CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2006 Supplement

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INTRODUCTION

Recommended rules.

9. Laboratory designators

fcc	(Fargo cereal crops unit – for QTL) Faris, J. USDA-ARS Cereal Crops Research Unit Northern Crop Science Laboratory Agricultural Research Center Fargo, ND 58105 USA farisj@fargo.ars.usda.gov
fcg	(Fargo cereal crops genomic DNA – for genomic DNA clones) Faris, J. USDA-ARS Cereal Crops Research Unit Northern Crop Science Laboratory Agricultural Research Center Fargo, ND 58105

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fcp	(Fargo cereal crops PCR - for PCR markers) Faris, J. USDA-ARS Cereal Crops Research Unit Northern Crop Science Laboratory Agricultural Research Center Fargo, ND 58105 USA farisj@fargo.ars.usda.gov
fcu	(Fargo cereal crops cDNA – for cDNA clones) Faris, J. USDA-ARS Cereal Crops Research Unit Northern Crop Science Laboratory Agricultural Research Center Fargo, ND 58105 USA farisj@fargo.ars.usda.gov
unlp	Castro, A.M. Genetics Faculty of Agricultural Sciences, UNLP, CC31, 1900-La Plata, Argentina amcastro@isis.unlp.edu.ar

Gene Symbol

Almt.	Malate transporter (GeneBank AB081803).
Lvl.	Loaf volume.
Vrt-2.	Mads-box (GenBank DQ022679) {10294}.

DNA Markers

A number of previously unlisted chromosome 6A *Xgwm* markers (719 and above) are given in {0604}.

Group 5L

Add:

XPhyC-5A,B,D {10289}.		PCCF2/PCCR1 clone.	
The analysis of 7 SNPs, of the differential presence of a MITE and of a 12-bp deletion in the *PhyC-5A* locus in 81 wheat cultivars is described in {10288}.			

1. Gross Morphology

Line 6. Change to: 4. Spelt and macha wheat *q c S-D1a* or *q C S-D1a*. **v:** Spelt and macha groups (including *vavilovi*).

1.3. Sphaerococcum

S-D1b.	**v:**	*T. antiquorum* K-56397 & K-56398 {10234}.

4. Aluminium Tolerance

Alt2.

Add at end of section: Malate transporter *Almt-D1* gene (GeneBank AB081803) is completely linked to aluminium tolerance in chromosome arm 4DL between SSR markers *Xwmc48b* and *Xwmc331* in a similar region to *Alt2* {10285}. *Almt1* transgenic expression in barley conferred an Al-activated efflux of malate with properties similar to those of *Al*-tolerant wheat {10286}.

QTL: Atlas 66 / Century: A QTL in the region *Xdgm125-4DL* - *Xwmc331-4DL* accounted for nearly 50% of the phenotypic variation in root growth rate in hydroponic solution {10265}. An Al-activated malate transporter (*LMT1*) was earlier mapped to the same location {10266}.

5.3. Red/purple coleoptiles

Add to the end of the section:

The *Rc* gene appears to encode a transcription activator of late biosynthesis genes involved in the light-regulation of anthocyanin synthesis (studies carried out on CS(Hope 7A) substitution line) {10317}.

9. Brittle Rachis

Insert note: Brittle rachis in *T. durum* was defined as a spike that disarticulated when the tip was bent by 45° relative to the peduncle {10242}.

Br-A1.	[..., *Br-A2* {10280}.	**it:**	ANW10A = LD222*7 / LDN-DIC DS 3A {10242}.
		ma:	*Xgwm2-3A* - 3 cM - *Br-A1* - 8 cM - *Xgwm666-3A.1/Xbarc356-3A/Xbarc19-3A/Xgwm674-3A/Xcfa2164-3A* {10280}.
Br-B1.	[..., *Br-A3* {10280}.	**it:**	ANW10B = LD222*7 / LDN-DIC DS 3B {10242}.
		ma:	*Xbarc218-3B* - 22 cM - *Br-B1* – 2 cM *Xwmc-3B* {10280}.
		tv:	Senatore Cappelle PI 242646 {10242}; Sammartinara {10242}; others {10242}.
The presence of *Br-B1* in some durums apparently does not lead to significant shattering under conditions of Mediterranean agriculture {10242}.			
Br-D1.		**dv:**	*Ae. tauschii* KU2126 10227}.
		ma:	In *Ae. tauschii*: *Br*^{t} - 19.7 cM - *Xgdm72-3D* {10227}.

17. Dormancy

Continue section: 'In cross Zen /CS': Insert as the second sentence: '*QPhs.ocs.3A-1* was localised to a 4.6 cM interval flanked by *Xbarc310-3A* and *Xbcd907-3A* {10245}.'

Add at end: *Qphs.ocs-4A.1* may be the same as a QTL in AC Domain / Haruyutaka due to tight linkage with *Xcdo785-4A* {10245}.

QPhs.ocs. 4B.1, a CS allele contributing to dormancy, was located in the region of *Xgwm495-4B* {10245}.
In cross SPR 8198 (dormant) / HD2329, *QPhs.occsu-3A* was located in the *Xgwm155-3A* – *Xwmc153-3A* region with R^2 = 75% across 6 environments (10261).
QTL analyses in several crosses {10275} indicated a common region in chromosome 4A associated with dormancy; dormant genotypes included AUS1408, SW95-50213 and Halberd. The location was consistent with Japanese and U.K. work even though different flanking markers were involved.

19. Earliness per se

Eps-1A^m.	Add to: **ma:** ……{0364}, within a 0.9 cM region within the *VAtpC - Smp* region {10246}.

QTL: Add: '*QEet.fcu.5AL* identified in *Xfcp359-5A* - *Xfcp231-5A* interval (R^2 = 0.38), at or near the *Q* locus in Grandin / BR34 {10256}. Grandin was the earlier parent.

20. Flowering Time

Add at end of section:
Heading date QTL: CI 13227 / Suwon 92 RIL population: AFLP marker – 2.6 cM – *QHd.pser-2DS* – 121.1 cM – *Xgwm261-2D* {10269}. This QTL could be *Ppd-D1*{10269}.
Karl 92*2 / TA 4152-4 F2:F4 population: Two QTLs, *QHd.ksu-2D,* associated with *Xgwm261-2D* (R^2 = 0.17), and *QHd.ksu-3D,* associated with *Xgwm161-2D* 9 (R^2) {10273}.

23. Frost Resistance

Fr-A2.	**ma:**	Insert the following sentence as the third sentence in the existing text: Eleven different *Cbf* transcription factors were identified at the *Fr-A2* locus {10302}.

24. Gametocidal Genes

24.1. Gametocidal activity

Sd1.	**ma:**	Proximal to *Lr19* and distal to *Xpsr165-7D* {10255}.

Sd2. Add note following the entry. "Zhang et al. {10255} question the existence of this gene and alternatively suggest a duplication or deletion event influencing the transmission.

26.2. Epistatic inhibitors of glaucousness

Iw2.	**ma:**	In *Ae. tauschii: Iw2* - 30.1 cM - *Xgdm35-2DS* {10227}.

28. Grain Hardness/Kernel texture

Insert before the par. 'Using proteomic analysis….' Two QTLs, *QHa.ksu-3B*, associated with *Xksum9-3B* (R^2 = 0.09, and *QHa.ksu-5D(Ha), associated with Xcfd-5D* (R^2 = 0.3), were identified in Karl*2 / TA 4152-4 {10273}.

29. Grain Quality parameters

29.7. Starch characteristics

Insert as the first sentence: The Isoamylase-1 gene from *Ae. tauschii* (*Iso-1*) complements the deficient rice sugary-1 mutant line {10295}.

29.8. Loaf volume

Lvl1 [{10312}]. *Lvl 1* {10312}. 3A {10312}. **v:** Cappelle Desprez*7 / Bezostaya 1 3A {10312}. **ma:** *Xgwm720-3A* - *Lvl1* appeared to be located in the *Xgwm2-3A* - *Xgwm720-3A* region {10312}.

