CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2010 SUPPLEMENT

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Add to Designators:

stm	Matthew Hayden DPI Victorian Agrobiosciences Centre 1 Park Dr Bundoora, Vic. 3083, Australia

Morphological and Physiological Traits

5.Anthocyanin Pigmentation

The genetic determinants of anthocyanin pigmentation of various tissues are largely located in homoeologous regions in group 7, viz. 7BS (*Rc-B1, Pc-B1, Plb-B1, Pls-B1*) and 7DS (*Rc-D1, Pc-d1, Plb-D1*), and appear to be linked clusters rather than multiple alleles on each chromosome {10700}. Their relationship with genes for purple auricle and purple pericarp are still not clear.

5.2. Purple/Red auricles. Purple leaf base/sheath

Pc/Pls/Plb {10692}.	7B {10692}.	**tv:**	TRI 15744 (IPK GeneBank, Gatersleben) {10692}.
		ma:	*Xgwm951-7B* – 6.7 cM – *Pc/Pls/Plb* – 8.2 cM – *Pp1* – 8.9 cM – *Xgwm753-7B* {10692}.

5.4. Purple/red culm/straw/stem.

Pc/Pls/Plb {10692}.	**tv:**	TRI 15744 (IPK GeneBank, Gatersleben) {10692}.
	ma:	*Xgwm951-7B* – 6.7 cM – *Pc/Pls/Plb* – 8.2 cM – *Pp1* – 8.9 cM – *Xgwm753-7B* {10692}.

5.6. Purple glume

Pg {10692}.	2A {10692}.	**tv:**	TRI 15744 (IPK GeneBank, Gatersleben) {10692}.
	ma:	*Xgwm328-2A* – 19.2 cM – *Pg* – 1.4 cM – *Pp3* – 5.1 cM – *Xgwm817-2A* {10692}.	

5.7. Purple leaf blade

Plb {10692}.	7B {10692}.	**tv:**	TRI 15744 (IPK GeneBank, Gatersleben).
		ma:	*Xgwm951-7B* – 6.7 cM – *Pc/Pls/Plb* – 8.2 cM – *Pp1* – 8.9 cM – *Xgwm753-7B* {10692}.

17.Dormancy (Seed)

Pre-harvest sprouting

QTL

Insert following the Rio Blanco entry:

RL4452 (red seeded, low PHS tolerance) / AC Domain (red seeded, high PHS tolerance): DH lines: Genes associated with falling number, germination index and sprouting index contributing to PHS were located on chromosomes 3A, 4A (locus-2) and 4B in AC Domain and 3D, 4A (locus-1) and 7D in RL4452 {10671}.

SPR8198 (red seeded, PHS tolerant) / HD2329 (white seeded, PHS susceptible): RIL population: 7 QTL located on chromosomes 2AL, 2DL, 3AL and 3BL, the most important on 2AL and 3AL {10670}.

Sun325B (dormant white seeded) / QT7475 (semi-dormant white seeded), both parents with the chromosome 4A QTL: DH population: A QTL was located in the *Xgwm77-3B* – *Xwmc527-3B* interval ($R^2 = 0.19$) in the approximate region of the *R-B1* locus {10669}.

23. Frost Resistance

Fr-1.

Add as a note:

Studies using *Vrn-1* induced and natural mutants suggest that differences in frost tolerance previously associated to *Fr-1* are actually pleiotropic effects of *Vrn-1* {10708}.

26.Glaucousness (Waxiness/Glossiness)

NEW: 26.3. Spike glaucousness

Spike glaucousness is recessive {10666}.

Ws {10666}.	1AS {10666}.	**bin:**	1AS1-0.47-1.00 {10666}.
	v:	Svenno {10666}.	
	ma:	*BJ23702a* – 3.5 cM – *Tc95235* – 4.8 cM – *Bla* {10666}.	
ws {10666}.	**v:**	Ciccio {10666}.	

27.Glume Colour and Awn Colour

27.7. Awn colour

Add at end of section:

Bla1 {10666}.	1AS {10666}.	**bin:**	1AS1-0.47 {10666}.
	v: Svenno {10666}.	**ma:**	*TC95235* – 4.8 cM – *Bla1* {10666}.

