V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2012 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 11th International Wheat Genetics Symposium held in Brisbane, Australia, and the 2009, 2010, and 2011 Supplements (Annual Wheat Newsletter 55:256-278; 56:256-278; 57:303-321) are available from the Komugi (http://www.shigen.nig.ac.jp/wheat/komugi/top/top.jsp) and GrainGenes (http://wheat.pw.usda.gov/GG2/Triticum/wgc/2008/) websites. The Wheat Gene Catalog is not included as part of the IWGS proceedings and, therefore, cannot be cited as part of them.

Laboratory Designators

\textit{Iwa} iSelect 9,000 SNP wheat chip A
Wheat SNP consortium
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10. Boron Tolerance

*Bol.*

**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 *Bol* and was predictive of the responses of 94 Australian wheat genotypes {10833}: *Xbarc32-7B* – 2.4 cM – *Xaww5L7* – 1.2 cM – *Xbarc182-7B/Bol* – 1.2 cM – *Xpsr680/Xmww2062-7B* {10833}.

**ma:** *Xbarc32-7B* – 2.6 cM – *Xaww7L7/Bol* {10834}.

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

**Add note:**

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

At the beginning of the last paragraph in the exiting file insert:

**Boron efficiency**

11. Cadmium Uptake

Low uptake is dominant.

**Cdul.**

**Add:** ‘; corrected to 5BL {10894}.’

**tv:** Fanfarran {10894}.

**bin:** 5BL9 0.76-0.79.

**ma:** *Xfcp2-5B* – 12 cM – *Cdul* – 3 cM – *ScOPC20* {10894}; *ScOPC20/Xrz575-5B/XBG608197* – 0.5 cM – *Cdul/XbF293297/XRF474090/Os03g53590 (Xusw15-5B)* – 0.2 cM – *XBF474164* {10895}.

*Cdul* is close to *Vrn-B1* {10895}.

**cdul.**

**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}.


17. Dormancy (Seed)

17.1. Vivipary

Insert above the present entry for *Vp-A1*.

Alleles of *Vp-A1* were recognized 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.
Higher germination index.

**Vp-A1f** \{10919\}.  
\textbf{v}: Yumai 34 \{10919\}  
\textbf{c}: 545 bp \{10919\}.  
Higher germination index.

Insert after the present \textit{Vp-B1} entry.

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

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

26. \textbf{Glaucousness (Waxiness/Glossiness)}  
26.1. \textbf{Genes for glaucousness}  
26.2. \textbf{Epistatic inhibitors of glaucousness}  
Add to existing comment:  
Although maps constructed from three tetraploid crosses suggested that \textit{w1} and \textit{Iw1} could be at different loci, allelism of \textit{w1}, \textit{W1}, and \textit{Iw1} = \textit{Vir} remain unresolved \{10815\}.

40. \textbf{Height}  
40.1. \textbf{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. \textbf{Reduced Height : GA-sensitive}  
\textit{Rht8}.  
Add at end of section:  
Allele sizes for \textit{Xgwm261} in U.S. eastern and central wheat winter cultivars are given in \{10868\}.  

\textbf{Rht14}.  
To the note add ‘10818’ to the reference.  

\textbf{Rht16}.  
To the note add ‘10818’ to the reference.  

\textbf{Rht18}.  
To the note add ‘10818’ to the reference.  

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

46. \textbf{Leaf Tip Necrosis}  
\textit{Ltn}.  
\textbf{c}: Putative ABC transporter \{10862\}.

48. \textbf{Male Sterility}  
48.1. \textbf{Chromosomal}  
\textit{Ms1376} \{10814\}.  
Sterility is dominant.  
\textbf{v}: \textit{TR1376A} \{10814\}.  
Male fertile counterpart: TR1376B \{10814\}.  
\textit{Ms1376} was discovered among progenies of a transgenic family of Xinong 1376 containing the leaf senescence-inhibiting gene \textit{P}_{\textit{SAG12-IPT}} \{10814\}.  

\begin{verbatim}  
261  
\end{verbatim}
54. Nuclear-Cytoplasmic Compatibility Enhancers

Add: \(\text{scs}^a\) {10878}.

\[\text{ma: } Xbcd1449.2-1A - 0.6 \text{ cM - scs} - 2.3 \text{ cM - } Xbcd12-1A\]
{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.**

**R-A1a.**

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.**

**R-B1a.**

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.**

**R-D1a.**

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}.