29.9 Dough rheological properties

QTL: In a Cranbrook / Halberd DH population, environmental factors were a major determinant of dough extensibility whereas additive effects of alleles at the high and low molecular weight glutenin loci determined dough strength {10247}.

New Section: Growth rate and Early Vigour

QTL analyses in *Aegilops tauschii*: chromosomes 1D, 4D, and 7D carried QTLs for relative growth rate, biomass allocation, specific leaf area, leaf area ratio, and unit leaf rate. Chromosome 2D had QTLs for rate and duration of leaf elongation, cell production rate, and cell length. Chromosome 5D harbored QTLs for total leaf mass and area, number, and growth rate of leaves and tillers {10293}.

39. Height

39.2. Reduced height: GA sensitive

Rht4.	2BL {10249}.	**ma:**	Associated with *Xwmc317-2B* {10249}.
Rht5.	3BS {10249}.	**ma:**	Approximately 10 cM from *Xbarc102-3B* {10249}.
Rht8.		**v:**	Chuan Mai 18 {10249}.
		ma:	Close linkage with *Xwmc-2D* {10249}. A survey of Chinese cultivars showed 13 alleles of *Xgwm261-2D* {10284}.
Rht9.	Add: , 5AL {10249}	**v:**	Mercia 12 {10249}.
		ma:	Close linkage with *Xwmc410-4A* {10249}.
Rht13.	Add: , 7BS	**ma:**	Associated with *Xwms577-7B* {10249}.

39.3 Reduced height: QTL

QHt.fcu-4BL {10256}.	**ma:**	Associated with *Xbarc125-4B* (R^2 = 0.57) {10256}.
	Reduced height allele in Grandin {10256}.	
QHt.fcu.6AS {10256}.	**ma:**	Associated with *Xbarc23-6A* - *Xcp201-6A* (R^2 = 0.07) {10256}.
	Reduced height allele in BR34 {10256}.	

QHt.crc-4B {10287}.	4B {10287}.	**ma:**	Linked to *Rht-B1* (LOD 7.7) in RL4452 / AC Domain {10287}.

	Associated with QTLs for lodging and 1000-grain weight.		
QHt.crc-4D {10287}.	4D {10287}.	**ma:**	Linked to *Rht-D1* (LOD 30.9) in RL4452 / AC Domain {10287}.
	Associated with QTLs for lodging, 1000-grain weight, yield, height, and test weight.		
QHt.crc-2D {10287}.	2D {10287}.	**ma:**	Linked to BE497718-260 (LOD 4.2) in RL4452 / AC Domain {10287}.
QHt.crc-5B {10287}.	5B {10287}.	**ma:**	Linked to *Xwmc640-5B* (LOD 6.1) in RL4452 / AC Domain {10287}.
QHt.crc-7A {10287}.	7A {10287}.	**ma:**	Linked to *Xwmc139-7A* (LOD 3.3) in RL4452 / AC Domain {10287}.
QHt.crc-7B {10287}.	7B {10287}.	**ma:**	Linked to *Xgwm333-7B* (LOD 3.3) in RL4452 / AC Domain {10287}.

45. Leaf Tip Necrosis

Add to existing entry for *Ltn.*

Ltn1 {10281}.	[*Ltn* {1361}].	**v2:**	Parula *Ltn2* {10281}.
	ma:	Associated with *Xgwm295-7D* and *Xgwm130-7D* {10218}.	

Ltn2 {10281}.	**v:**	1B {10281}.	Wheats with *Yr29/Lr46* {10281}. See *Yr29, Lr46.*
	v2:	Parula *Ltn1* {10281}.	
	ma:	*Xwmc44-1B* - 1.4 cM - *Xbac24prot* - 9.5 cM - *Ltn2* - 2.9 cM - *Xbac17R........Xgwm140-1B* {10281}. *Xgwmc44-1B* - 3.6 cM - *Ltn2* - 2.1 cM – *XtG818/XBac17R........Xgwm140-1B* {10281}.	

According to Messmer et al. {0031} LTN may be caused by several QTLs and is affected by genetic background and environment.

46. Lodging

QLd.crc-3D {10287}.	3D {10287}.	**ma:**	Linked to *Xgwm191-3D* (LOD 3.7) in RL4452 / AC Domain {10287}.

New Section: Maturity time

QTL:

QMat.crc-3B {10287}.	3B {10287}.	**ma:**	Linked to *Xwmc231-3B* (LOD 3.0) in RL4452 / AC Domain {10287}.
QMat.crc-4A {10287}.	4A {10287}.	**ma:**	Linked to *Wx-B1* (LOD 6.1) in RL4452 / AC Domain {10287}.

QMat.crc-7D {10287}.	7D {10287}.	**ma:**	Linked to *Xgwm130-7D* (LOD 17.5) in RL4452 / AC Domain {10287}.

50. Meiotic Characters

50.2. Pairing homoeologous

Add note at end of *Ph1*section: A complex *Ph1*candidate structure comprising at least one 5B-specfic member of the *cdc2* complex multigenic cluster (involved in chromosome condensation), a unique repeat structure with similarities to repeats on chromosome 3B, and a heterochromatic sub-telomeric insertion from chromosome 3AL was identified {10240}.

57. Polyphenol Oxidase (PPO) Activity

Add after the first paragraph: STS marker PPO18 based on a polyphenol oxidase (*PPO*) gene (GenBank AY596268) was closely linked to SSR markers *Xgwm312* and *Xgwm294* on chromosome arm 2AL. PPO18 explained 28-43% of the variation in PPO activity in the cross Zhongyou 9507 / CA9632 {10290}.

58. Red Grain Colour

R-B1.	**ma:**	*Xwmc29-3B* - 5 cM - *R-B1* - 5 cM - *Xbarc-3B* {10280}.

63. Response to Vernalization

Replace the existing material in this section with the following:

Vrn-1{1398}. [Synonymous with *TaVRT-1* {10019}]. Orthologous series in long arms of chromosomes of homoeologous group 5. *Vrn-1* is a MADS-box gene similar to Arabidopsis *APETALA1* {10014}. Spring types are associated with mutations in the promoter or the first intron {10014,10198,10202,10288}. Reduction of *Vrn-1* transcripts in transgenic hexaploid spring wheat delays flowering {10300}.

Vrn-2{1398}. Orthologous series in chromosomes of homoeologous group 4. *Vrn-A*^{m}*2* was located in *T. monococcum* {279} on chromosome 5A^{m} on the 4A^{m} translocated region. *Vrn-A*^{m}*2* was mapped to the distally located *Xwg114-5A* - *Xwec87-5A* region {0312}. *Vrn-H2* (sh/sgh1) occurs in barley chromosome 4H {1455} and is probably orthologous to *Vrn-A*^{m}*2* based on comparative maps {279,767}. *Vrn-2* is a zinc-finger / CCT domain transcription factor (*ZCCT1*) {10299}, and repressor of flowering down-regulated by vernalization and short days {10301}. Reduction of *Vrn-2* transcripts in transgenic hexaploid winter wheat accelerates flowering {10299}.

Vrn-A2a {279}.	Winter habit, dominant in diploid wheat {279}.	**dv:**	G1777 {279}; G3116 {279}.
Vrn-A2b {279}.	Spring habit, recessive in diploid wheat.	**dv:**	DV92 {279}; PI 355517 {10299}; PI 345242 {10299}; PI 352475 {10299}; PI 277137 {10299}.
Contains a non-functional mutation in the CCT domain {10299}.			
Vrn-A2c {10299}.	Spring habit, recessive in diploid wheat.	**dv:**	PI 352484 {10299}; PI 323437{10299}; PI 286068 {10299}; PI 591871 {10299}; PI 542474 {10299}; PI 428175 {10299}; PI 237659 {10299}; PI 221329 {10299}; PI 225164 {10299}; PI 377662 {10299}; PI 377648 {10299}; PI 362610 {10299} .
Complete deletion of the *ZCCT1* gene {10299}.			