29.Grain Quality Parameters

29.2. Flour, semolina and pasta colour

To the paragraph on Ph82-2 / Neixinag add:

A further study confirmed major QTL on chromosomes 1RS (R^2 = 0.319) and 7A (R^2 = 0.339); minor QTL occurred on 1A and 4A {10716}.

60.Response to Photoperiod

Ppd-D1. Add note:

Jagger amplified the 414 bp band {10466} associated with daylength sensitivity whereas 2174 amplified the 288 bp band associated with insensitivity {10722}.

63.Response to Vernalization

Replace the current preamble with:

The requirement for vernalization is particularly important for winter cereals to avoid cold injury of the sensitive floral organs during the winter. In wheat, vernalization requirement is controlled by four major genes designated *Vrn-1, Vrn-2*, *Vrn-3,* and *Vrn-4.* The first three genes were identified using map based cloning approaches {10014,10299,10421}. The *Vrn-1* gene encodes a MADS-box transcription factor closely related to the Arabidopsis *AP1 / FRUITFULL* family, responsible for the transition of the shoot apical meristem from the vegetative to reproductive stage in wheat {10014}. Deletions in the promoter (*Vrn-A1a, Vrn-A1b*) {10198} or the first intron of this gene (*Vrn-A1c*, *Vrn-B1a, Vrn-D1a*) {10202} are the most common sources of spring growth habit among landraces and commercial cultivars of polyploid wheat worldwide {10617,10695,10709}.

The *Vrn-2* locus produces two linked and related proteins designated ZCCT1 and ZCCT2, characterized by the presence of a putative zinc finger and a CCT domain {10299}. Deletions and mutations involving both the ZCCT1 and ZCCT2 genes are frequent in diploid wheat and are associated with recessive alleles for spring growth habit {10299}. Among the cultivated tetraploid and hexaploid wheat species the *Vrn-B2* gene is generally functional whereas the *Vrn-A2* gene is not {10710}. At least one functional copy of *Vrn-2* combined with homozygous recessive alleles at all three *Vrn-1* loci is required to confer winter growth habit in hexaploid wheat.

The *Vrn-B3* locus (formerly known as *Vrn-5* or *Vrn-B4*) is homologous to the Arabidopsis *FT* gene {10421}. This dominant allele, found in the variety Hope, is associated with the insertion of a transposable element in the *Vrn-B3* promoter. Natural variation at the *Vrn-A3* and *Vrn-D3* loci has been also described in hexaploid wheat {10533}. *Vrn-3* promotes the transcription of *Vrn-1* and accelerates flowering {10421}.

The *Vrn-D4* allele for early flowering was originally identified in the Australian cultivar Gabo {671} and was backcrossed into Triple Dirk to develop the isogenic line TDF {1172}. This locus was mapped on the centromeric region of chromosome 5D between markers *Xcfd78* and *Xbarc205* {10711}. Natural variation for flowering time at the centromeric region of homoeologous group 5 chromosomes has been found, so far, only in the D genome. Incorrect TDF seed stocks generated initial confusion about the existence of *Vrn-D4* but molecular markers are now available to separate the incorrect stocks {10711}. Using genetic analyses, Iwaki et al. {10003} found the *Vrn-D4* allele for spring growth habit occurred with a higher frequency in India and neighboring regions.

Vrn-1

Add to the preamble before the first gene entry:

A polymorphism between Jagger and 2174 was associated with *vrn-A1a*. A point mutation occurred in exon 4 {10695}; 17 of 19 genotypes surveyed, including Jagalene, carried the 2174 mutation and only Jagger and Overley carried the Jagger allele {10695}.

Vrn-B1a.	**c:**	GenBank AY74603.1 {10695}.
Vrn-B1b {10695}.	**v:**	Alpowa {10695}.
	c:	GenBank FJ766015. Relative to *Vrn-B1a* (Triple Dirk B), *Vrn-b1b* has a G-C SNP at position 1656 and a 36 bp deletion at 1661-1696 {10695}.
vrn-B1.	**c:**	AY747604.1 {10695}.

