3B-206* {10403}.	
The relationship of *Fhb1* to *Fhs1* or *Fhs2* {1096}is unknown.			
Fhb2. Change '6B' to '6BS'.	**v:**	pbE85 {10444}	
	v2:	Sumai 3 *Fhb1* {10225}.	
	ma:	Change present entry to: '*gwm133-6B* - 4 cM - *Fhb2* - 2 cM - *Xgwm644-6B* {10225}.'	
Add note: The relationship of *Fhb2* to *Fhs1* or *Fhs2* {1096}is unknown.			

In the third paragraph following the listing of *Qfhs.ifa-5A* (relates to Ning 7840 / Clark) add: Three RGA sequences putatively assigned to chromosome 1A explained 3.37 - 12.73% of the phenotypic variation in FHB response among F7 and F10 populations {10364}. STS marker FHBSTS1A-160 was developed from one of the RGA.

Following the entry for Frontana / Remus add:
Frontana (MR) / Seri 82 (S), F3 and F3:5 populations: QTL were located in chromosomes 1BL (R^2 = 7.9%), flanked by AFLP markers, 3AL (R^2 = 7.7%), flanked by *Xgwm720-3A* and *Xgwm121-3A* , 7AS (R^2 = 7.6%), flanked by an AFLP and *Xgwm233-7A* {10349}.

Following Wangshuibai /Alondra add:
Wangshuibai / Annong 8455: RIL population: CIM analysis over 2 years detected QTL for FHB response on chromosomes 3B (R^2 = 0.17) and 2A (R^2 = 0.12), and for DON levels in 5A (R^2 = 0.13), 2A (R^2 =0.85) and 3B (R^2 = 0.06) {10447}. The regions

involved were *Xgwm533.3B - Xbarc133-3B*, *Xgwm425-2A*, and *Xgwm186-5A - Xgwm156-5A* {10447}

In a reciprocal backcross analysis of Chris monosomics / Frontana, Frontana chromosomes 3A, 6A and 4D reduced visibly diseased kernels, kernel weight and DON content, whereas Frontana chromosomes 2A, 2B, 4B and 7A increased the same traits {10398}.

At end of section add:
<u>Tetraploid wheat</u>

Qfhs.crc-2BL {10445}.	**tv:**	Strongfield {10445}.
	ma:	Spanning 16 cM, this QTL peaking on *Xgwm55-2B* explained 23% of the phenotypic variation {10445}.
Qfhs.ndsu-3AS {10402}.	**sutv:**	LDN-DIC3A {10402}.
	tv:	*T. dicoccoides* {10402}.
	ma:	Located in an interval spanning 29.3 cM this QTL accounted for 37% of the phenotypic variation; peak marker, *Xgwm2-3A* {10402}.
Qfhs.crc.6BS {10445}.	**tv:**	*T. turgidum* var. *carthlicum* cv. Blackbird {10445}.
	ma:	Spanning 23 cM and peaking on *Xwmc397* this QTL accounted for 23% of the phenotypic varia tion {10445}.
Qfhs.fcu-7AL {10401}.	**sutv:**	LDN-DIC 7A {10401}.
	tv:	*T. turgidum* var. *dicoccoides* PI 78742 {10401}.
	ma:	Located in an interval spanning 39.6 cM this QTL accounted for 19% of the phenotypic variation in a RIL population of Langdon / LDN-DIC 7A; nearest marker *Xbarc121-7AL* {10401}.

Strongfield / *T. carthlicum* (Blackbird): Field resistance identified in chromosome 2BL (*Xgwm55-2B*), and 6BL (*Xwmc397-6B*) (coincident with *Fhb2* {10225}).

82.2. Disease: Crown rot caused by *Fusarium pseudograminearum, F. culmorum* and other *Fusarium* species.
Add: W21MMT70 / Mendos: DH population: three consistent QTL for seedling resistance were identified with CIM; there were located in chromosomes 5D and 2D (resistance alleles from W21MMT70) and 2B (resistance allele from Mendos) {10358}.

83.Reaction to *Heterodera avenae* Woll.

Cre5.	**v:**	Continue present text with: However a contribution of the *Cre5* region was detected in Trident / Molineux {10343}.
	ma:	Associated with the *Xgwm359-2A* (R^2 = 8%) - *Xwmc177-2A* (R^2 = 7%) region in Trident / Molineux {10343}.
Cre8.	**ma:**	Associated with the *Xgdm147-6B* (R^2 =24%) - *Xcdo247-6B* (R^2 = 12%) region in Trident / Molineux {10343}.

