CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2012 SUPPLEMENT

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Morphological and Physiological Traits

10. Boron Tolerance

Bo1.	**v:**	Additional genotypes {10833,10834}.
	tv:	Kalka {10834}; Linzhi 10834}; Niloticum {10834}; additional genotypes {10834}.
	ma:	Add: Co-dominant PCR marker AWW5L7 co-segregated with *Bo1* and was predictive of the responses of 94 Australian wheat genotypes {10833}; *Xbarc32-7B* – 2.4 cM – *Xaww5L7* – 1.2 cM – *Xbarc182-7B/Bo1* – 1.2 cM – *Xpsr680/Xmwg2062-7B* {10833}; *Xbarc32-7B* – 2.6 cM – *Xaww7L7/Bo1* {10834}.

QTL: Cranbrook (moderately tolerant) / Halberd (tolerant): DH population; QTLs for tolerance were identified on chromosomes 7B and 7D {10832}.

Add note:
For a review of boron tolerance in wheat, see {10835}.

At be beginning of the last paragraph in the exiting file insert:
<u>Boron efficiency</u>

11. Cadmium Uptake

Low uptake is dominant.

Cdu1.	Add: '; corrected to 5BL {10894}.'	**tv:**	Fanfarran {10894}.
	bin:	5BL9 0.76-0.79.	
	ma:	*Xfcp2-5B* – 12 cM – *Cdu1* – 3 cM – *ScOPC20* {10894}; *ScOPC20/Xrz575-5B/XBG608197* – 0.5 cM – *Cdu1/XbF293297/XBF474090/Os03g53590 (Xusw15-5B)* – 0.2 cM – *XBF474164* {10895}. *Cdu1* is close to *Vrn-B1* {10895}.	

cdu1.	**tv:** DT369 {10894}.

12. Chlorophyll Abnormalities

12.2. Chlorina

cn-A1a.	**i:**	ANK-32 {10820}.
cn-A1d.	**itv:**	ANW5A-7A {10820}.
Two mutants in diploid wheat are reported in {10820}.		
	ma:	Hexaploid wheat: *Xhbg234-7A* – 8.0 cM – *cn-A1* – 4.3 cM – *Xgwm282/Xgwm332-7A* {10820}; Tetraploid wheat: *Xbarc192-7A* – 19.5 cM – *cn-A1* – 11.4 cM – *Xgwm63-7A* {10820}; Diploid wheat: *Xgwm748-7A* – 29.2

		cM – *cn-A1* – 33.3 cM – *Xhbg412-7A* {10820}.

17. Dormancy (Seed)

17.1. Vivipary

Insert above the present entry for *Vp-A1*.
Alleles of *Vp-A1* were recognised using STS marker A17-19 {10919}.

Vp-A1{10919}.	3AL {10919}.				
	Vp-A1a {10919}.	**v:**	Nongda 311 { 10919}.	**c:**	599 bp {10919}.
	Higher germination index.				
	Vp-A1b {10919}.	**v:**	Wanxianbaimaizi {10919}; Yannong 15 {10919}.		
		c:	596 bp {10919}.		
	Lower germination index.				
	Vp-A1c {10919}.	**v:**	Jing 411 {10919}.	**c:**	593 bp {10919}.
	Higher germination index.				
	Vp-A1d {10919}.	**v:**	Xiaoyan 6 {10919}.	**c:**	590 bp {10919}.
	Lower germination index.				
	Vp-A1e {10919}.	**v:**	Zhengzhou 6 {10919}; Bainong 64 {10919}.		
		c:	581 bp {10919}.		
	Higher germination index.				
	Vp-A1f {10919}.	v:	Yumai 34 { 10919}	**c:**	545 bp {10919}.
	Higher germination index.				

Insert after the present *Vp-B1* entry.

Vp-D1 {10919}.	3DL {10919}.	AJ400714 {10919}.	
	Vp-D1a {10919}.	**v:**	81 Chinese wheat cultivars { 10919}.
	c:	5 pairs of primers {10919}.	

17.2. Pre-harvest sprouting

Continue under the Rio Blanco cross:
Qphs.psweru-3A was fine mapped to a 1.4 cM region flanked by two AFLP markers and was tightly linked to *Xbarc57-3A* and seven other AFLP markers {10893}.

26. Glaucousness (Waxiness/Glossiness)

26.1. Genes for glaucousness

26.2. Epistatic inhibitors of glaucousness

Add to existing comment:

Although maps constructed from three tetraploid crosses suggested that *w1* and *Iw1*^{DIC} could be at different loci, allelism of *w1, W1* and *Iw1*^{DIC} = *Vir* remain unresolved {10815}.

40. Height

40.1. Reduced Height : GA-insensitive

At end of section add:
…….are given in {10404} and those for eastern and central U.S. eastern and central winter wheat cultivars are given in {10868}.

40.2. Reduced Height : GA-sensitive

Rht8.

Add at end of section: Allele sizes for *Xgwm261* in U.S. eastern and central wheat winter cultivars are given in {10868}.

Rht14. To the note add ‘,10818’ to the reference**.**

Rht16. To the note add ‘,10818’ to the reference**.**

Rht18. To the note add ‘,10818’ to the reference**.**

Rht22 {10857}.	7AS {10857}.	**tv:**	Aiganfanmai {10857}.
	ma:	*Xgwm471-7A* – 29.5 cM – *Rht22* – 20.1 cM – *Xgwm350-7A* {10857}.	

46. Leaf Tip Necrosis

Ltn.	**c:**	Putative ABC transporter {10862}.

48. Male Sterility

48.1. Chromosomal

Ms1376 {10814}.	Sterility is dominant.	**v:**	TR1376A {10814}.
Male fertile counterpart: TR1376B {10814}. *Ms1376* was discovered among progenies of a transgenic family of Xinong 1376 containing leaf senescence-inhibiting gene P_{SAG12}-*IPT* {10814}.			

54. Nuclear-Cytoplasmic Compatibility Enhancers

scs.	Add: scs^{ti} {10878}.	**ma:**	*Xbcd1449.2-1A* – 0.6 cM – *scs* – 2.3 cM – *Xbcd12-1A* {10878}.

60. Red Grain Colour

Correct and add to the first paragraph: ‘……Himi & Noda {10107} provided evidence that the *R* genes were wheat forms of Myb-type transcription factors (*Tamyb10-3A, Tamyb10-3B* and *Tamyb10-3D*). Genetic evidence is provided in {10838}’.