Vrn-1 genotypes in Pacific Northwest USA wheats are listed in {10695}.

The *Vrn3, Vrn4* and *Vrn5* sections can be replaced as follows. Some references may need to be deleted as a consequence.

Vrn3{1398}.

Replace the existing section with:

This designation was previously given to an orthologous series in homoeologous group 1 and was predicted from orthology with *Vrn-H3* (*Sh3*) in barley chromosome 1H

{1455,1316}. However, the *Vrn-H1* location proved erroneous {10421} and any genes located in homoeologous group 1 should not be designated as *Vrn3*.

Vrn4 {279}.	[*Vrn5* {771,769}, *Vrn-D5* {10004}].		5D{10002}.5DL{10004}.	
	bin:	Centromeric region.	**i:**	Triple Dirk F {10711}.
	s:	CS (Hope 7B) *VrnD1a* {768}.		
	v2:	Gabo *Vrn-B1a*{1172}. Hope *Vrn-a1a* {1424}. IL47/*Vrn-A1a*{10005}.		
	ma:	*Xgdm3*-5D – 11.5 & 4.5 cM – *Vrn4* {10004}. Located in a 1.8 cM interval flanked by markers *Xcfd78-5D* and *Xbarc205-5D* {10711}.		

Vrn4 was mapped on the centromeric region of 5D between markers
Incorrect TDF seed stocks generated confusion about *Vrn-D4* existence {10711}. Eight land races with only *Vrn4* were detected in {10003}; others combined *Vrn4* with other *Vrn* genes. Stelmakh {1424} doubted the existence of *Vrn4*. Goncharov {10108} confirmed the existence of *Vrn4* but failed to confirm its location on chromosome 5D.

Add:

***Vrn5*.** The pre- existing section can be deleted because this gene is the same as *Vrn4*.

Aneuploid and whole chromosome substitution experiments showed that all group 1 chromosomes of wheat carry genes affecting response to vernalization {773}.

At the end of entire section add:

Stem elongation in winter wheat: In regions where wheat is used as a dual purpose crop for grazing and grain production a relatively long vegetative phase is required to maximize the vegetative tissue and to delay the stem elongation phase. Variation in this attribute occurs among winter wheats such as Jagger (early stem elongation) and 2174 (late elongation).

In a Jagger / 2174 RIL population, QTL for stem elongation included *QSte.ocs-5A* (associated with the *Vrn-A1* locus, *Qste.ocs-1BL*, *Qste.ocs-2D* (associated with the *Ppd-D1* locus) and *Qste.ocs-6A* {1010}. In 2007 the respective R^2 values were 0.289, 0.155, 0.067 and 0.058. Jagger alleles on chromosomes 5A, 1B and 6A promoted stem elongation whereas the allele on chromosome 2D had a delaying effect {10722}.

Proteins

77.Proteins

77.1. Grain protein content

Enter above the heading ‘Durum’

Ning 7840 / Clark: RILs: QTLs from Ning 7840 were detected on chromosomes 3AS (*Xwmc749-3AS* – *Xgwm 369-3AS*; R^2 = 0.09 – 0.11) and 4B (*Xgwm368-4B* – *Xwmc617-4B*, R^2 = 0.08 – 0.11) {10702}.

Pathogenic Disease/Pest Reaction

78.Reaction to Barley Yellow Dwarf Virus

***Bdv3*.**	**v:**	Add: P98134 {10159}.	**ma:**	A SSR-BDV marker is described in {10159}.

Bdv3 in wheat shows distorted inheritance that varies with genetic background {10159}.

NEW SECTION. Reaction to *Bipolaris sorokiniana*

Diseases: Spot blotch and common root rot

Spot blotch

QTL

Yangmai 6 (R) / Sonalika (S): RIL population: AUDPC was controlled by four QTL derived from Yangmai 6, viz. *QSb.bhu-2AL* (*Xbarc353-2A – Xgwm445-2A*, R^2 = 0.148), *QSb.bhu-2BS* (*Xgwm148-3B – Xgwm375-2B*, R^2 = 0.205), *QSb.bhu-5BL* (*Xgwm67-5BL – Xgwm371-5BL*, R^2 = 0.386) and *QSb.bhu-6DL* (*Xbarc173-6D – Xgwm732-6DL*, R^2 = 0.225) {10719}.