QTL: ***Qcre.srd-1B*** was located to the *Xwmc719-1B* (R^2 = 12%) - *Xgwm140-1B* (R^2 = 12%) region in Trident / Molineux (10343).

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

H13.	6DS {10388}.	**v:**	PI 562619 {10388}; SW34 = Langdon / *Ae. tauschii* RL 5544 {10388}.
		ma:	*Xcfd132-6D* - 3.7 cM - *H13* {10388}.
H22.	1D {1199}, 1DS {10381}.		
		v:	KS85WGRC01 = *Ae. tauschii* TA1644 / Newton // Wichita {1199}; PI 572542 {10388}.
		ma:	*Xgdm33-1D* - 1.0 cM - *H22*- 0.3 cM - *Xhor2KV-1D* - 0.5 cM - *Xgpw7082-1D* {10381}.
H23.		**v:**	PI 535766 {10388}.
H24.		**v:**	PI 535769 {10388}.
H26.	3DL {10388}.	**v:**	SW8 = Langdon / *Ae. tauschii Clae* 25 {10388}.
		ma:	*Xcfd211-3D* - 7.5 cM - *H26* - 2.9 cM - *Xwgc7330-3D* - 4.0 cM - *Xgwm3-3D* {10388}.

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

Stb6.		**v:**	Amigo {10448}; Arina {10448}; Amada {10448}; Atlas 66 {10448}; Ble Seigle {10448}; Bon Fermier {10448}; Chinese Spring {10448}; Gene {10448}; Heines Kolben {10448}; Hereward {10448}; Poros {10448}; Senat {10448}; Shafir m{10448}; Tadinia {10448}.
		v2:	Bulgaria 88 *Stb1* {10448}. Veranopolis *Stb 2* {10448}. Israel 493 *Stb3*{10448}.
Stb10.	1D.		Kavkaz-4500 L.6.A.4.
Stb11.	1BS.	**v:**	TE9111, JIC W 9996.
Stb12.	4AL.		Kavkaz-4500 L.6.A.4.
Stb13 {10347}.	Confers resistance to Canadian cultures MG96-13 and MG2 {10347}.		
	7BL {10347}.	**v:**	DH line 90S05B*01 {10347}; DH line 98S08C*03 {10347}.
		v2:	Salamouni *Stb14* {10347}.
		ma:	*Xwmc396-7B* - 9 cM - *Stb13* 10347}; *Xwmc396-7B* - 7 cM - *Stb13* {10347}.
Stb14 {10348}.	Confers resistance to Canadian isolate MG2 but not to MG96-13 {10347}.		
	3BS {10348}.	**v:**	DH line 98S08A *09 {10348}.
		v2:	Salamouni *Stb13* {10347}.
	ma:		*Xwmc500-3B* - 2 cM - *Stb14* - 5 cM - *Xwmc632-3B* {10348}.
Stb15 {10341}.	Confers resistance to Ethiopian culture IPO88004 {10341}.		
	6AS {10341}.	**v:**	Riband {10341}.
		v2:	Arina *Stb6* {10341}.
		ma:	*Stb15* - 14 cM - *Xpsr904-6A* {10341}.

QTL:
A weak QTL, *QStb.psr-7D.1*, giving partial resistance to Portuguese isolate IPO92006, was detected in the *Xcdo475b-7B* - *Xswm5-7B* region in chromosome 7DS {10341}.

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

89.2. Sensitivity to SNB toxin

Replace or update present entries with the following**:**

Snn1 {10008}**.**	Sensitivity to toxin SnTox1 is dominant {10008}.		1BS {10008}.
	s:	CS- DIC 1B {10008}.	
	v:	CS {10008}; Grandin {10008}; Kulm {10008}; ND 495 {10008}.	
	ma:	*Snn1* - 4.7 cM - *XksuD14-1B* {10008}.	
snn1.	**v:**	Br34 {10008}; Erik {10008}; Opata 85 {10008}.	

QTL: ITMI population: A major QTL, coinciding with *Snn1*, was located in chromosome 1BS ($R^2 = 0.58$, 5 days after inoculation), minor QTL were found in 3AS, 3DL, 4AL, 4BL, 5DL, 6AL and 7BL (10009).