R-A1.	**v:**	Rio Blanco {10839}.
	ma:	*Xwmc559-3A* – 16.3 cM – *R-A1/Xgwm155-3A* – 4.5 cM – *Xwmc153-3A* {10839}.

	R-A1a.	**ma:**	Based on *Tamyb10-A1* sequences this allele in CS lacks the ability to bind DNA due to deletion of the first half of the R2 repeat of the MYB domain {10838}. The *R-A1a* allele in Norin 17 has a 2.2 bp insertion in the second intron that appears to prevent transcription {10838}.
R-B1.	**ma:**	*Xgwm4010-3B* – 1.6 cM – *R-B1* – 4.6 cM – *Xgwm980-3B* {10839}.	
	R-B1a.	**ma:**	Based on the *Tamyb10-B1* sequence this allele in CS has a 19 bp deletion of the CCG repeat region causing a frameshift mutation {10838}.
R-D1.	**ma:**	*Xgwm2-3D* – 15.4 cM – *R-D1* – 3.2 cM – *Xgwm4306-3D* {10839}.	
	R-D1a.	**ma:**	No *Tamyb10-D1* sequence was detected in lines with this allele indicating that it may be a deletion {10838}.

Add note at the end of this section:
Functional markers based on *Tamyb10* sequences are given in {10838}.

62. Response to Photoperiod

The following sections are updated on the listing in the 2009 supplement.

Ppd-A1.

	Ppd-A1a {10612}.	**tv:**	GS100, Kofa (1027-bp deletion in the promoter) {10612}; GS105, Svevo (1117-bp deletion in the promoter) {10612}. A survey of *Ppd-A1* alleles is reported in {10915}.
GS100 and GS105 had different deletions relative to GS101 and GS104, respectively, and both were consistently a few days earlier flowering than their near-isogenic counterparts with *Ppd-A1b* {10612}.			

Ppd-B1.

	Ppd-B1a{0063}.	[*Ppd2*{1566}].	2BS {1566,1268,1269}.
	i:	H(C) = Haruhikari*5 / Fukuwasekomugi {10611}. H(D) = Haruhikari 5*/ Fukuwasekomugi *Ppd-D1a* {10611}.	
	s:	Cappelle-Desprez*/CS 2B{0058}.	
	v:	CS{1268}; Spica{557}; Timstein{1269}.	
	v2:	Sharbati Sonora *Ppd-A1a*{887}. Fukuwasekomugi *Ppd-D1a* {10611}.	
	c:	Varieties with the photoperiod insensitive allele have more than one *Ppd-B1* copy per chromosome 2B: two copies in Récital, three copies in Sonora 64, Timstein and C591, and 4 copies in Chinese Spring {10881}.	
	Ppd-B1b [{10611}],{10881}.		
	v:	Cappelle-Desprez {10881}; Cheyenne {10881}; Norstar {10881}; Renan {10881}; Paragon {10881}; Beaver {10881}.	
	v2:	Haruhikari *Ppd-D1b* [{10611}].	
	c:	Varieties with the photoperiod sensitive allele have a single *Ppd-B1* copy per chromosome 2B {10881}.	

63. Response to Salinity

63.3. Sodium exclusion

Add after Nax1 and Nax2:

QTL for Na^+ exclusion and seedling biomass under salt stress were detected in the cross Berkut/Krichauff on chromosomes 2A (*Nax1* region) and 6A (*cfd080-barc171-6A*) {10917}.

65. Response to Vernalization

Vrn-A1.

Vrn-A1.	**ma:**	*Xgwm271-5A* – 6.5 cM – *Vrn-A1* – *Xbarc232-5A* {10880}.

Insert heading:

<u>Dominant spring habit alleles at the *Vrn-A1* locus</u>

As currently listed based on the 2010 Supplement and earlier lists:

<u>Recessive winter habit alleles at the *Vrn-A1* locus</u>

	vrn-A1.	Copy number variation for *vrn-A1* was detected in IL369 (2 copies) {10202}, Malacca (2 copies) and Hereward (3 copies). Higher copy number was associated with later flowering or with increasing requirement for vernalization (i.e. longer exposure to cold is needed to achieve full vernalization) {10881}.		
	vrn-A1a [{10198}].	*vrn-A1a* {10198}.	**v:**	Claire {10880}; Triple Dirk C {10880}.
			v2:	Chinese Spring *Vrn-D1a* {10880}.
			c:	GenBank AY616455 {10198}.
	vrn-A1b {10881}.		**v:**	IL369 {10202}; Malacca {10881}.
			c:	GenBank JF965396 {10881}.
This allele has two copies of the gene, possibly arranged in tandem although the physical structure is unknown. Both copies are distinguished from Chinese Spring *vrn-A1a* by a SNP in exon 7 (T in Malacca, C in Chinese Spring). One copy also has a SNP in exon 4 (T in Malacca, C in Chinese Spring). Sequenced cDNAs from Malacca show that both copies are expressed {10881}.				
	vrn-A1c {10881}.		**v:**	Hereward {10881}.
			c:	GenBank JF965397 {10881}.
A comparison of Claire (*vrn-A1a*), Malacca {*vrn-A1b*} and Hereward (*vrn*-A1c} indicated that increasing gene copy number is associated with lateness{10881}.				
Two winter alleles were identified based on an SNP in exon 4 {10656}:				
	vrn-A1v {10916}.		**v:**	Don Ernesto INTA {10916}; Jagger {10916}; Norin 61 {10916}; Opal {10916}.
	vrn-A1w{10916}.		**v:**	Bezostaya {10916}; Bavicora M 92 {10916}; Kavkaz {10916}; Gennson 81 {10916}; Seri M 82 {10916}; Wichita {10916}.

Vrn-B1.		**ma:**	*Tsn1* – 14.8 cM – *Vrn-B1* – 0.7 cM – *Xwmc75-5B* {10880}.
	Vrn-B1c {10880}.	**tv:**	*T. turgidum* ssp. *carthlicum* PI 94749 {10880}.
		c:	GenBank JN817430, contains a 5,463 retrotransposon

			insertion in the 5’ UTR region {10880}.