79.Reaction to *Blumeria graminis* DC.

79.1. Designated genes for resistance

Pm3. Insert the following note at the end of section:

Alleles *Pm3b, Pm3d* and *Pm3f* were detected in Scandinavian varieties using allele-specific markers {10681}.

Pm40.	**v:**	Yu24 {10539}; Yu {10539}; Partial amphiploid TAI7047 {10539}.
	ma:	Replace present entry with: *Xwmc426-7B* – 5.9 cM – *Xwmc334-7B* – 0.2 cM – *Pm40* – 0.7 cM – *Xgwm297-7B* – 1.2 cM – *Xwmc364-7B* {10539}.

Add to genotype lists: Scandinavian wheats {10681}.

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

PmCn17 {10686}.	1BS = 1BL.1RS {10686}.	**v:**	Chuannong 17 {10686}.
		al:	*S. cereale* R14 {10686}.
PmHNK {10706}.	3BL {10706}.	**v:** **ma:**	Zhoumai 22 {10706}. *Xgwm108-3BL* – 10.3 cM – *PmHNK* – 3.8 cM – *Xwmc291-3BL* {10706}.

79.4. QTLs for resistance to *Blumeria graminis*

Bainong 64 (R) / Jingshuang 16 (S), DH lines: Four QTL from Bainong 64: *Qpm,caas.1A*, *Xbarc148-1A – Xwmc550-1A* interval, R^2 = 0.074-0.099; *QPm.caas-4DL* proximal to *Xwmc331-4D*, R^2 = 0.15-0.23; *QPm.caas-6BS*, proximal to *Xbarc79-6BS*, R^2 = 0.09-0.13; and *QPm.caas-7AL*, proximal to *Xbarc174-7AL*, R^2 = 0.067-0.071{10680}.

Lumai 21 (R) / Jingshuang 16 (S), F_3 lines: Three QTL from Lumai 21: *QPm.caas-2BS*, *Xbarc98-2BS – Xbarc1147-2BS* interval, R^2 = 0.106-0.206; *QPm.caas-2BL*, *Xbarc1139-2BL – Xgwm47-2BL* interval, R^2 = 0.052-0.101; and *QPm.caas-2DL*, *Xwmc18-2DL –*

Xcfd233-2DL interval, R^2 = 0.057-0.116 {10707}.

82.Reaction to *Fusarium graminearum*

82.1.Disease: Fusarium head scab, scab

Cansas / Ritmo: Add at end of section:
More detailed mapping led to the relocation of the 5B QTL to chromosome 1BL. The renamed *Qfhs.lfl-1BL* reduced FHB severity by 42% relative to lines lacking it {10698}. This gene was also present in Biscay, History and Pirat {10698}.

Soissons (relatively resistant) / Orvantis (susceptible): Soissons carried *QFhs.jic-4D* (R^2 = 0.106 – 0.161) associated with *Rht-D1a* (tall allele) {10718}. FHB susceptibility tended to be associated with the *Rht-D1b* allele (10718}. Supporting studies with NILs indicated that the presence of *Rht-B1b* led to reduced type 2 resistance relative to presence of *Rht-B1b* or the tallness alleles at both loci {10718}.

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

To follow the Kukri / Janz entry:
Lang (S) / CSCR6 (R): RIL population: tested under controlled conditions with *F. pseudograminearum* and *F. graminearum*: *Qcrs.cpi-3BL* from CSCR6, R^2 = 0.49 and *Qcrs.cpi-4B* from Lang, R^2 = 0.23 {10703}.

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

H18.	**v:**	Redland {10715}.

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

89.2. Sensitivity to SNB toxin

Tetraploid wheat Add to the present (2009) text:
In a reevaluation of this work Faris and Friesen {10688} attributed all of the variation in SNB response to the presence or absence of SnTox1.
ma: *Xbcd183-5B* – 1.2 cM – *Tsn1/Xbcd1030-5B* – 2.4 cM – *Xrz575-5B* {10688}.