64. Restorers for Cytoplasmic Male sterility

64.1. Restorers for *T. timopheevii* cytoplasm

Rf3. Add: **v:** R18 {10222}; R9034 {10222}. **ma:** Mapped as a QTL in the region *Xbarc207-1BS - Xgwm131-1BL - Xbarc61-1BL* in crosses R18 / ND36 and R9034 / ND36 {10222}.

Add note at end of section: Minor restorer effects were associated with *Xbarc330-5A* in R18 and *Xgdm130-7D* in R9034 {10222}. The relationships of these QTL with previously located restorers in chromosomes 5A {860} and 7D (*Rf2*) are unknown.

67. Segregation Distortion

Add introductory note: ‘See also, 24. Gametocidal Genes’

69. Stem Solidness

Insert introductory statement: Solid stem, caused by increased pith in normally hollow stem regions, is associated with resistance to wheat stem sawfly, *Cephus cinctus*.

72. Tiller Inhibition

At end of section add note: A QTL of large effect on spike number per plant in a DH population of Fukuho-Komugi / Oligoculm mapping to the *Hg - Xpsp2999(Glu3)-1A* region {10218} probably corresponds to *Tin1*.

75. Yield and Yield Components

75.1. Grain weight

75.1.2. 1000-grain weight

QGwt.crc-3D {10287}.	3D {10287}.	**ma:**	Linked to *Xgwm341-3D - Xwmc552-3D* (LOD 4.3) in RL4452 / AC Domain {10287}.
QGwt.crc-4A {10287}.	4A {10287}.	**ma:**	Linked to *Xgwm494-Xgwm162* (LOD 6.7) in RL4452 / AC Domain {10287}.

QGwt.crc-6D {10287}.	6D {10287}.	**ma:**	Linked to *Xgwm325-6D* - *Xgwm55-6D* (LOD 3.9) in RL4452 / AC Domain {10287}.

75.1.3. Test weight (New sub-section)

QTL:

QTwt.crc-1B {10287}.	1B {10287}.	**ma:**	Linked to *Xgwm374.1-1B* (LOD 3.9) in RL4452 / AC Domain {10287}.
QTwt.crc-1D {10287}.	1D {10287}.	**ma:**	Linked to *Xgdm126-1D* (LOD 5.8) in RL4452 / AC Domain {10287}.
QTwt.crc-2D {10287}.	2D {10287}.	**ma:**	Linked to *Xgwm349-2D* - *Xbarc59-2D* (LOD 5.2) in RL4452 / AC Domain {10287}.
QTwt.crc-3B {10287}.	3B {10287}.	**ma:**	Linked to *Xwmc635-3B* - *Xbarc164-3B* (LOD 15.4) in RL4452 / AC Domain {10287}.
QTwt.crc-3D {10287}.	3D {10287}.	**ma:**	Linked to *Xbarc71-3D* (LOD 5.2) in RL4452 / AC Domain {10287}.
QTwt.crc-5D {10287}.	5D {10287}.	**ma:**	Linked to *Xgdm63-5D* - *Xwmc765-5D* (LOD 5.3) in RL4452 / AC Domain {10287}.

75.4. Grain yield

QYld.crc-2B {10287}.	2B {10287}.	**ma:**	Linked to *Xgwm257-2B* (LOD 9.4) in RL4452 / AC Domain {10287}.
QYld.crc-4A {10287}.	4A {10287}.	**ma:**	Linked to *Xgwm130-4A* (LOD 4.4) in RL4452 / AC Domain {10287}.
QYld.crc-2A {10287}.	2A {10287}.	**ma:**	Linked to *Xgwm339-2A* (LOD 3.0) in RL4452 / AC Domain {10287}.

77. Proteins

77.1. Grain protein content

Insert following entry *Pro2*:

Gpc-B1b {10296}. *QGpc.ndsu-6Bb* {632,0071}, *Gpc-6B1* {10229}. 6BS. **ma:** Mapped to a 0.3 cM interval flanked by *Xucw79-6B and Xucw71-6B* {10229}. *Xcdo365-6B* - 1.5 cM - *Gpc-B1* - 1.2 cM - *Xucw67-6B* {10296}. A high-throughput codominant marker, *Xuhw89-6B,* was then mapped less than 0.1 cM from *Gpc-B1* {10297}.

Gpc-B1 affects senescence and maturity in addition to grain protein content with *Gpc-B1b* from *T. dicoccoides* accelerating senescence and maturity {10298}.

77.2 Enzymes

77.2.1. Acid phosphatase

Acph-D2 [{10309}].	*Acph1* {10309}.	2DL {10309}.	

	dv:	*Acph-D2*$_{100}$ and *Acph-D2*$_{95}$ alleles distinguished accessions of *Ae. tauschii* ssp. *tauschii* and *strangulata*, respectively {10309}.
	ma:	Cent….*Acph-D2* - 4 cM - *Xgwm157-2D* {10309}.

77.2.11. Lipoxygenase

Replace with the following: The wheat *Lpx-1* gene in wheat corresponds to barley *LoxA* (GenBank L35931). The *Lpx-B1* locus is duplicated, with the *Lpx-B1.1* and *Lpx-B1.2* loci corresponding to GenBank sequences DQ474240 and DQ474241, respectively. The *Lpx-B1b* allele corresponds to a deletion associated with a 4.5-fold reduction in lipoxygenase activity. The *Lpx-2* gene in wheat corresponds to the barley *LoxC* gene (GenBank L37358) whereas the *Lpx-3* gene in wheat corresponds to the barley *LoxB* gene (GenBank L37359).

Lpx-A1{516}.	[*Lpx-B1* {516}].	4AL {516}.	**v:**	CS {516}.
	ma:	*Xksu919(Lpx-1)-4A*{0091}.		
Lpx-B1{516}.	[*Lpx-A1* {516}].	4BS{516}.	**v:**	CS {516}.
	ma:	*Xcn110(Lpx-1)-4B*{0269,0367}.		
Lpx-B1a {1533}.	[*Lpx-A1a* {936}].		**v:**	CS.
Lpx-B1b {1533}.	[*Lpx-A1b* {936}].		**v:**	Bosanka {1533}.
Lpx-B1.1 {10303}.		4BS {10303}.	**ma:**	*Xksm62-4B* - 8 cM - *Lpx-B1.1* - 13 cM - *Xwmc617b-4B* {10303}.
Lpx-B1.1a {10303}.			**tv:**	UC1113 {10303}.
Lpx-B1.1b {10303}.			**tv:**	Kofa, deletion {10303}.
Lpx-B1.2 {10303}.		4B {10303}.	**v:**	CS.
Lpx-D1 {516}.		4DS {516}.	**v:**	CS.
Lpx-E1 {518}.		4ES {518}.	**ad:**	CS/*E. elongata.*
Lpx-H1 {716}.		4H {716}.	**ad:**	CS/Betzes.
Lpx-A2 {516}.		5AL {516,10303}.	**v:**	CS.
	ma:	*Xksu919(Lpx-2)-5A* {0091}.		
Lpx-B2 {516}.		5BL {516,10303}.	**v:**	CS.
	ma:	*Xksu919(Lpx-2)-5B*{0091}; *Xcn111(Lpx-2)-5B* {0269}.		
Lpx-D2 {516}.		5DL {516}.	**v:**	CS.
Lpx-E2 {518}.		5EL {518}.	**ad:**	CS/*E. elongata*.

Lpx-H2 {716}.		5H {716}.	**ad:**	CS/Betzes.
Lpx-S^{s}***2*** {1140}.		5S^{s} {1140}.	**ad:**	CS/*Ae. searsii*.
Lpx-V2 {242}.		5V.	**ad:**	CS/*D. villosum*.
Lpx-A3 {10303}.		4AL {10303}.	**tv:**	UC1113 (GenBank DQ474244) and Kofa (GenBank DQ474242) {10303}.
	ma:	*Xwmc617a-4A* - 10 cM - *Lpx-A3* - 15 cM - *Xgwm192b-4A* {10303}.		
Lpx-B3 {10303}.		4B {10303}.	**tv:**	UC1113 and Kofa (GenBank DQ474243) {10303}.