Proteins

80. Proteins

80.2. Enzymes

80.2.33. Phytoene synthase

Psy-A1.			
	Psy-A1t {10920}.	v:	WAWHT2074 {10920}.
		ma:	*Xgwm344-7A* – 3.9 cM – *Psy-A1t* – 9.9 cM – *Xcfa2257a-7A* {10920}.
		c:	HM006895 {10920}.
Associated with a higher flour b* value.			

80.2.38. Flavone 3-hydroxylase (EC 1.14.11.9)

F3h-A1 {10823}.	2AL {10823}.	**v:**	CS {10823}.
	ma:	*Xgwm1067-2A* – 2.1 cM – *F3h-A1* – 11.4 cM – *Xgwm1070-2A* {10823}.	
F3h-B1 {10823}.	2BL {10823}.	**v:**	CS {10823}.
	ma:	*F3H-B1/Xgwm1067-2B* – 11.4 cM – *Xgwm1070-2B* {10823}.	
F3h-D1 {10823}.	2DL {10823}.	**v:**	CS {10823}.
	ma:	*Xgwm877-2D* – 1.8 cM – *F3h-d1/Xgwm1264-2D* – 22.7 cM – *Xgwm301-2D* {10823}.	
F3h-B2 {10823}.	2AL {10823}.	**v:**	CS {10823}.
	ma:	*Xgwm1070-2B* – 30.1 cM – *F3h-B2* {10823}. Located in the terminal region near *Xgwm1027-2B* {10823}.	

80.2.39. Zeta-carotene desaturase

Zds-A1 {10905}.	2A {10905}.	**tv:**	Langdon {10905}
Zds-B1 {10905.	2B {10905}.	**tv:**	Langdon {10905}.
Zds-D1 {10906}.	2DL {10906}.	**v:**	CS {10906}.
	Zds-D1a {10906}.	*TaZDS-D1a* 10906}.	
	v:	CA9632 {10906}. Many Chinese wheat and 80 CIMMYT lines {10906}.	
	Zds-D1b {10906}.	*TaZDS-D1b* {10906}.	
	v:	Ning 99415-8 {10906}; Zhengzhou 9023 {10906}; Zhongyou 9507 {10906}; Zhoumai 13 {10906}.	

Cv. Zhongyou 9507 has lower yellow flour pigment content, preferred for Chinese steamed bread and dry Chinese noodles. A QTL in the *Zds-D1a* region explained 18.4% of the variation in yellow pigment content in Zhongyou 9507 / CA 9632 {10906}.

80.2.40. Carotenoid beta-hydroxylase (non-heme di-iron type)

HYD are non-heme di-iron b-hydroxilases that act primarily on b-carotene

Hyd-A1 {10913}.	2AL {10913}.	**tv:**	Kronos {10913}.
		v:	UC1041 {10913}.
Hyd-B1 {10913}.	2BL {10913}.	**tv:**	Kronos {10913}.
		v:	UC1041 {10913}.
Hyd-D1 {10913}.	2DL {10913}.	**tv:**	Kronos {10913}.
		v:	UC1041 {10913}.
Hyd-A2 {10913}.	5AL {10913}.	**tv:**	Kronos {10913}.
		v:	UC1041 {10913}.
Hyd-B2 {10913}.	4BL {10913}.	**tv:**	Kronos {10913}.
		v:	UC1041 {10913}.
Hyd-D2 {10913}.	4DL {10913}.	**tv:**	Kronos {10913}.
		v:	UC1041 {10913}.

80.3. Endosperm storage proteins

80.3.1. Glutenins

80.3.1.3. Glu-3

***Glu-A3*.**

Due to an error made in an earlier update, add:

Glu-A3ax [{10116}].	6.1 {10116}.	**tv:**	Buck Cristal {10116}.
The designation of this protein (subunit 6.1) as an allele of *Glu-A3* was deduced from its electrophoretic mobility and awaits confirmation through mapping studies.			

***Glu-B3*.**

Due to an error made in an earlier update, delete:

Glu-B3z [{10116}].	6.1 {10116}.	**tv:**	Buck Cristal {10116}.

80.3.3. Other endosperm storage proteins

80.5.8. Puroindolines and grain softness protein

After the second last paragraph of notes starting ‘In *T. monococcum* the gene order…….’ Add a new paragraph:
The soft kernel trait was transferred to durum {10899}.

80.5.9 Endosperm-specific wheat basic region leucine zipper (bZIP) factor storage activator

Spa-A1 (10908}.	1AL {10909}.	**v:**	Recital {10909}.
Spa-B1 {10908}.	1BL {10909}.		**v:** Recital {10908}.
	ma:	*Glu-B1* – 1.3 cM – *Spa-B1* {10909}.	
	Spa-B1a {10908}.	**v:**	Chinese Spring {10909}; Recital {10908}; Australian

			genotypes listed in {10908}.
	Spa-B1b {10908}.	**v:**	Renan {10909}; Australian genotypes listed in {10908}.
Spa-D1 {10908}.	1DL {10909}.	**v:**	Recital {10909}.

After testing an earlier hypothesis that SPA genes affected wheat quality, analyses conducted by both {10908} and {10909} obtained no evidence supporting a significant effect and attributed any variation to the closely linked *Glu-B1* locus.

Pathogenic Disease/Pest Reaction

81. Reaction to Barley Yellow Dwarf Virus

Bdv3. Add note:
Further translocations lines with *Bdv3* are described in {10882}.

82. Reaction to *Bipolaris sorokiniana*

Sb1 {10855}.	Partial resistance.	7DS {10855,10856}.
	i:	HUW234Ltn+ {10855}.
	v:	Saar {10856}; Lines with *Lr34/Yr18/Pm38/Sr57* - see Reaction to *Puccinia triticina,* Reaction to *Puccinia striiformis,* Reaction to *Blumeria graminis,* Reaction to *Puccinia graminis,* Leaf tip necrosis.
	ma:	Pleiotropic or closely linked with *Lr34/Yr18/Pm38/Sr57* located between *Xgwm1220-7DS* and *Xswm10-7DS* (1.0 cM interval) {10856}; see also Reaction to *Puccinia triticina,* Reaction to *Puccinia striiformis,* Reaction to *Puccinia graminis* and Reaction to *Blumeria graminis.*
	c:	Putative ABC transporter {10862}.

83. Reaction to *Blumeria graminis* DC.

83.1. Designated genes for resistance

Pm3.