90.Reaction to *Puccinia graminis* Pers.

Sr31.	**ma:**	A SCAR marker, $SCSS30.2_{576}$ was developed {10359}.

91.Reaction to *Puccinia striiformis* Westend.

91.1. Designated genes for resistance to stripe rust

Yr3a.		**i:**	Taichung 29*6 / Vilmorin 23 {10370}.
			Yr3 (*YrV23*) - *Xwmc356-2B*, 9.4 cM {10370}.
Yr5.		**ma:**	Co-segregation with AFLP marker S19N93-140 and 0.7 cM with S23M41-310 {10435}.
Yr7.		**i:**	Taichung 29*6 / Lee {10371}.
		ma:	*Yr7* - *Xgwm526-2B*, 5.3 cM {10371}.
Yr9.		**ma:**	*Yr9* - 3.7cM - *Xgwm582-1BL* {10365}.
Yr15.		**v:**	Boston {0330}; Cortez {0330}; Legron {0330}.
Yr17.		**v:**	Kris {10336}.
		ma:	Characterised by null alleles for *Xwmc382-2A* and *Xwmc407-2A* {10336}.
Yr24.	*YrCH42.*	**v:**	Chuanmai 42 {10339}; Synthetic 769 {10339}.
		tv:	Decoy 1 {10339}.
		ma:	*Xbarc187-1B* -2.3 cM -*Yr24* -1.6 cM - *Xgwm498-1B* {10339}.
Yr24 is identical to *Yr26* {10339,939}.			
Yr26.			
Yr26 is identical to *Yr24* {10339,939}.			
Yr32.		**v:**	Deben {10336}.

Yr34.	Change to:	**v:**	AUS22857 {10040}; WAWHT2046 = AUS91389 {10040}.
		ma:	Change current entry to:'*Xgwm410.2-5A* - 8.2 cM - *B1* - 12.2 cM - *Yr34* {10040}'.
Yr39 {10416}**.**	HTAP resistance.		7BL {10416} .
		v:	Alpowa {10416}.
		ma:	Closely linked to several RGAP markers {10416}.
Yr40 {10328}.	Derived from *Aegilops geniculata.*		5DS (5DL.5DS-T5MS^G {10328}.
		v:	TA5602 {10328}; TA5603 {10328}.
		al:	*Ae. geniculata* (= *ovata*) ($U^sU^sM^gMM^g$) TA10437 (10328).
	ma:		Completely linked with distinctive alleles of *Gsp*, *Xfbb276* and *Xbcd873* {10328}. Completely linked with *Lr57* {10328}.

At end of section add: Genotype list: Chinese common wheats {10369}.

91.2. Temporarily designated genes for resistance to stripe rust

YrAlp {10416}.	1BS {10416}.	**v:**	Alpowa *Yr39*{10416}.
		ma:	*YrAlp* -15.2 cM - *Xgwm18-1B* - 1.1 cM - *Xgwm11-1B* (10416) and more closely linked to RGAP markers {10416}.
YrSp {10352}.	*YrSp* {10353}.		2B {10352,10353}, probably 2BL.
		i:	Avocet*3 / Spaldings Prolific {10353}; Taichung*6 / Spaldings Prolific {10352}.
		v:	Spaldings Prolific {10352,10353}.
		ma:	*YrSp* - *Xwmc-2B* 12.1cM {10352}.
YrV23 {10370}.	Presumed to be *Yr3a*.	**v:**	Vilmorin 23 {10370}.
YrZH84 {10331}.	7BL {10331}.	**v:**	Annong 7959 {10331}; Zhoumai 11 {10331}; Zhoumai 12 {10331}.
		v2:	Zhou 8425B *Yr9* {10331}.
		ma:	*Xwmc276-7B* - 0.6 cM - *Xcfa2040-7B* - *YrZH84* - 4.8 cM - *Xbarc32-7B* {10331}.
Yrns-B1.		**ma:**	As a QTL, *Yrns-B1* was located in a 3 cM interval between *Xgwm493-3B* and *Xgwm1329-3B* {10383}.

91.3. Stripe rust QTLs

Multi-cross analyses detected QTL in chromosomes 2AS (*Yr17*), 2AL (*Yr32*), 2BL (*Yr5/Yr7*) region and 6BL {10336}.