77.2.32 Phytoene synthase

Phytoene synthase, which condenses two molecules of geranyl geranyl diphosphate to produce phytoene, is the first of specific enzyme necessary for carotene biosynthesis in plants.

77.2.32.1 Phytoene synthase 1 (E.C. 2.5.1.32)

Homology with the same gene in rice (*Psy1*) {10230}.

Psy1-A1 {10230}.	7AL {10230}.	**tv:**	Kofa {10230}.
Psy1-B1 {10230}.	7BL {10230}.	**tv:**	Kofa {10230}.

77.2.32.2 Phytoene synthase 2 (E.C. 2.5.1.32)

Homology with the same gene in rice (*Psy2*) {10230}.

Psy2-A1 {10230}.	5A {10230}.	**tv:**	Kofa {10230}.
Psy2-B1 {10230}.	5B {10230}.	**tv:**	Kofa {10230}.

77.2.33 Isoamylase 1

Iso-1[{10295}].	*ISA-1* {10295}].	**dv:**	*Ae. tauschii* {10295}.

Endosperm storage proteins

77.3.1.1. Glu-1

Glu-A1

Add:

Glu-A1w {10327}.		2.1* {10327}.	**v:**	KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.
Glu-A1x [{10327}].		2’ {10327}.	**v:**	TRI14165/91 {10327}.

Glu-B1

Add:

Glu-B1bh {10327}.		13+22* {10327}.	**v:**	KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.
Glu-B1bi {10327}.		13+22.1 {10327}.	**v:**	KU-1135 {10327}.
Glu-B1bj {10327}.		14*+15* {10327}.	**v:**	TRI11553/92 {10327}.
Glu-B1bk {10327}.	[*Glu-B1be* {10327}].	6.1+22.1 {10327}.	**v:**	Steiners Roter Tiroler, Hercule, Schwabenkorn, SP3, Rouguin {10327}.
Glu-B1bl {10327}.	[*Glu-B1bf* {10327}].	6.1 {10327}.	**v:**	KU-3418, KU-3446, TRI4613/75 {10327}.
Glu-B1bm {10327}.	[*Glu-B1bg* {10327}].	13*+19* {10327}.	**v:**	Rechenbergs Früher Dinkel, Renval, Zeiners Weißer Schlegel, KU-3410, TRI9885/74, SP1 {10327}.

Add to the end of the section: Although alleles *Glu-B1i* encoding subunits 17+18, and *Glu-B1bc* encoding subunits 6+17, apparently share a common subunit (Ax17 and By17, respectively) it is not clear that this is in fact true.

Primers were designed to distinguish subunit By8 from By8*, for distinguishing subunit By9-containing alleles from non-By9 alleles, and for diagnosing the presence of *Glu-B1f*.

Glu-D1

Add:

Glu-D1bp {10327}.		2.1'+12 {10327}.	**v:**	KU-1034 {10327}.
Glu-D1bq.	[*Glu-D1bp(t)* {10304}].	2.6+12 {10304}.	**v:**	Jinbaojin, Hongkedongmai, Hongdongmai, Baidongmai {10304}.

At the end of the section for *Glu-D1* add:

The complete sequence of this subunit was determined {10319}.

Glu-A1-1

Add:

Glu-A1v {10327}.		2.1* {10327}.	**v:**	KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.
Glu-A1w [{10327}].		2' {10327}.	**v:**	TRI14165/91 {10327}.

Glu-B1-1

Add:

Glu-B1-1ae {10327}.		14* {10327}.	**v:**	TRI11553/92 {10327}.

Glu-B1-1af {10327}.		6.1 {10327}.	**v:**	Steiners Roter Tiroler, Hercule, Schwabenkorn, SP3, Rouguin, KU-3418, KU-3446, TRI4613/75 {10327}.

Glu-B1-2

Add:

Glu-B1-2ac {10327}.		22* {10327}.	**v:**	KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.
Glu-B1-2ad {10327}.		22.1 {10327}.	**v:**	KU-1135, Steiners Roter Tiroler, Hercule, Schwabenkorn, SP3, Rouguin {10327}.
Glu-B1-2ae {10327}.		15* {10327}.	**v:**	TRI11553/92 {10327}.
Glu-B1-2af {10327}.		19* {10327}.	**v:**	Rechenbergs Früher Dinkel, Renval, Zeiners Weißer Schlegel, KU-3410, TRI9885/74, SP1 {10327}.

Glu-D1-1

Glu-D1-1l. Replace the entry that currently reads: '*Glu-D1-1l*{1578}. 1.5 {1578}. **dv:** *Ae. tauschii*' with:

Glu-D1-1l {1578}.	1.5{1578}, Dtx1.5 {10306}.	**dv:**	*Ae. tauschii* accession SQ-214 {10306}.
A restriction enzyme based method named the 'restricted deletion method' was used to characterise the ORF of this subunit {10306} (as in the case of subunit Dty10 encoded by *Glu-D1-2u* {10306}. Allele-specific PCR markers were developed based upon SNPs located at the non-repetitive N-terminal {10320}.			

Add:

Glu-D1-1t [{10304}].	2.6 {10304}.	**v:**	Jinbaojin, Hongkedongmai, Hongdongmai, Baidongmai {10305}.
Glu-D1-1u [{10327}].	2.1' {10327}.	**v:**	KU-1034 {10327}.

Glu-D1-2

Add:

Glu-D1-2u [{10306}].	Dty10 {10306}.	**dv:**	*Ae. tauschii* accession SQ-214 {10306}.
A restriction enzyme based method named the 'restricted deletion method' was used to characterise the ORF of this subunit {10306} (as in the case of subunit 1.5 (or Dtx1.5 {10306}) encoded by *Glu-D1-1l* {10306}. This subunit was first recognised as being different from subunit 10 encoded by *Glu-D1-2b* in hexaploid wheat in {10307}.			

77.3.1.2. Glu-2

Glu-B2

Add:

Glu-B2c {10215}.	12* {10215}.	**tv:**	Alcala la Real {10215}.

77.3.1.3 Glu-3

Add at end of the preamble:

A novel storage protein gene with chimerical structure was isolated from the old Hungarian cultivar Bánkúti 1201, containing ?-gliadin sequences in the 5’ region, LMW-glutenin sequences in the 3’ region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated *Ch1* to *Ch8*, seem to derive from four ?-gliadin and three LMW-glutenin sequences and are probably the result of crossing over between the loci *Gli-1* and *Glu-3*. However, the precise recombinational mechanism that gave rise to them has yet to be elucidated {10307}.

Glu-A3

Add:

Glu-A3q {10215}.	[*Glu-A3i* {10215}].	5+20 {10215}.	**tv:**	Fanfarron {10215}.

Glu-B3

Add:

Glu-B3aa {10215}.	[*Glu-B3l* {10215}].	1+3+13*+16 {10215}.	**tv:**	Blancal de Nules {10215}.

77.3.2. Gliadins

Add to the end of the preamble:

‘A novel storage protein gene with chimeric structure was isolated from the old Hungarian cultivar Bánkúti 1201, containing ?-gliadin sequences in the 5’ region, LMW-glutenin sequences in the 3’ region and a frameshift mutation leading to a completely new polypeptide in the C-terminal region. A further seven recombinant prolamin genes were subsequently isolated. The eight genes, designated *Ch1* to *Ch8*, seem to derive from four ?-gliadin and three LMW-glutenin sequences and probably resulted from crossing over between *Gli-1* and *Glu-3*. However, the precise recombinationalal mechanism that gave rise to them has yet to be elucidated {10307}.

Transcriptome analysis showed the presence of proteins called avenin-like a and b. The former contained a duplicated sequence of about 120 residues and corresponded to the LMW-gliadins. The latter were not previously characterised, but may form part of the glutenin fraction and hence influence quality. These avenin-like proteins showed higher expression levels in three *Aegilops* species (*Ae. caudata*, *Ae. cylindrica* and *Ae. tauschii*) than in common wheat {10321}.’