	Pm3a.	**v:**	Madrid {10843}; Merker {10843}; Robigus {10843}; Tabasco {10843}.
	Pm3b.	**v:**	Enorm {10843}.
	Pm3d.	**v:**	Vergas {10843}.
	Pm3e.	**v2:**	Cortez *Pm5* allele {10843}.
		m**a:**	*Pm3e* – 7.1 cM – *Xwmc818-1A* {10843}.
	Pm3f.	**v:**	Viza {10843}.

Pm21.	**bin:**	6VS 0.45-0.58 {10859}.

	ma:	Potentially useful markers are provided in {10918}.
	c:	*Pm21* is likely the serine/threonine kinase gene *Stpk-V* {10859}.

Pm31.	This gene designation {0301}is not valid; subsequent studies {10918} showed the gene was *Pm21*.

Pm46 {10847}.	Partial resistance.	4DL {10847,10678}.	
		bin:	Distal to break point 0.56 FL {10678}.
	i:	RL6077 = Thatcher*6 / PI 250413 {10847,10678}.	
	ma:	Pleiotropic or closely linked with *Lr67/Yr46/Sr55* and associated with *Xgwm165-4D* and *Xgwm192-4DL* {10847,10678}.	

Pm47 {10912}.	Recessive.	*PmHYLZ* {10912}.	7BS {10912}.	
	bin:	7BS-1 c-0.27.	**v:**	Hongyanglazi {10912}.
	ma:	*Xgpw2097-7B* – 0.9 cM – *Pm47* – 3.6 cM – *Xgwm46-7B* {10912}.		

83.2. Suppressors of *Pm*

SuPm8. Add comment following the present entry:
Pm8 was suppressed when locus *Pm3* is transcribed (including Chinese Spring and Thatcher which have no currently detectable *Pm3* resistance alleles) {10828}.

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

PmG16 {10886}.	7AL {10886}.	**bin:**	7AL16 0.86-0.90.
	tv:	*T. dicoccoides* G18-16 {10886}.	
	ma:	*Xgwm1061/Xgwm344-7A* – 1.2 cM – *PmG16/wPt-1424/wPt6019* – 2.4 cM – *wPt-0494/wPt9217/Xwmc809-7A* {10886}.	

PmHNK54 {10897}.	2AL {10897}.	**bin:**	2AL1 C-0.85.
	v:	Zheng 9754 {10897}.	
	ma:	*Xgwm372-2A* – 5 cM – *PmHNK54* – 6.0 cM – *Xgwm312-2A* {10897}.	

Ml3D32 {10892}.	5BL {10892}.	**bin:**	5BL 0.59-0.76.	
	tv:	*T. dicoccoides* I222 {10892}.	**v:**	3D232 {10892}.
	ma:	*Xwmc415-5B* – 1.3 cM – *Ml3D232* – 3.3 cM – *CJ832481* {10892}. Co-segregation with 8 EST markers including an NBS-LRR analogue {10892}.		

MlAB10 {10873}.	2BL {10873}.	**bin:**	2BL6 0.89-1.00.
	v:	NC97BGTAB10 PI 604036 {10873}.	
	tv:	*T. dicoccoides* PI 471746 {10873}.	
	ma:	*Xwmc445-2B* – 7 cM – *MlAB10* {10873}.	

New: Reaction to *Cephalosporium gramineum*

Disease: Cephalosporium stripe

QTL:
Coda (more resistant) / Brundage (less resistant): RIL population: 7 QTLs identified based on whiteheads; three from Coda – *QCs.orp-2D.1* (nearest marker *C*, $R^2 = 0.11$),

QCs.orp-2B (nearest marker *Xwmc453-2B*, $R^2 = 0.08$), and *QCs.orp-5B* (nearest marker *Xgwm639-5A*, $R^2 = 0.12$) and four from Brundage (*QCs.orp-2D.2* (nearest marker *Xbarc206-2D*, $R^2 = 0.04$), *QCs.orp-48* (nearest marker *wpt-3908,* $R^2 = 0.05$), *QCs.orp-5A.1* (nearest marker *wpt-3563*, $R^2 = 0.08$), *QCs.orp-5A.2* (nearest marker *B1*, $R^2 = 0.05$) {10836}.

87. Reaction to *Fusarium* spp.

87.1. Disease: Fusarium head scab, scab

Fhb4 {10884}.	*Qfhi.nau-4B* {10282}.	4BL {10282,108831}.		
	bin:	4BL5-0.86-1.00.	**i:**	Mianyang 99-323*4/Nanda 2419 / Wangshibai {10885}.
	v2:	Wangshuibai *Fhb5*{10884}.		
	ma:	Located in a 1.7 cM segment flanked by *Xhbg226-4B* and *Xgwm149/Xmag4580-4B* {10883}.		
Although plants with *Fhb4* were taller than the recurrent parent, the height difference was not associated with the *Rht-B1* locus {10885}.				
Fhb5 {10896}.	*Qfhi.nau-5A* {10282}.	5AS {10896}.		
	bin:	C-5AS3 0.75.	**i:**	Mianyang 99-323 and PH691 backcross derivatives selected for *Qfhi.nau-5A* {10896}.
	v2:	Wangshuibai *Fhb4* {10896}.		
	ma:	Mapped to a 0.3 cM interval between *Xbarc117/Xbarc358/ gwm293/Xgwm304-5A* and *Xgwm415-5A* {10896}.		

Ernie (I) / MO 94-317 (S): RIL population: 3 QTLs on chromosomes 3BSc, 4BL and 5AS accounted for 31 and 42% of the total phenotypic variances for DON and Fusarium damaged kernels (FDK), respectively. A minor QTL ($R^2 = 0.04$) for FDK was on chromosome 2B {10831}.

Add at end of this section:

Six of 9 NIL pairs made by MAS for *Xgwm0181-3B* earlier located near a FCR QTL on 3BL

Grandin (S) / PI 277012 (I): DH population: Two QTLs, *Qfhb.rwg-5A.1* on 5AS ($R^2 = 0.06\text{-}0.2$) and *Qfhb.rwg-5A.2* on 5AL ($R^2 = 0.12 – 0.2$) conferred type I and II resistance and reduced DON content {0147}. The new QTL on 5AL was closely but not completely linked with gene *q* which is present in PI 277012 {10860}.