90.Reaction to *Puccinia graminis* Pers.

Sr6.	**bin:**	2DS5-0.47-1.00 {10714}.
	ma:	*Sr6* – 1.1 cM – *Xwmc453-2D* – 0.4 cM – *Xcfd43-2D* {10714}.

Sr35.	**ma:**	*Sr35* was mapped to a 5.1 cM interval between *XBF483299* and *XCJ656351* in diploid wheat {10712}.	
Sr49 {10704}. 5BL {10704}.		**v:**	AUS 28011 {10704}.
		ma	*Sr49* – *Xwmc471*-5BL, 7.8 cM {10704}.

Genotype lists: {Add: ,10697}

91.Reaction to *Puccinia striiformis* Westend.

91.1. Designated genes for resistance to stripe rust

Yr4.	Undesignated allele.	The information listed below is based on the similarity of the resistance genes in Rubric and Avalon.		
	YrRub {10720}.	3BS {10720}.	**bin:**	3BS3-0.87-1.00 {10720}.
	v:	Avalon {10720}; Bolac {B008}; Emu S {10720}; Rubric AUS33333 {10720}.		
	ma:	*Yr4* – 2.9 cM – *Xcfb3530*-3B – 2.4 cM – *Xbarc75-3B* {10720}.		

The conclusion that *YrRub* is *Yr4* is based on specificity similarities and the presence of the *Xcfb3530*$_{150}$ and *Xbarc75*$_{132}$ alleles in the five genotypes listed above. The 3BS location is not consistent with that listed below for *Yr4a* and *Yr4b*.

***Yr38*.**	**v:**	Recombinants with shorter segments – 07M4-39, 07M4-157 and 07M4-175 are reported in {10691}.

Yr43 {10673}.	2BL {10673}.	**v:**	IDO377s = PI 591045 {10673}; Lolo {10673}; many IDO377s derivatives {10673}.
	ma:	*Xwms501-2B* – 11.6 cM – *Xwgp110-2B* – 4.4 cM – *Yr43* – 5.5 cM – *Xwgp103-2B* – 12.8 cM – *Xbarc139-2B* {10673}.	

Yr44 {10673}.	*YrZak* {10674}.	2BL {10674}.	**v:**	Zak = PI 607839 {10674}.
	ma:	*XSTS7/8/Yr5* – 12.7 cM – *Yr44* – 3.9 cM – *Xwgp100* – 1.1 cM – *Xgwm501-2B* {10674}.		
Yr45 {10677}.	3DL {10677}.	**v:**	PI 181434 {10677}.	
	ma:	*Xbarc6-3D* – 0.9 cM – *Xwmc656-3D* – 6.9 cM – *Xwp118-3D* – 4.8 cM – *Yr45* – 5.8 cM – *Xwp115-3D* {10677}.		

This gene is highly effective and confers resistance to all North American *Pst* pathotypes.

Yr46 {10678}.	Adult plant resistance.	4D {10678}.	
	i:	RL6077 = Thatcher*6 / PI 250413 {10678}.	
	v:	PI 250413 {10678}.	
	ma:	Close linkage with *Xcfd71-4D* and *Xbarc98-4D* estimated at 4.4 cM, and *Xcfd23-4D* at 5.2 cM (all on the same side of *Yr46*) {10678}.	
Yr47 {10679}.	5BS {10679}.	**bin:**	5BS5-0.71- 0.81.
	v:	AUS28183 = V336 {10679}.	
	ma:	5 +/- 2 cM proximal to *Lr52* {10679}.	

This is a seedling resistance gene (IT 1CN), effective against the main Australian groups of *Pst*. V336 is the original source of *Lr52*.

Yr48 {10705}.	Adult plant resistance.	5AL {10705}.	**bin:**	5AL23.
	v:	UC1110 (S) / PI 610750 RIL 167 (R) {10705}.		
	ma:	Co-segregated with *Vrn2*, Be495011, *Xcfa2149-5AL*, *Xgpw2181a-5AL*, *Xwmc74-5AL*, and *Xwmc410-5AL* {10705}. *Xwmc727-5AL* – 4.4 cM – *Yr48* – 0.3 cM – *Xwms291-5AL* {10705}.		