77.3.3. Other endosperm storage proteins

Before the preamble add the sub-heading:

’77.3.3.1. Triticin proteins’

Replace the preamble with:

‘The triticin proteins {1360} or [Triplet proteins {1357}] are storage globulins with homology to pea legumins and related proteins in oats, rice and several dicotyledonous species {1360}. Triticin gene segments including its hypervariable region were PCR-amplified, with preferential amplification of *Tri-D1* for the only pair of primers giving consistent results {10322}.

77.4.4. Inhibitors (dimeric) of heterologous alpha-amylases

Add to the end of the preamble:

‘Three genome allele specific primer sets were designed for the 3BS and 3DS a-amylase inhibitors in cv. Chinese Spring, based upon SNPs. Their validity was confirmed in 15 accessions of *Triticum urartu*, *Triticum monococcum, Aegilops tauschii* and *Triticum dicoccoides*. The results offered support that the 24 kDa dimeric a-amylase inhibitors in cultivated wheat are encoded by a multigene family {10323}, previously proposed, as the result of phylogenetic analysis of sequences characterised by cSNPs, in {10324}.’

77.5.6. Waxy proteins

Add after the ***Wx-B1b*** entry:

‘An ELISA-based method was developed for distinguishing wheat lines carrying this null allele {10325}.’

77.5.8. Puroindolines and grain softness protein

Changes:

Under ***Pina-D1a***

Delete dv: ‘TA1583 (GenBank AY252029) *Pinb-D1a, Gsp-D1b*{03105}’

Under ***Pina-D1c***

Delete dv: ‘TA2536 (GenBank AY251998) *Pinb-D1i, Gsp-D1d*{03105}’

Under ***Pina-D1d***

Change: GenBank ‘AY251963’ to ‘AY252012’; change ‘AY251948’ to ‘AY251996’; add to dv: ‘TA2536 (GenBank AY252043){03105}’.

Under ***Pina-S1***

Add after TA2368 ‘(GenBank AY622787)’; add after TA1789 ‘(GenBank AY622788)’, add after TA1777 ‘(GenBank AY622789)’.

Under ***Pina-S*^{sh}*1***

Add after TA1999 ‘(GenBank AY622796)’.

Under ***Pina-S*^{l}*1***

Add after TA1912 ,(GenBank AY622790)’; add after TA1921 ‘(GenBank AY622791)’.

Under ***Pina-S*^{s}*1***

Add after TA1355 ‘(GenBank AY622792)’.

Under ***Pina-A*^{m}*1***

Add after TA2026 ‘(GenBank AY622786)’; add after TA2037 ‘(GenBank AJ242715)’; add after TA581 ‘(GenBank AY622786)’.

Add new allele after *Pina-D1n*:

Pina-D1o{10311}. **dv:** *Ae. tauschii* RM0182 (GenBank AY608595) {10311}.
Pina-D1p {10316}. **v:** *T. aestivum* Jing771 (GenBank AY599893) {10316}.

Pinb:

Make the following changes to current entries:
Under ***Pinb-D1h***
After TA2369 add ‘(GenBank AY251983)’; after TA2527 add ‘(GenBank AY251965)’; after TA1649 add ‘(GenBank AY251963)’.
Under ***Pinb-D1i***
After TA2436 add ‘(GenBank AY251947)’.
Under ***Pinb-D1j***
After TA1559 add ‘(GenBank AY251962)’, after TA1691 add ‘(GenBank AY251964)’.
Under ***Pinb-D1q***
Add: ‘**v:** Jingdong 11 {10313 }.’.
Under ***Pinb-A***^{m}***1***
First entry should read, ‘**dv:** *T. monococcum* DV92 (cultivated) cds (GenBank AJ242716) complete BAC sequence (GenBank AY491681), G3116 (spp. aegilopoides){0083}’.
After second entry delete ‘is identical to allele Pina-D1h{03105}’.
Add: ‘*T. monococcum* TA2025 (GenBank AY622797{10315}; *T. monococcum* TA2026 (GenBank AY622798){10315}, *T. monococcum* TA183 (GenBank AY622799){10315}’.
Under ***Pinb-S1***
After TA2368 add ‘(GenBank AY622797)’, after TA1789 add ‘(GenBank AY622802)’, after TA1777 add ‘(GenBank AY622803)’.
Under ***Pinb-S***^{b}***1***
After TA1954 add ‘(GenBank AY622807)’ after TA1942 add ‘(GenBank AY622808)’.
Under ***Pinb-S***^{l}***1***
After TA1912 add ‘(GenBank AY622800)’, after TA1921 add ‘(GenBank AY622804)’.
Under ***Pinb-S***^{s}***1***
After TA1837 add ‘(GenBank AY622805)’.
Change ‘TA1355’ to ‘TA2355 (GenBank AY622806)’.
Under ***Pinb-S***^{sh}***1***
After TA1999 add ‘(GenBank AY622809)’.

New entries:
Pinb-D1v [{10305}]. [*Pinb-D1i(t)* {10305}]. **v:** Qingdao Landrace 1{10305}; Qitoubai {10305}; Shijiazhuang 34 {10305}; Zigan {10305}.
Pinb-D1w {10314}. **dv:** *Ae. tauschii* 002 (GenBank DQ257553){10314}; *Ae. tauschii* ssp. *tauschii* TA1704 (GenBank AY649747){ 10315}; *Ae. tauschii* spp. *anathera* TA2381 (GenBank AY649747){10315}.
Pinb-D1x {10316}. [*Pinb-D1q* {10316}]. **v:** Jing 771 (GenBank AY640304){10316}.
Pinb-D1y {10316}. [*Pinb-D1r* {10316}]. **v:** Tachun 3 (GenBank AY598029){10316}.
Pinb-D1z {10316}. [*Pinb-D1p* {10316}]. **v:** Dahuangpi (GenBank AY581889) {10316}.

General note at end of Puroindoline section: ‘Ikeda et al {10305} reported a double-null with apparently no *Pina-D1* or *Pinb-D1* genes present in **v:** Bindokku, Cheyenne 'A', Chosen 68, Saiiku 18, Saiiku 44, and tentatively assigned it *Pina-D1b/Pinb-D1h(t)*. How this deletion compares with the double null mutation reported by Tranquilli et al. {10077} which was assigned *Pina-D1k/Pinb-D1q* is unknown’.

Pathogenic Disease/ Pest Reaction

79. Reaction to *Blumeria graminus*

Pm3.
Pm3a. Sequence AY939880 {10292}.
Pm3d. Sequence AY939881 {10292}.
Pm3f. Sequence DQ071554 {10292}.

At the end of the *Pm3* section add: The *Pm3a*, *Pm3b*, *Pm3d* and *Pm3f* alleles form a true allelic series based on sequence analysis {10292}.

Pm16.	Add: 5B {10217}.	**v:**	Line 70281 = Norman /*3 Beijing 837 {10217}.
		ma:	*Pm16* - 5.3 cM - *Xgwm159-5B* (10217).

Add note: To account for the different chromosome locations a 4A-4B translocation was suggested {10217}. Based on the 5B location and similar disease responses *Pm16* and *Pm30* may be the same {10217}.

Pm30. Add note: *Pm30* could be the same as *Pm16* {10217}.

Pm33. **v:** Delete the present entry and enter the present v2 entry as v. **ma:** *Xgwm536-2B* - 18.1 cM - *Pm33* - 1.1 cM - *Xwmc317-2B* - 1.1 cM - *Xgwm111-2B* - 1.8 cM - *Xgwm383-2B* {10205}.

Pm34 {10241}.	5DL {10241}.	**v:**	PI 604033 = NC97BGTD7 = Saluda*3 / *Ae. tauschii* TA2492 {10241}.
		dv:	*Ae. tauschii* TA2492 {10241}.
		ma:	*Xbarc177-5D* - 5.4 cM - 2.6 cM - *Xbarc144-5D* {10241}.