Nanda 2419 / Wangshuibai: Above <u>Type IV resistance</u> add:

Backcross-derived NILs with *Qfh.nau-2B, Qfhs.nau-3B, Qfhi.nau-4B* (syn. *Fhb4*), and *Qfhi.nau-5A* were developed with Mianyang 99-323 as the recurrent parent {10884}.

Wheaton (I) / Haiyanzhong: RIL population: Four QTLs, *Qfhb.uhgl-7D* [syn. *Qhb.hyz-7D*], nearest marker *Xwmc121-7D*, $R^2 = 0.16 – 0.2$), *Qfhb.uhgl-6B.1* [*Qhb.hyz-6B.1*], $R^2 = 0.4$), *Qfhb.uhgl.6B.2* [*Qhb.hyz-6B.2*], $R^2 = 0.07$), *QFhb.uhgl-5A* [*Qhb.hyz-5A*], $R^2 = 0.04 – 0.07$) were from Haiyanzhong, and *QFhb.uhgl-1A* [*QFhb.ughl-1A*], $R^2 = 0.05$) was from Wheaton {10837}.

To the paragraph beginning: In a reciprocal backccross of Chris……….. {10398}' add: Further study of the 3A, 6A and 4D reciprocal substitution lines indicated that chromosome 3A of Frontana had the largest effect on incidence, severity, spread and kernel damage, 4D less so and 6A possibly not at all (10900}.

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

2-49 / W21MMT70: DH lines: Three QTLs for seedling resistance, viz. *QCr.usq-1D.1*, and a weaker QTL on chromosome 7A from 2-49 and *QCr.usq-3B.1* ($R^2 = 0.41$) from W22MMT70 {10883}.

Following the entry Lang (S) / CSCR6 add:
Six of 9 NIL pairs made by MAS for *Xgwm01081-3B* earlier located near the 3BL QTL {10703} in CSCR6 showed significant differences ($P<0.01$) in crown rot response {10891}.

Sunco / 2-49: DH population: Three QTLs for seedling resistance, viz. *QCr.usq-1D.1* and *QCr.usq.4B.1* ($R^2 = 0.19$) from 2-49 and *QCr.usq-2B.1I* from Sunco {10883}.

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

H26.	**bin:**	3DL3-0.81-1.00.	
	Add note:		
H26 is very close to *H32* {10846}.			
H32.	**bin:**	3DL3-0.81-1.00.	
	ma:	*Xrwgs10-3D* – 0.5 cM – *H32/Xrwgs11-3D* – 0.5 cM – *Xrwgs12-3D* {10846}.	
	Add note:		
H32 is very close to *H26* {10846}.			

Add to temporary symbols:

HNC09MDD14 [*Hf-NC09MDD14* {10844}].		6DS {10843}.	
	v:	NC09MDD14 PI 656395{10843}.	
	dv:	*Ae. tauschii* TA2492 and/or TA2377 {10843}.	
	ma:	*Xgdm36-6D* – 1.5 cM – *HNC09MDD14/Xcfd123-6D* {10843}. *HNC09MDD12* could be allelic to, but is different from, *H13* {10843}.	

91. Reaction to *Meloidogyne* spp.

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

Stb9 {10027}.		Culture IPO89011.	2BL {10027}.	
	v:	Courtot {10027}; Tonic {10027}.		
	ma:	*Xfbb226-2B* – 3 cM – *Stb9* – 9 cM – *XksuF1b-2B* {10027}.		
Stb16 [{10879}].		Seedling and adult plant resistance.	*Stb16q* {10879}.	
	3DL {10879}.	**v2:**	Synthetic W-7976 *Stb17* {10879}.	
	ma:	Associated with *Xgwm494*-3D and mapped as a QTL, $R^2 = 0.4 – 0.7$ in seedling tests and 0.28 – 0.31 in mature plants {10879}.		

Stb17 {10879}.	Adult plant resistance.	5AL {10879}.	
	v2:	Synthetic W-7976 *Stb16* {10879}.	
	ma:	Associated with *Xhbg247-5A* and mapped as a QTL, R^2 = 0.12 – 0.32 {10879}.	
Stb18 {10827}.	Confers resistance to IPO0323, IPO98022, IPO98046 {10827}.		
	6DS {10827}.	**v2:**	Balance *Stb6 Stb11* {10827}.
	ma:	Mapped as a QTL located in a 8.8 cM region spanned by *Xgpw3087-6D* and *Xgpw5176-6D* {10827}.	

QTL: Add at end of section:
Apache / Balance: Analyses with a panel of *M. graminicola* cultures identified QTLs on chromosomes 1BS (Apache, considered to be *Stb11*), 3AS (Balance, considered to be *Stb6*), 6DS (Balance, named as *Stb18*), 7DS (Apache, considered to be *Stb4*) and 7DL (Apache) {10827}.

Florett / Biscay (S): RIL population: two QTL for APR located on chromosomes 3B and 6D {10901}.

Tuareg / Biscay (S): RIL population: two QTL for APR were located on chromosomes 4B and 6B {10901}.

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

93.1. Genes for resistance

QTL
Salamouni / Katepwa: RIL population: Two QTL, *QSnb.fcu-1A* (*Snn4*) (R^2 = 0.24) and *QSnb.fcu-7A* (R^2 = 0.16) were associated with SNB response to isolate Sn99CH 1A7a {10867}.

93.2. Sensitivity to SNB toxin

Snn4. Add: **v:** Salamouni {10867}.
Snn4. Add: **v:** Katepwa {10867}.

95. Reaction to *Puccinia graminis* Pers.

Sr6.	**ma:**	Add: *Xgwm102*-2D – 0.9 cM – *Xgpw94049-2D* – 5.6 cM – *Sr6* – 1.5 cM – *Xwmc453/Xcfd43-2D* {10870}.	
Sr21.	**dv:**	After the Einkorn entry insert: Dv92 *Sr35*; G2919 *Sr35* {10876}.	
Sr22.	**bin:**	Add: 7AL-13 0.83-0.89 {10869}.	
	ma:	Add: Recombined lines with shortened introgressions from diploid wheat are reported in {10869}; the shortest was U5616020-154.	
Sr24.	**v:**	Ernest {10845}; Keene {10845}.	
	ma:	*Xbarc71-3Ag* was considered a better marker for *Sr24* than STS Sr24#12 {10845}.	
	1BL.	**tr:**	Add: Millenium {10845}.