Avocet S / Pavon76: QTL identified in 1BL (*Xgwm259*), 3BS (PstAATMseCAC2), 4BL (*Xgwm495*), 6AL (*Xgwm617*), 6BL (PstAAGGMseCGA1) {10443}.

92.Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr1.		**ma:**	Add: 'Mapped to a 0.7 cM interval in *Ae. tauschii* and a 0.075 cM interval in wheat {10408}. A candidate gene for *Lr1*, *Lr1RGA1*,

		encoding a CC-NBS-LRR protein co-segregated with *Lr1* {10408}.’.	
Lr3c.	**v:**	Blava {10345}.	
Lr10.	**ma:**	*Lr10* was cloned – it has a CC-NBS-LRR structure, syn, *T10rga1* GeneBank AY270157 {10442}.	
Lr17a.	**v:**	Jagger {10346}.	
Lr17b.	**v2:**	Contra *Lr13* {10345}; Kalasz *Lr13* {10345}; Riband *Lr13* {10345}; Sarka *Lr13* {10345}.	
Lr19.	**ma:**	RAPD, SCAR and SSR markers co-inciding with, or flanking, *Lr19* in a derivative of Knott’s Agatha Mutant 28 (C80.1) were reported in {10379}.	
Lr21.		*Lr40* {1200,10415}.	
	v2:	WGRC16 = TAM107*3 / *Ae. tauschii* TA 2460 *Lr39* {220,10415}.	
	dv:	*Ae. tauschii* TA2460 *Lr39* {220,10415}.	
	ma:	*Xksu-1D* is part of *Lr21* {10420}. *Lr21* was cloned and shown to have a NBS-LRR structure {10420}.	
Lr22a.	**ma:**	*Xgwm296-2DS* - 2.0 cM - *Lr22a* {10446}.	
Lr24.	**ma:**	SCAR markers were developed in {10368}.	
Lr34.	**v:**	Arina*3/Forno {10380}; Bezostaya {10387}; Condor {10387}; Cook {10387}; Forno {10066,10380,10387}; Fukuho-Komugi {10387}; Otane {10387}.	
	ma:	*Lr34……XsfrBF473324* - 0.5 cM - *Xsfr.cdo475*-7D - 0.7 cM - *Xswm10*-7D {10380}. A 150bp allele (b) of STS *CsLV34*, derived from wEST BQ788742 was identified in most wheats with *Lr34*; *CsLV34a* - 0.4 cM - *Lr34* {10387}.	
Lr39.		Add existing **v:** and **dv:** entries from *Lr41* and add ‘,10415’ after each reference.	
	v2:	WGRC16 = TAM107*3 / *Ae. tauschii* TA 2460 *Lr39* {220,10415}.	
	dv:	*Ae. tauschii* TA2460 *Lr21* {220,10415}.	
Lr40 {1200}.		Deleted. Shown to be *Lr21* {10415}.	
Lr41 {215}.		Deleted. Shown to be *Lr39* {10415}.	
Lr43 {218}.		Deleted. WGRC16 shown to have *Lr21* and *Lr39* {10415}.	
Lr57 {10328}.		Derived from *Aegilops geniculata.*	5DS (5DL.5DS-T5MS^G {10328}.
	v:	TA5602 {10328}; TA5603 {10328}. Since TA5602 and TA5603 are fourth backcross selections to WL711, they likely also carry *Lr13*.	
	al:	*Ae. geniculata* (= *ovata*) ($\mathrm{U^SU^SM^GM^G}$ TA10437) {10328}.	
	ma:	Completely linked with distinctive alleles of *Gsp*, *Xfbb276* and *Xbcd873* {10328}. Completely linked with *Yr40* {10328}.	
Lr58 {10375}.		Derived from *Aegilops triuncialis.*	2BL {10375} = T2BS.2BL-2^{t}L(0.95).
	v:	TA5605 = WL711*4 / Ae. triuncialis TA10438 *Lr13* {10375}.	
	al:	*Ae. triuncialis* TA10438 {10375}.	
	ma:	TA5605 possesses *Ae. triuncialis* alleles of RFLP markers *XksuH16*, *XksuF11* and *Xbg123* in the terminal region of chromosome 2BL {10375}.	
Lr59 {10399}.		1AL (probable centric fusion {10399}.	
	v:	Line 0306 {10399} = *Ae. peregrina*-680 / 2*CS // 5*W84-17 {10399}.	
	al:	*Ae. peregrina* (UUSS, 2n = 28) 680 {10399}.	
Lr60 {10400}.		*LrW2* {0305}.	1DS {10400}.

	v:	RL6172 {0305} = Thatcher*3/V860.