Single resistance genes were identified on chromosome 7AL in hexaploid germplasms NC96BGTA4 (a *T. monococcum* derivative) and NC99BGTAg11 (a *T. timopheevii* subsp. *armeniacum* derivative). The genes were proximal to *Pm1* and considered to be different from each other, although possibly allelic {10274}.

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

PmPs5A {10205}.	2AL {10205}.	**v:**	AM4 {10205}.
		tv2:	*T. turgidum* subsp.. *carthlicum* pS5 *Pm33* {10205}.
		ma:	*Xgwm356-2A* - 10.2 cM - *PmPS5A*. *PmPS5A* is located at or near the *Pm4* locus {10205}.

Mlzec1 {10227}. Update symbol: previously listed in 2005 as *MlZec.* **ma:** *Xwmc356-2B* - 2.0cM - *PmZec1* {10227}.

Add general note at end of section: ‘APR to powdery mildew was completely associated with *Yr18/Lr34* in a population of Thatcher / RL6058.

XX. Reaction to *Cephus cinctus*

Insect pest: Wheat stem sawfly.
See 69: Stem solidness.

81. Reaction to *Diuraphis noxia*

Insert the relevant PI numbers and add reference '10277' for the following **i:** entries:

Dn1. Betta-Dn1: PI 634768, Tugela Dn1: PI 591932.

Dn2. Betta-Dn2: PI 634769, Karee-Dn2: PI 663774, Tugela-Dn2: PI 634772.

Dn5. Add reference 10310 to the 7DL chromosome location, i.e., 7DL {287,10310}.

Insert the following note: Issues relating to the confused arm location and mapping of *Dn5* is discussed in {10310}.

Dn8. Karee-Dn8: PI 634775.

Dn9. Betta-Dn9: PI 634770.

QTL: A QTL, *QDn.unlp.6A*, for antixenosis was associated with *Xgwm1393-6AL* and *Xgwm1150-6Al* in a CS / CS (Synthetic 6A) DH population {10216}.

82. Reaction to *Fusarium graminearum*

82.1

Fhb1 {10214}.	*QFhs.ndsu-3BS* (9925,0175}.		3BS {9925}.
	i:	Lines to be named.	
	v:	At least one reference genotype	
Fhb2 {10225}.	6B {10225}.	**v:**	2 contrasting stocks to be placed in a national germplasm collection. Please advise pedigree designations and accession numbers
		v2:	BW278 *Fhb1* {10225}.
		ma:	*Xgwm-6B* - 2.6cM - *Fhb2* – 3.1cM - *Xgwm644-6B* {10225}.

Add to notes following *Fhb1*: W14 (R) / Pioneer 2684 (S) population: QTL in 3BS and 5AS accounted for 33%, 35% and 31% of the phenotypic variation for disease spread, kernel infection and DON accumulation in greenhouse experiments, and 34% and 26% of variation for FHB incidence and severity in the field {10239}. Flanking markers were *Xbarc133-3B* & *Xgwm493-3B* and *Xbarc117-5A* & *Xbarc56-5A* {10239}.

QTL:

Dream (R) / Lynx (S) RIL population. Following inoculation with *F. culmorum* 4 QTL for AUDPC were identified on chromosomes 6AL (R^2 = 19%), 1B (12%), 2BL (11%) and 7BS (21%). The resistance allele in 1B came from Lynx and was associated with T1BL.1RS {10260}.

Insert at end of Nanda2419(S) / Wangshuibai(R): 'Type I resistance (% infected plants) in this cross was attributed to 10 chromosome regions among which *Qfhi.nau-4B* (*Xwmc349-4B* - *Xgwm149-4B* - r^2 = 0.175), *XFhi.nau-5A* (*Xwmc96-5A* - *Xgwm304-5A* -

R^2 = 0.27) and *Qfhi.nau-5B* (*Xgwm408-5B* - *Xbarc140-5B*) from Wangshuibai were detected in at least 3 of 4 years {10282}. A significant additive effect of QTL on 6D and 2A was also observed {10282}.'

Insert following Wangshuibai / Wheaton: 'Wangshuibai / Seri 82: F3:F5 population: QTL on chromosomes 3BS (*Xgwm533-3B* - *Xs18/m12-3B*) and 2DL (*Xgwm539-2D* - *Xs15/m24-2D*) accounted for 17% and 11%, respectively, of the phenotypic variance (10264).

Wangshuibai / Alondra 'S': A stable QTL was associated with *Xgwm533-3B* in each of 3 years, QTLs in 5B (*Xgwm335-5B*), 2D and 7A were detected in 2 years {10268}.'

Chokwang (R) / Clark (S):

Qfhb.ksu-5DL.1 associated with *Xbarc239-5D* (R^2 = 0.24) {10276}, *Qfhb.ksu-4BL.1* associated with *Xbarc1096-4B* (R^2 = 0.13){10276}, and *Qfhs.ksu-3BS.1* marginally associated with the region of *Fhb1* (R^2 = 0.1) {10276}.

Add at end of section: Bobwhite plants transformed with AtNPR1, an *Arabidopsis thaliana* gene that regulates activities of SAR, displayed a heritable type II response equal to that of Sumai 3 {10237}.

DH 181 (R) (Sumai 3 / HY 386 Seln.)

Type I Res.	2DS, 3AS, 3BS, 3B Cent. region, 4DL, 5AS, 6BS {10213}.

In cross Patterson (open) / Goldfield (closed) RILs, narrow flower opening width was correlated with FHB resistance. The major QTL effect associated with narrow flower opening and low FHB incidence occurred in map interval *Xbarc200* - *Xgwm210* (29% of variation in FHB incidence); these genes were probably located in chromosome 2BS {10243}.

<u>Insert before 'Field resistance:'</u>

<u>Type 1 resistance and DON accumulation</u>: Hobbit Sib / *T. macha* 4A DH population: Both traits were assigned to a small region distal to *Xgwm601-4A* and co-segregating with *Xgwm165-4A* {10254}.

New Section: Reaction to *Fusarium pseudograminearum*

Crown rot

QTL

Analysis of partial seedling resistance in a DH population of 2-49 (partially Resistant) / Janz (susceptible) indicated major QTL in chromosomes 1D (R^2 = 0.21) and 1A (R^2= 0.09) and minor QTL in 2A, 2B (from Janz), 4B and 7B {10132}.

85 Reaction to *Mayetiola destructor*

H3. Insert note after chromosome location: Based on the location of *H9* on chromosome 1AS, *H3* may also be located on chromosome 1AS {10231,10252}. **v:** Ike {10252}.

H5. **v:** Magnum {10252}.

H6. Insert note after chromosome location. Based on the location of *H9* on chromosome 1AS, *H6* may also be located on chromosome 1AS {10231,10252}.

H9. Add:‘1AS {10231,10252}.’ **ma:** *STS-Pm3* – 1.7cM - *$SOP005_{909}$* - 0.6cM - *Xksu11/Xcnl76/Xgdm33-1A* – 0.5cM - *Xgwm176/Xpsp2999/Xcfa2153-1A* - 0.5cM - *Xbarc263-1A* - 1.2cM - *H9*- *Xwmc24-1A* {10231}. *Xcfa2153-1A* - 0.5 cM - *H9* - 0.3 cM - *Xbarc263-1A* {10252}.

H10. May be identical to H9 {10252}. Add: , 1AS {10252}. **ma:** *Xcfa2153-1A* - 0.5 cM - *H10* - 1.3 cM - *Xbarc263-1A* {10252}. *Xrapd9-2-1000/Xpsp2999-1A/Xgpw7072-1A* - 2.2 cM - *H10* {10252}.

H11. Add: ,1AS {10252}. **ma:** *Xcfa2153-1A* - 0.3 cM - *H11* - 1.7 cM - *Xbarc363-1A* {10252}.