Sr30.	**ma:**	*Xcfd12-5D* – 9.0 cM – *Sr30* – 16.6 cM – *Xgwm292-5D* {10858}.
	Add note:	
According to {10858} Webster RL6201 carries a second gene *SrW* that confers resistance to the race Ug99 group.		

Sr31.	**ma:**	*Xscm09-1R*$_{208}$ {10845}.

Sr35.	**bin:**	3AL8 0.85-1.00.	**i:**	Marquis*5/G2919 {10876}.
	dv:	DV92 *Sr21* {10876}; G2919 *Sr21* {10876}.		
	ma:	Add: Mapped in diploid wheat within to a 2.2 – 3.1 cM region between *Xbf483299* and *XCJ656351* and corresponding to a 174 kb region in *Brachypodium* {10876}.		

Sr36.	**ma:**	*Xgwm429-2B* – 0.8 cM – *Sr36/Xstm773-2/Xgwm319/Xwmc477-2B* {10824}; *Xgwm319-2B* – 0.9 cM – *Sr36/Xstm773-2/Xwmc477-2B* {10824}; Of four markers *Xwmc477-2B* was the best, but it is not a perfect marker {10845}.

Sr39.		Add note:
A Ti2BL.2BS-2SS-2BS translocation (10872} separated from *Sr47* in DAS15 could contain *Sr39* – see *SrAEs7t*.		

Sr40.	**ma:**	*Xwmc661-2B* – 6.4 cM – *Sr40* – 0.7 cM – *Xwmc344-2b* – 2.0 cM – *Xwmc477-2B* {10825}; *Xwmc661-2B* – 7.8 cM – *Sr40* – 2.5 cM – *Xwmc474-2B* – 1.0 cM – *Xwmc477-2B* {10825}.

Sr47.		Add to chromosome location: ‘,2BS {10872}’.	
Add note:		Further chromosome engineering on DAS15 showed that the alien segment carried two resistance genes. The gene on 2BL was considered to be *Sr47* based on low infection type. The second gene located in 2BS produced a low infection type similar to *Sr39* and was located in a similar position to that gene {10872}.	
	2B = 2BL-2SL-2BL.2BS	**tv:**	RWG 35 {10872}; RWG 36 {10872}.
	ma:	Located in the interval *Xgwm47-2B – Xgpw4165-2B* {10872}.	

Sr48.	Update:	**v:**	To be provided.	**v2:**	Arina *Sr56* AUS 91457{10851}.

Sr54 {10816}.	2DL {10816}.	**v2:**	Norin 40 *Sr42* {10816}.

Sr55 {10847}.	Adult plant resistance.	4DL {10847,10678}.
	bin:	Distal to break point 0.56 FL {10678}.
	i:	RL6077 = Thatcher*6 / PI 250413 {10847,10678}.
	ma:	Pleiotropic or closely linked with *Lr67* and *Yr46* and associated with *Xgwm165-4D* and *Xgwm192-4DL* {10847,10678}.

Sr56 {10851}.	Adult plant resistance.	*QSr.Sun-5BL* {10565}.		
	5BL {10565,10851}.	**bin:**	5BL16.	
	v:	AF533 {10851}.	**v2:**	Arina *Sr48* AUS 91457{0138}.

	ma:	*Xgwm118-5BL* – 13.6 cM – *wPt9116* – 5.4 cM – *Sr56* – 6.9 cM – *wPt0484* {10851}.
In the earlier QTL analysis of an Arina/Forno population *QSr.Sun*-5BL accounted for 12% of the PVE {10565}. In the present study of an Arina/Yitpi RIL population stem rust response segregated as a single gene. The response phenotype was 40-50 MS-S.		

Sr57 {10861}.	Adult plant resistance.	7DS {10861}.	
	bin:	7DS4.	
	su:	Lalbahadur(Perula7D) GID 5348503 and GID 5348496 {10861,10862}.	
	v:	Chinese Spring {10861}; Wheats with *Pm38/Lr34/Yr18*, see Reaction to *Blumeria granminis*, Reaction to *Puccinia striiformis*, Reaction to *Puccinia triticina*, Leaf tip necrosis.	
	ma:	See Reaction to *Puccinia triticina*.	
	c:	Putative ABC transporter {10862}.	
Further evidence for the effects of this gene on stem rust response can be found in {299, 10565,10733,10863,10864,10865,10866}.			

SrAes7t {10872}.	2BS = T2BL.2BS-2SS-2BS {10872}.			
	v:	Line 0797 {10872}.	**ma:**	Sr39#50s {10741,10872}.
SrAes7t may be identical to *Sr39* {10872}.				
SrWeb {10858}.	2BL {10858}.	**v2:**	Webster RL6201 *Sr30* {10858}.	
	ma:	*Xgwm47-2B* – 1.4 cM – *SrWeb* – 12.5 cM – *Xwmc332-2B* {10858}.		
Sr1RS^{Amigo} {10845}.	1AS (T1AL.1RS) {389,1624}.			
	v2:	Amigo *Sr24* {1464,10845}.	**ma:**	*Xscm09-1R*$_{224}$ {10845}.
This alien segment also carries *Pm17* – see *Pm17*.				

QTL:
RL6071 / RL6058 (R): RIL population: RL6058, a Tc backcross line with *Lr34/Sr57* is more resistant than Tc. Enhancement of resistance in both Kenya and North America was attributed to a QTL in the region *wPt5044 – Xgwm-2B* in chromosome 2BL {10902}.

96. Reaction to *Puccinia striiformis* Westend.

96.1. Designated genes for resistance to stripe rust

Yr5.	**ma:**	*Xwmc175-2B* – 1.1 cM – *YrSTS-7/8* – 0.3 cM – *Yr5* – 0.4 cM – *Xbarc349-2B* {10826}.
Yr15.	**ma:**	*Xwmc128/Xgwm273/Xgwm582-1B* – 0.4 cM – *Yr15/Xwgp34/Xgwm413/Xbarc8* {10826}.
Yr18.	**c:**	Putative ABC transporter {10862}.
Yr46.	Add note:	
Pleiotrophic or closely linked with *Sr55* and *Lr67*.		

Yr47.
Update the existing entry to the following:

Yr47 {10679}.	5BS {10679}.	**bin:**	5BS5-0.71- 0.81.
	v:	AUS28183 = V336 {10679}; AUS28187 {10679}.	
	ma:	*Xgwm234-5B* – 10.9 cM – *Lr52* – 4.1 cM – *Yr47* – 9.6 cM – *Xcfb309-5B* {10679}; *Xgwm234-5B* – 10.2 cM – *Lr52* – 3.3 cM – *Yr47* – 8.2 cM – *Xcfb309-5B* {10679}.	