PI 610750 = Synthetic 205 (Croc 1 / *Ae. tauschii*) / Kauz) {10705}.

Genotype list: ……., U.K. wheats {10697}.

91.2. Temporarily designated genes for resistance to stripe rust

YrC142 {10667}.	1BS {10667}.	**v:**	Synthetic CI142 = Gaza / Boy // *Ae. tauschii* 271 {10667}.
	ma:	Located in the *Yr24/Yr26* region close to *Xbarc187-1B* and *Xgwm273-1B* {10667}.	

Although postulated to be unique this gene is likely *Yr24/Yr26*.

YrCn17 {10686}.	1BS = 1BL.1RS {10686}.	**v:** **dv:**	Chuannong 17 {10686}. *S. cereale* R14 {10686}.
YrP81 {10696}.	2BS {10696}.	**v:**	P81 {10696}; Xu29 {10696}.
	ma:	*Xgwm429-2B* – 1.8 cM – *YrP81* – 4.1 cM – *Xwmc770-2B* {10696}.	

91.3. Stripe rust QTL

Pingyuan 50 (R) / Mingxian 169 (S): DH population: APR: *QYrcaas-2BS* (*Xbarc13-2BS – Xbarc230-2BS*, R^2 = 0.05-0.09), *QYr.caas-5AL* (*Xwmc410-5AL – Xbarc261 - 5AL*, R^2 = 0.05- 0.2), *QYrcaas-6BS* (*Xgwm361-6BS – Xbarc136-6BS*, R^2 = 0.05 – 0.08) {10693}.

Renan (R) / Recital (S)RIL population: Tested for AUDPC in 1995/6 and 2005/6 with pathogen isolates avirulent and virulent, respectively, for *Yr17*: *QYr.inra-2AS.2*, (= *Yr17*), R^2 = 0.45, 1995/6; *QYr.inra-2AS.1*, R^2 = 0.9, 2005/6; *QYr.inra-2BS*, R^2 = 0.11 & 0.13, *QYr.inra-3Bcent*, R^2 = 0.06 in 2005/6; *QYr.inra-6B*, R^2 = 0.04 &0.06; from Renan; and *QYr.inra-2AS.1*, R^2 = 0.09; *QYr.inra-3DS*, R^2 = 0.08 & 0.12 from Recital. Other QTL were effective only at certain growth stages {10689}.

Express / Avocet S: RIL population: Relative AUDPC for high temperature APR was controlled by *QYrex.wgp-6AS*, R^2 = 0.326, interval *Xgwm334-6A – Xwgp56-6A*; *QYrex.wgp-3BS*, R^2 = 0.274, interval *Xgwm299-3B – Xwgp66-3B*, *QYrex.wgp.1BL*, R^2 = 0.094, interval *Xwmc631-1B – Xwgp78-1B* {10672}. When rust phenotyping was based on infection type only the 6S and 3BL QTLs were evident {10672}.

92.Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr11.	**v:**	Saluda {10699}.
Lr13.	**v2:**	Beaver *Lr26* {1032}.
Lr17		
Lr17a.	**v2:**	Fuller *Lr39* {10699}.
Lr26.	**v2:**	Beaver *Lr13* {10687}.

Lr34.	**v:**	Lantian 12 {10682}; Libellula {10682}; Strampelli {10682}.

Add to the sentence:

'STS marker csLV34 was used to confirm………..in Australian cultivars {10493}' and Hungarian materials {10701}.

Add to the notes following this entry:

Diagnostic markers based on the gene sequence are reported in {10713}; AC Domain, Cappelle Desprez, H-45, Jagger, Newton, RL 6077, and H-45 do not carry *Lr34* {10713}.