H13. Add: , 6DS {10251}. **ma:** *Xgdm36-6D* – 2.7 cM - *H13/Xcfd132-6D* - 1.1 cM - *Xcfd213-6D* {10251}.

H23. Add: , 6DS {10251}. **v:** Change to: KS89WGRC03 = TA1642 /2*Wichita {442,10251}. **al:** *Ae. tauschii* TA1642 {10251}. **ma:** Maps to same region as *H13* {10262}.

H15. Insert note after chromosome location. Based on the location of *H9* on chromosome 1AS, *H15* may also be located on chromosome 1AS {10231}.

H32. **ma:** Modify entry to: *Xgwm3-3D* - 1.7cM - *H32* - 1.7 cM - *Xcfd-3D* {10137}.

Hdic {10262}. 1AS {10262}. **v:** KS99WGRC42 {10262}. **tv:** *T. dicoccum* PI 94641 {10262}. **ma:** *Xcfa2153-1A* - 1.4 cM - *Hdic* - 0.6 cM - *Xgwm33-1A* {10262}.

H_{WGRC4} {10251}. 6DS 10251}. **v:** KS89WGRC04 = TA1695 /3*Wichita {10251}. **ma:** Allelic with *H13* {10251}.

87. Reaction to *Mycospaerella graminicola*

Stb6.		**v2:**	Kavkaz-K4500 *Stb7 Stb10 Stb12* {10011}; TE 9111 *Stb7 Stb11*{10012}.
Stb7.		**v2:**	Kavkaz-K4500 *Stb6 Stb10 Stb12* {10011}; TE 9111 *Stb6 Stb11* {10012}.
		ma:	*Stb7* was closer to *Xwmc313-4A* than to *Xwmc219-4A* {10011}.
Stb10.	1D {10011}.	Confers resistance to cultures IPO94269 and ISR8036, but not to IPO87019 {10011}.	
		v2:	Kavkaz –K4500 L.6.A.4 *Stb6 Stb7 Stb12* JIC.W9995 {10011}.
		ma:	Associated with *Xwmc848-1D* {10011}.
Stb11.	1BS {10012}.	Confers resistance to isolate IPO90012 {10012}.	
		v2:	TE 9111 {10012} *Stb6 Stb7* {10012}.
		ma:	Distal to *Xbarc008-1B* {10012}.

Stb12 {10011}.	4AL {10011}.	Confers resistance to cultures ISR398, ISR8036 and IPO87019 {10011}.	
		v2:	Kavkaz-K4500 *Stb6 Stb7 Stb10* {10011}.
		ma:	*Stb12* was closer to *Xwmc219-4A* than to *Xwmc313-4A* {10011}.

89. Reaction to *Phaeosphaeria nodorum*

Add to list of QTL: Forno (S) / Oberkulmer spelt (R). Among 204 RILs leaf and glume responses were genetically different but correlated ($R^2 = 0.52$). Ten QTL for glume blotch (SNG) were detected, 6 from Forno. A major QTL ($R^2 = 35.8\%$) was associated with *q*. Eleven QTLs (4 from Forno) affected leaf blotch; 3 of these (chromosomes 3D, 4B and 7B) with $R^2 > 13\%$ were considered potential candidates for MAS {10250}.

90. Reaction to *Puccinia graminis*

Sr22. **ma:** *Xcfa2123-7A* - 6cM - *Sr22* - 5.9 cM - *Xcfa2019-7A* {10263}.

Sr26. **ma:** A PCR marker, Sr26#43 was reported in {10257}.

Sr31. Add at end of section: *Sr31* seems to be different from the rye-derived gene in Amigo and related materials {10270}.

Genotype lists: Add ',10270'.

91. Reaction to *Puccinia striiformis*

Yr18. ***v2:*** Parula *Yr29* {10281}. **ma:** *Xgwm120-7D* - 0.9 cM - *Yr18* - 0.7 cM - *Xgwm295-7D* {10259}.

Yr29. **s:** Lalbahadur(Parula 1B) {10281}. **v2:** Attila *Yr27* {10281}; Parula *Yr18* {10281}. **ma:** *Xwmc44-1B* - 1.4 cM - *Xbac24prot* - 9.5 cM - *Yr29* - 2.9 cM - *Xbac17R........Xgwm140-1B* {10281}. *Xgwmc44-1B* - 3.6 cM - *Yr29* - 2.1 cM - *XtG818/XBac17R........Xgwm140-1B* {10281}.
Associated with *Ltn2* and *Lr46*.
Yr36. For gene name insert additional reference, i.e. {10138,10272}. **ma:** *Nor-B2****….****Xucw68-6B* - *Xucw69-6B/Xbarc101-6B/Yr36* - *Xucw66-6B* {10272}. *Yr36* is 2-4 cM proximal to *Gpc-B1* {10272}.

Yr38 {10224}.	*YrS12* {10204}.	6A (6AL-6L^{sh}•6S^{sh}) {10224}.

	v:	Line 0352-4 = *Ae. sharonensis*-174 / 9*CS // 3*W84-17 /3/ CS /4/ W84-17 {10224}.
	al:	*Ae. sharonensis*-174 {10224}.

91.2. Temporarily designated genes for resistance to stripe rust

YrCK {10220.10221}.	Temperature sensitive (10219).	2DS {10220}.	**v:**	Cook *Yr34* {10219,10220,10221}; Sunco *Yr34* {10220}.
YrCN19 {10228}.		2BS {10228}.	**v:**	AIM {10228}; AIM6 {10228}; Chuannong 19{10228}.
	ma:	Complete linkage to a 391bp allele of *Xgwm410-2BS* {10228}.		

91.3. Stripe rust QTLs

Insert as the second paragraph:

Camp Remy / Recital: 217 RILs. Six QTLs for APR were detected over 4 years. *QYr.inra-2BL* ($R^2 = 0.42 – 0.61$) corresponded largely to seedling resistance gene *Rsp* and possibly *Yr7*. The other genes were *Qyr.inra-2AL, QYr.inra-2BL, QYr.inra-2DS* (perhaps *Yr16*), *QYr.inra-5BL.1* and *QYr.inra-5BL.2* {10279}.

Insert at end of section: ‘Four QTLs were detected in a multiple cross analysis {10283}: Chromosome 2AL (probably *Yr32* in Deben, Kris and Soloist), 2AS (probably *Yr17* in Kris), 2BL (*Xwmc149-2B* – *Xwmc317a-2B* in Deben) and 6BL (*Xwmc397-6B* – *Xwmc105b-6B* in Soloist and Kris).’

92. Reaction to *Puccinia triticina*

Lr3a. **ma:** *UBC840*$_{540}$ - Lr3a, 6 cM {10263}.

Lr9. **i:** Add: Lines listed in {10244}. **ma:** Before the last entry insert: ‘SCAR markers were developed in {10244}’. The last entry in this section should appear as a separate note at the end of the *Lr9* section.

Lr13. **v2:** Add ‘*Lr46’* to genotype of Parula.

Lr19. 7DL. **i:** Sears’transfer 7D-7Ag no. 1 {10255}. **ma:** Located in the *Xwg420-7Ag* - *Xmwg2062-7Ag* interval {10255}.

Add note at end of this entry: ‘Secondary translocation line I-96 derived from Sears’ 7D-7Ag no. 1 involved *Lr19* being located in an intercalary segment with low yellow pigment and lacking *Sd1* {10255}.’

7AL. **v:** Lines I-22 and I-23 {10255}.

Add note: ‘*Lr19* in lines I-22 and I-23 retaining yellow pigment but lacking *Sd1* was transferred to durum {10255}.’

7BL. Add: One of these lines with the shortest 7Ag segment, Lr19-149-299, was used in a further cycle of recombination {10278}.

Lr20. **ma:** *Lr20 – STS638,* 7.1 cM {10263}.

Lr24. Add at end of section: ‘A PCR marker, Sr24#12 was confirmed across all sources of Lr24 {10257}.’