Update:

Yr48 {10705}.	Adult plant resistance.	Syn. *Qyr.ucw-5AL* {10705}.	5AL {10705}.
	bin:	5AL23 0.87-1.00.	
	v:	UC1110 (S) / PI 610750 RIL 4 = GSTR 13504 & RIL 167 = GSTR 136 {10705}.	
	ma:	*Xwmc727-5AL* – 3.7 cM – *Vrn-A2* – 0.1 cM – *Yr48/BE444566-5AL/Xcfa2149-5AL/Xgpw2181a-5AL/Xwmc74-5AL/Xwmc410-5AL* {10705}.	

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

Yr50 {10849}.	Derived from *Th. intermedium.*	4BL {10849}.		
	v:	CH233 {10849}.	**ma:**	cent….*Xbarc1096-4B* – 6.9 cM – *Yr50* – 7.2 cM – *Xbarc-4B* {10849}.
Yr51 {10850}.	4AL {10850}.	**bin:**	4AL4-0.80-100.	
	v:	Line 5515 AUS 91456 {10850}.	**v2:**	AUS 27858 Gene 2 {10850}.
	ma:	*wPt4487* – 9.8 cM – *Yr51* – 4.4 cM – *wPt0763* – 7.9 cM – *Xgwm160-4B* {10850}.		
Yr52 {10852}.	Adult plant resistance.	7BL {10852}.		
	bin:	7BL-3 0.86-1.00.	**v**:	PI 183527 {10852}; PI 660057 = Avocet S / PI 183527 F4-41{10853}.
	ma:	*Xbarc182-7B* – 1.2 cM – *Yr52* – 1.1 cM – *Xwgp5258* – 5.7 cM – *Xcfa2040-7B* {10852}.		
Yr53{10854}.	2BL {10854}.	**tv:**	PI 480148 {10854}.	
	v:	Avocet S / PI 480148 F5-128{10854}.		
	ma:	*Xwmc441-2B* – 5.6 cM – *Yr53* – 2.7 cM – *XLRRrev/NLRRrev*$_{350}$ – 6.5 cM – *Xwmc149-2B* {10853}. *Yr53* was estimated to be 35 cM distal to *Yr5* based on an F2 allelism test, but on an integrated map this distance was about 20 cM.		

96.2. Temporarily designated genes for resistance to stripe rust

YrAS2388 {10822}.	**dv:**	*Ae. tauschii* AS2388 {10822}.
	ma:	*Xwmc617-4DS* – 34.6 cM – *YrAS2388* – 1.7 cM – *Xwmc285-4DS* {10822}.
YrR61 {10914}.	*QYr.uga*-2AS 10914}.	2AS {10914}.
	v:	Pioneer 26R61 = PI 612056 {10914}.
Yrxy1 {10829}.	High temperature resistance.	
	v:	Mingxian 169 / Xiaoyan 54 F$_3$-4-14 {10829}.
	v2:	Xiaoyan 54 *Yrxy2* {10829}.
	ma:	*Xbarc49-7AS* – 15.8 cM – *Yrxy1* with closer flanking RGA markers {10829}.

Yrxy2 {10829}.	High temperature resistance.		
	v:	Mingxian 169 / Xiaoyan 54 F_3-4-30 {10829}.	
	v2:	Xiaoyan 54 *Yrxy1* {10829}.	
	ma:	*Xwmc794-2AS* – 4.0 cM – *Yrxy2* – 6.4 cM – *Xbarc5-2AL* {10829}.	

96.3. Stripe rust QTLs

Pioneer 26R61 (R) / AGS2000 (S): RIL populations: Two QTLs, *QYr.uga-2AS* (R^2 = 0.56) flanked by *Xbarc124-2A* and *Xgwm359-2A* (also named *YrR61*) and *QYr.uga-6AS* (R^2 = 0.06) {10914}. Minor QTLs were also on other chromosomes.

UC1110 (MR) / PI 610750 (MR)**:** RIL population: *Qyr.ucw-3BS* ex UC1110, R^2 = 0.22, associated with *Xgwm522-3B.1*. This marker differs from *Xgwm533-3B.2* that is associated with *Yr30* {10705}; *Qyr.ucw-5AL*, R^2 = 0.1, ex PI 61075 – syn. *Yr48* {10705}; *Qyr.ucw-2BS*, R^2 = 0.045, ex UC1110, located in the centromeric region near *Xwmc474-2BS* {10705}, *Qyr.ucw-2AS*, R^2 = 0.023, ex PI 61725, near *wPt-5839* (10705}.

Stephens I / Platte (S): RIL population; 13 QTL were identified across several environments; significant QTL x environment interactions suggested that plant stage specificity, pathogen genotype and temperature as well as host genotype were important in determining rust response {10890}.

92.Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr11.	**v:**	Panola {10830}.	**v2:**	Jamestown *Lr18* {10830}.
Lr17.				
	Lr17a.	**v:**	Santa Fe {10830}.	
Lr18.	**v2:**	Jamestown *Lr11* {10830}.		
Lr19.	**v:**	Dobrynya {10821}; Ekada 6 {10821}; L505 {10821}; Samsar {0108}; Volgouralskaya {10821}.		
	v2:	Kinelskaya Niva *Lr23* {10821}.		
Lr32.	**i:**	RL6086 = Tc*7//Rl5713/Marquis K {10874}; BW196 = Katepwa*6//RL5713/2*Marquis K {10874}.		
	ma:	*Xbarc128-3D* – 9.1 cM – *Lr32* – *Xwmc43/Xbarc235-3D* {10874}.		
Lr34.	**v:**	2174 {10888}. List of U.S. hard wheats in {10888}. Pedigree charts showing the presence of *Lr34* in various Canadian wheat classes are given in {10889}.		
	ma:	Further markers for *Lr34* and various marker-positive haplotypes that lack leaf rust resistance are described in {10887,10888}.		
	c:	Putative ABC transporter, GenBank FJ436983, in CS {10862}. Further confirmation of the ABC transporter is provided in {10887}.		
Lr39.	**v:**	Postrack {10830}.		