Lr39.	**v:**	Overley {10699}.	**v2:**	Fuller *Lr17a* {10699}.
***Lr56*.**		**v:**	Recombinants with shorter segments – 07M4-39, 07M4-157 and 07M4-175 – are reported in {10691}.	
Lr66.	3A = 3A-$3S^S$.	**v:**	Correct to: 07M127-3.	
Lr67 {10675}.	Adult plant resistance.	4DS {10675}.		
	i:	RL6077 = Thatcher*6 / PI 250413 {10675}.		
	v:	PI 250413 {10676}.		
	ma:	Associated with *Xcfd71-4D* {10675}. Pleiotrophic with *Yr46*. Close linkage with *Xcfd71-4D* and *Xbarc98-4D* estimated at 4.4 cM, and *Xcfd23-4D* at 5.2 cM (all on the same side of *Lr67/Yr46*) {10678}.		

Genotype lists: Under Chinese cultivars add {…, 10682}.

Add to:***LrZH84.***	**v:**	Zhoumai 11 {10682}.

92.3. QTLs for reaction to *P. triticina*

Beaver / Soissons DH population: QTL for resistance to Australian pathotypes were located on 4-6 chromosomes over 3 years; the most consistent being 1B (1BL.1RS), 4BS (proximal to *Xbarc20-4B*) and 5AS (*QTLBvr5AS,* proximal to *Xbarc10-5A*) and in the vicinity of *wPt-8756* and *wPt-1931* {10687}.

Add at end of section:

TA4152-60 / ND495 DH population: Four QTL for APR, *QLr.fcu-3AL* (*Xcfa2183-3AL* – *Xgwm666-3AL*, R^2 = 0.18), *Qlr.fcu-3BL* (*Xbarc164-3BL* – *Xfcp544-3BL*, R^2 = 0.19), *Qlr.fcu5BL*, and *Qlr.fcu-6BL* (*Xbarc5-6BL* – *Xgwm469.2-6BL*, R^2 = 0.12) were from TA4152-60 and *Qlr.fcu-4DL* (*Xgdm61-4DL* – *Xcfa2173-4DL*, R^2 = 0.13) was from

ND495 {10717}. The 3AL QTL conferred seedling resistance to all 3 races, and the 3BL gene gave race-specific seedling resistance to one race. *Qlr.fcu-3BL* was effective only in the presence of an allele associated with *Xgwm359-5DS* {10717}.

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

After the introductory paragraph add:

A review is provided in {10690}.

97.3. Resistance to tanspot

Tsr6 {10668}.	Resistance is recessive.	2BS {10668}.	
	v:	ND-735 {10688}.	
	ma:	*Xwmc382-2B* – 15.3 cM – *wPt-0289* – 4.6 cM – *Tsr6* – 18.7 cM – *Xwmc-2B* {10668}.	

According to {10668} *Tsr6* should be identical to *tsc2* (see Insensitivity to tan spot toxin (chlorosis)).

96.Reaction to Soil-Borne Cereal Mosaic

SbmTmr1 {10683}.	5D {10683}.	**v:**	TAM 107-R7 {10683}.
SBWMV {10685}.	5D {10685}.	**v:**	KS96WGRC40 {10685}.
		dv:	*Ae. tauschii* TA2397 {10685}.
	ma:	*Xcfd010-5DL* – 9.5 cM – *SBWMV* – 11.1 cM – *Xbarc144-5D* {10685}.	

The relationship of this gene to *Sbm1* is not known.

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

Bt10.	6DS {10721}.	**ma:**	*Bt10/FSD_RSA* – 19.3 cM – *Xgwm469-6D* – 1.8 cM – *Xwmc749-6D* {10721}.

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

Utd1 {10684}.	5BS {10684}.	**tv:**	D93213 {10684}; P9163-BJ08*B {10684}; VIR 51658 {10684}.
	ma:	SCAR – 3.2 cM – *Utd1* – 5.9 cM – *Xgwm234-5B* {10684}.	

102.Reaction to Wheat Streak Mosaic Virus

Wsm1.	**v:**	Mace {10694}.

Genetic Linkages

Chromosome 2BL

Yr5	-	*Yr44*	42 cM {10673,10674}.
Yr5	-	*Yr43*	65.5 cM {10673}.

Yr44	-	*Yr43*	13.1 cM {10673}.

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