Lr28. **ma:** A linked RAPD marker, $S421_{640}$ was converted to a TPSCAR, $SCS421_{570}$ {10236}.

Lr34.	**v2:**	Parula *Lr13 Lr46* {1374}.	
	ma:	*Xgwm120-7D* - 0.9 cM - *Lr34* - 2.7 cM - *Xgwm295-7D* {10259}.	

Lr46.	**s:**	Lalbahadur(Parula 1B) {10281}.	**v:**	Attila {10281}.
	v2:	Parula *Lr13 Lr34* {10281}.		
	ma:	*Xwmc44-1B* - 1.4 cM - *Xbac24prot* - 9.5 cM - *Lr46* - 2.9 cM - *Xbac17R........Xgwm140-1B* {10281}. *Xwmc44-1B* - 3.6 cM - *Lr46* - 2.1 cM - *XtG818/XBac17R........Xgwm140-1B* {10281}. *XSTS1BL2* - 2.2 cM - *Lr46 / XSTS1BL9* - 2.2 cM - *XSTS1BL17* {10326}.		

Associated with *Ltn2* and *Yr29.*

Lr51. **ma:** A CAPS marker was developed from *XAga7-1B* {0308}.

Lr52. **ma:** *Lr52* - 16.5 cM - *Xgwm443-5B* {10035}.

Lr56 {10224}.	*LrS12* {10204}.	6A (6AL-$6S^{sh}$L•$6S^{sh}$S) {10224}.		
	v:	Line 0352-4 = *Ae. sharonensis*-174 / 9*CS // 3*W84-17 /3/ CS /4/ W84-17 {10224}.		
	al:	*Ae. sharonensis*-174 {10224}.		
LrKr1 {10233}.	**v:**	Thatcher {10233}.	**v2:**	Kanred *LrKr2* {10233}.
LrKr2 {10233}.	**v2:**	Kanred *LrKr1* {10233}.		
LrMq1 {10233}.	**v:**	Marquis {10233}.		

Add following the temporary designations: ‘A potentially novel resistance gene was located in chromosome 5BS of Iranian landrace PI 289824. *Xgwm234-5B* - 8.9 cM - *Lr* - 2.3 cM - STS $Xtxw_{200}$ {10253}.

Under ‘Complex genotypes’ at end of section add:

Alsen: *Lr2a Lr10 Lr13 Lr23 Lr34* {10223}.

Norm: *Lr1 Lr10 Lr16 Lr13 Lr23 Lr34* {10223}.

93. Reaction to *Pyrenophera tritici-repentis*

93.2 QTL

Grandin (S) / BR34 (R) RILs: QTL in 1BS, *QTs.fcu-1BS*,(13-29% of variation depending on race) and 3BL, (13-41%) were involved in resistance to 4 races. Five other QTL showed race specific responses {10248}.

94. Reaction to *Sitodiplosis mosellana* (Gehin)

Sm1. **ma:** Add: *Sm1* was mapped to a 2.5 cM interval on chromosome 2BS flanked proximally by AFLP-derived SCAR marker *WM1* and distally by SSR *Xgwm210-2B* {10291}.

95. Reaction to *Schizaphis graminum*

Gb4. 7DL {10267}.

Gb4 is either closely linked or allelic to *Gb3* {10267}.

Gba {10267}.	7DL {10267}.	**v:**	TA4152L94 = CETA / *Ae. taushii* Wx1027 (10267).
	ma:	*Xwmc671-7D* - 34.3 cM - *Gba* - 20.7 cM - *Xbarc53-7D* {10267}.	
Gbb {10267}.	7DL {10267}.	**v:**	TA4252L24 = CROC 1 / *Ae. tauschii* Wx224 {10267}.
	ma:	*Xwmc671-7D* - 5.4 cM - *Gbb* - 20.2 cM - *Xbarc53-7D* {10267}.	
Gbc {10267}.	7DL {10267}.	**v:**	TA4063.1 = 68111 / Rugby // Ward // *Ae. tauschii* TA2477 {10289}.
	ma:	*Xgwm671-7D* -13.7 cM - *Gbc* - 17.9 cM - *Xgdm150-7D* {10267}.	
Gbd {10267}.		**v:**	TA4064.2 = Altar 84 / *Ae. tauscii* TA2841 {10267}.
	ma:	*Xgwm671-7D* - 7.9 cM - *Gbd* - 1.9 cM - *Xwmc157-7D* {10267}.	
Gbx1 {10267}.	*Gbx* [[10267]].	7DL (10267).	
	v:	KS89WGRC4 = Wichita / TA1695 // 2*Wichita {10267}.	
	dv:	*Ae. tauschii* TA1695 {10267}.	
	ma:	*Xwmc157-7D* - 2.7 cM - *Xgdm150-7D* {10267}.	
Gbx2 {10267}.	*Gbx* [{10267}].	**v:**	W7984 [{10267}].

	ma:	*Gbx2* was located 8.8 cm from *Gb3* {10267}.

***Gbz*.** **ma:** *Xwmc671-7D* - 3.9cM - *Gbz/Xwmc157-7D* - 5.1 cM - *Xbarc53* {10267}.

QTL: A QTL, *QGb.unlp.6A*, for antixenosis was associated with *Xgwm1009-6A* and *Xgwm1185-6A* in a CS / CS (Synthetic 6A) DH population {10216}.

96. Reaction to Soil-Borne Cereal Mosaic

Syn.: Soilborne wheat mosaic.

Add at end of section: 'A major QTL, *QSbv.ksu-5D*, ($R^2 = 0.38$) was found in Karl 92*2 / TA 4152-4 {10273}; the resistance was contributed by Karl 92'.

97. Reaction to *Tapesia yallundae*

***Pch1*.** Add: **ma:** *Ep-d1b* was a more reliable marker than the STS for selecting *Pch1* {10238}.

102. Reaction to Wheat Streak Mosaic Virus

Insert introductory note: Vectored by wheat curl mites, *Eriophyes tulipae* and *E. tosichella.* See: Resistance to colonization by *Eriophyes tulipae.* According to {10226} WSMV may also be seed-borne.

101. Reaction to Wheat Spindle Streak Mosaic Bymovirus

Insert introductory note: 'WSSMV is soil-borne and vectored by the fungus *Polymxa graminis.* This virus has some sequence similarity to Wheat Yellow Mosaic {10258}.'

Wss1 {10271}. Derived from *Haynaldia villosa.* 4D = T4VS.4DL {10271}.
v: NAU413 {10271}.

XX. Reaction to Wheat Yellow Mosaic Virus

WYMV is soil-borne and vectored by the fungus *Polymxa graminis.* This virus has some sequence similarity to Wheat Spindle Streak Mosaic {10258}.

YmYF {10258}.	2DL {10258}.	**v:**	Yangfu 9311 {10258}.

	ma:	*Xpsp3039-2D/Xwmc181-2D* - 0.7 cM - *Xwmc41-3D* - 8.1 cM - *Xgwm349-2D* {10258}.

Genetic Linkages

<u>Chromosome 7AS</u>

Sr22	-	*Lr20/Sr15/Pm1*	42 cM	{10263}

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Updates:

0308.	Replace present entry with: Helguera M, Vanzetti L, Soria M, Khan IA, Kolmer J & Dubcovsky J 2005 PCR markers for *Triticum speltoides* leaf rust resistance gene *Lr51* and their use to develop isogenic hard red spring wheat lines. Crop Science 45: 728-734.
10011.	Chartrain L, Berry ST & Brown JKM 2005 Resistance of wheat line Kavkaz-K4500 l.6.A.4 to Septoria triici blotch controlled by isolate-specific resistance genes. Phytopathology 95: 664-671.
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10105.	Update: ………septoria tritici blotch in wheat. Crop Science 44: 1403-1411.
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10137.	Sardesai N, Nemacheck JA, Subramanyam S & Williams CE 2005 Identification and mapping of *H32,* a new wheat gene conferring resistance to Hessian fly. Theoretical & Applied Genetics 111: 1167-1173.
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New:	
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