At the end of section: Under Genotype lists; to references after European cultivars add: {',10345'}.

92.3. QTLs for reaction to *P. triticina*

Avocet S / Pavon76: QTL identified included: 1BL (PstAFAMseCAC1&2), 4BL (*Xgwm368*), 6AL (*Xgwm617*), 6BL (PstAGGMseCGA1) {10443}.

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

93.1. Insensitivity to tan spot toxin

tsn1. **ma:** Replace the last entry with: *Xfgcg7-5B* - 0.4 cM - *Tsn1/Xfcg17-5B* - 0.2 cM - *Xfcg9-5B* {10207}; *Xfcg17-5B* - 0.2 cM - *Tsn1* - 0.6 cM - *Xfcg9-5B* {10207}; *Xfcp1-5B* and *Xfcp2-5B* delineated *Tsn1* to an interval of about 1 cM {10337}. *Tsn1* was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1/XBE425878/Xfcc/XBE443610* {10413}.

Add note: According to {10376} the same dominant allele, presumably *tsn1*, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea and 86ISMN 2137 in crosses with 6B-365.

Tsn2 {10344}.	Conditions resistance to race 3 {10344}.		3BL {10344}.
	sutv:	LDN (DIC-3B) {10344}.	
	tv:	*T. turgidum* no. 283, PI 352519 {10344}; *T. dicoccoides* Israel-A {10344}.	
	ma:	Identified as a QTL in region *Xgwm285-3B* - *Xwmc366.2-3B* (R2 = 91%) {10344}. Also classified as a single gene: *Xgwm285-3B* - 2.1 cM - *tsn2* - 15.2 cM - *Xwmc366.2-3B* {10344}.	
tsn3 {10394}.	3D {10394},3DS {10419}.		
	v:	XX41 = [Langdon / *Ae. tauschii* CI 00017] {10394}; XX45 {10394}; XX110 {10394}	
	dv:	*Ae. tauschii* CI 00017 {10394}.	
	ma:	*Xgwm2a* - *tsn3*, 15.3 cM, 14.4 cM and 9.5 cM in CS / XX41, CS / XX45 and CS /XX110, respectively {10419}.	
Resistances in XX41 and XX110 were recessive whereas that in XX45 was dominant – all three were hemizygous-effective{10394}. The genes were given different temporary designations {10394,10419}, but all will be considered to have a common gene until they are shown to be different.			
tsn4 (10350).	Resistance to race 1 (culture ASC1a) {10350}.		3A {10350}.
	v:	Salamouni {10350}.	

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Updates

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03105.	Massa AN Morris CF & BS Gill 2004 Sequence diversity of puroindoline-a, puroindoline-b and the grain softness protein genes in *Aegilops tauschii* Coss. Crop Science 44: 1808-1816.
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10008.	Change ‘2003’ to ‘2004’ and ‘Abstr.’ to ‘ Phytopathology 94: 1056-1060.
10009.	Change title and location to: Quantitative trait loci analysis and mapping of seedling resistance to Stagonospora nodorum leaf blotch in wheat. Phytopathlogy 94: 1061-1067.
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10225.	Update to: Cuthbert PA, Somers DJ & Brule-Babel 2007 Mapping of *Fhb2* on chromosome 6BS: a gene controlling Fusarium head blight field resistance in bread wheat (*Triticum aestivum* L.). Theoretical & Applied Genetics 114: 429-437.
10214.	2006. Theoretical & Applied Genetics 112: 1465-1472.
10224.	Change to 2006. In title change *Triticum sharonense* to *Aegilops sharonensis.* Euphytica 149: 373-380.
10225.	Replace present reference with: Cuthbert PA, Somers DJ & Brule-Babel A 2007 Mapping of *Fhb2* on chromosome 6BS: a gene controlling Fusarium head blight field resistance in bread wheat (*Triticum aestivum* L.). Theretical & Applied Genetics 114: 429-437.
10230.	Update to: Pozniak CJ, Knox RE, Clarke FR & Clarke JM 2007 Identification of QTL and association of a phytoene synthase gene with endosperm colour in durum wheat. Theoretical & Applied Genetics 114: 525-537.
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10302.	Add ‘6’ to the year of publication, i.e. ‘2006’.
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