Lr42.	Change the current listing to the following:			
	1D {218}.	**v:**	AR93005 {10840}; Fannin {10595}, but not confirmed with markers {10840}.	
	v2:	KS91WGRC11 *Lr24* {218,10840}.	**dv:**	TA2450 {218}.
	ma:	*Lr42* – 0.8 cM – *Xwmc432-1D* – 1.6 cM – *Xcfd-D1* {10840}.		

Lr48.	Add: , 2BS {10842}.	
	ma:	*Xwmc175-2B* – 10.3 cM – *Lr48* – 2.5 cM – *Xwmc332-2B* {10842}. Centromere – 27.5 cM – *Lr48* (est.) {10842}.

Lr52.	**v:**	Add: AUS28183 = V336 {10679}; AUS18187 {10679}.
	ma:	Add: *Xgwm234-5B* – 10.9 cM – *Lr52* – 4.1 cM – *Yr47* – 9.6 cM – *Xcfb309-5B* {10679}; *Xgwm234-5B* – 10.2 cM – *Lr52* – 3.3 cM – *Yr47* – 8.2 cM – *Xcfb309-5B* {10679}.

Lr58.	**ma:**	Add: A codominant STS marker *Xncw-Lr58-1* was based on the sequence of *XksuH16* {10819}.

Lr63.	Under *Lr63* change reference 10550 to 10875.	
	ma:	Replace existing text by '*Xbarc321/Xbarc57-3A* – 2.9 cM – *Lr63* {10875}.'

Lr65 {10848}.	*LrAlt* {10739}.	2AS {10739,10848}.
	v:	Selection ARK 0; {10848}; *T. spelta* Altgold Rotkorn {10739,10848}.
	ma:	*Lr65* – 1.8 cM – *Xbarc212-2A/Xwmc382-2A* – 2 cM – *Xgwm636* {10739}; *XE41M57-165* – 3 cM – *Lr65* – 2 cM – *Xbarc124/Xbarc222/Xgwm614-2A* {10848}. *Lr63* was estimated to be about 10 cM from *Lr17* {10848}.
Some plants of Altgold Rotkorn possess a second gene conferring IT 12C {10848}.		

Lr67.	Correct chromosome location to 4DL {10675}.	
	bin	C-0.53 {10675}; Distal to 0.56 {10678}.
	ma:	Replace first sentence with: *Xcfd71-4D* – 1.5 cM – *Lr67* {10675}.
Lr67 is pleiotropic or closely linked with *Sr55* and *Yr46*.		

Lr68 {10817}.		Adult plant resistance.	7BL {10817}.
	v:	Arula 1 CIMMYT GID 1847450 {10817}; Arula 2 CIMMYT GID 1847422 {10817}.	
	v2:	Parula *Lr3b Lr34 Lr46* {10817}.	
	ma:	Close linkage with several markers in chromosome arm 7BL and *Lr14b* in the Apav × Arula populations. Flanking markers are *Xpsy1-1* and *Xgwm146-7BL* at 0.4 and 0.6 cM. Gamma-irradiation induced deletion stocks of Arula 1 that lack *LrP* but have *Lr14b* were identified showing that the two genes are located at different closely linked loci {10817}.	

Lr69 {10903}.	3DL {10903}.	**v:**	Toropi-6.3 {10903}.

Lr70 {10904}.	5DS {10904}.	**v:**	Yet to be named selection of cross or backcross to Tc {10904}.

	v2:	KU3198 *LrXX* {108221}.	**ma:**	*Lr70 – Xgwm190-5D* {10904}.
LrXX is believed to be a known gene for resistance.				
Lr71 {10911}.		*LrARK12c* {10910}.	1B centromere region not resolved {10911}.	
	v:	LrARK12c = *T. spelta* Altgold Rotkorn selection {10910}. Common wheat reference line under increase {10911}.		
	ma:	*Xgwm11-1B* – 3.3 cM – *Xgwm18-1B* – 1.0 cM – *Lr71* – 1.3 cM – *Xbarc187-1B* – 0.5 cM – *Xbarc137-1B* {10911}.		

LrAlt. Delete this section.

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

98.2. Insensitivity to tan spot toxin (chlorosis)

Tsc2.	**v:**	Add: Katepwa (10871}.	**bin**	2BS3 0.84-1.00.
tsc2.	**v:**	Salamouni {10871}.	**tv:**	Altar 84 {10871}.
	ma:	*Xmag681-2B/XTC339813* – 2.7 cM – *Tsc/XBE444541* – 0.6 cM – *XBE517745* {10871}. An XBE444541 EST-STS co-segregating marker for *Tsc2* was developed and lines with *tsc2* produced a 505 bp fragment whereas those with *Tsc2* produced a 340 bp band {10871}.		

QTL
Salamouni / Katepwa: RIL population: variation at the *Tsc2* locus explained 54% of the variation in response to race DW5 {10871}.

NEW SECTION XX Reaction to *Sitobion avenae*

English grain aphid**.**

Sa1 [{10877}].	*RA-1* {10877}.	6AL {10877}.	**tv:**	C273 {10877}.
	ma:	*Xwmc179-6A* – 3.37 cM – *Sa1* – 4.73 cM – *Xwm580-6A* {10877}.		

99. Reaction to *Sitodiplosis mosellana* (Gehin)

Add:

QTL:

Reeder I / Conan: RIL population: *QSm.mst-1A*, flanked by *Xwmc59-1A* and *Xbarc1022-1A* was the most effective and constant QTL for reduced larval infection over two years (R^2 = 0.17 and 0.34) {10841}. RILs with this QTL in three genetic backgrounds had reduced infestations of 42% {10841}.

100. Reaction to *Schizaphis graminum* Rond. (*Toxoptera graminum* Rond.)

Gb3.	**bin**:	7DL3 0.82-1.00.	**v:**	TAM 112 {0194}.
	tv:	*Ae. tauschii* PI 268210 {10907}.		
	ma:	At the end of the present entry add: ….. – 0.8 cM – *Xbarc76-7D* {10169}. *H1067J6-R* – 0.7 cM – *Gb3* – 0.4 cM – *H1009B3-F* {10907}.		

107. Reaction to Wheat Streak Mosaic Virus

Wsm2 {10802,10898}.		**v:**	RonL {10898}.
	ma:	*Xgwm389-3B* – 30.8 cm – *Wsm2* – 45.2 cM – *Xgwm566-3B* {10898}.	

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