**Ppd-B1.**

**Ppd-B1a** {0063}.

**Ppd-B1b** {10811}.

**Ppd-D1.**

**Ppd-D1a** {10611}.

Functional markers based on \(Tamyb10\) sequences are given in {10838}.
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.**


Insert heading:
Dominant spring habit alleles at the Vrn-A1 locus
As currently listed based on the 2010 Supplement and earlier lists:

Recessive winter habit alleles at the Vrn-A1 locus

**vrn-A1.** Copy number variation for vrn-A1 was detected in IL369 (two copies) {10202}, Malacca (two copies) and Hereward (three 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.**

**Vrn-B1c** {10880}. ma: Tsn1 – 14.8 cM – Vrn-B1 – 0.7 cM – Xwmc75-5B {10880}.

tv: T. turgidum subsp. 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-A1t {10920}.

\[
\begin{align*}
\text{v:} & \text{ WAWHT2074 (10920).} \\
\text{ma:} & \text{ Xgwm344-7A – 3.9 cM – Psy-A1t – 9.9 cM – Xcfa2257a-7A (10920).} \\
\text{c:} & \text{ HM006895 (10920).}
\end{align*}
\]

Associated with a higher flour \(b^*\) value.

80.2.38. Flavone 3-hydroxylase (EC 1.14.11.9)

\[
\begin{align*}
F3h-A1 & \{10823\}. \quad 2\text{AL} \{10823\}. \quad \text{v:} \text{ CS (10823).} \\
\text{ma:} & \text{ Xgwm1067-2A – 2.1 cM – F3h-A1 – 11.4 cM – Xgwm1070-2A (10823).}
\end{align*}
\]

\[
\begin{align*}
F3h-B1 & \{10823\}. \quad 2\text{BL} \{10823\}. \quad \text{v:} \text{ CS (10823).} \\
\text{ma:} & \text{ F3H-B1/Xgwm1067-B1 – 11.4 cM – Xgwm1070 (10823).}
\end{align*}
\]

\[
\begin{align*}
F3h-D1 & \{10823\}. \quad 2\text{DL} \{10823\}. \quad \text{v:} \text{ CS (10823).} \\
\text{ma:} & \text{ Xgwm877-2D – 1.8 cM – F3h-d1/Xgwm1264-2D – 22.7 cM – Xgwm301-2D (10823).}
\end{align*}
\]

\[
\begin{align*}
F3h-B2 & \{10823\}. \quad 2\text{AL} \{10823\}. \quad \text{v:} \text{ CS (10823).} \\
\text{ma:} & \text{ Xgwm1070-2B – 30.1 cM – F3h-B2 (10823). Located in the terminal region near Xgwm1027-2B (10823).}
\end{align*}
\]

80.2.39. Zeta-carotene desaturase

\[
\begin{align*}
Zds-A1 & \{10905\}. \quad 2\text{A} \{10905\}. \quad \text{tv:} \text{ Langdon (10905).}
\end{align*}
\]

\[
\begin{align*}
Zds-B1 & \{10905\}. \quad 2\text{B} \{10905\}. \quad \text{tv:} \text{ Langdon (10905).}
\end{align*}
\]

\[
\begin{align*}
Zds-D1 & \{10906\}. \quad 2\text{DL} \{10906\}. \quad \text{v:} \text{ CS (10906).} \\
\text{TaZDS-D1a} & \{10906\}. \quad \text{v:} \text{ CA9632 (10906). Many Chinese wheat and 80 CIMMYT lines (10906).}
\end{align*}
\]

\[
\begin{align*}
Zds-D1b & \{10906\}. \quad \text{TaZDS-D1b (10906).} \\
\text{v:} & \text{ Ning 99415-8 (10906); Zhengzhou 9023 (10906); Zhongyou 9507 (10906); Zhoumai 13 (10906).}
\end{align*}
\]

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

\[
\begin{align*}
\text{Hyd-A1} & \{10913\}. \quad 2\text{AL} \{10913\}. \quad \text{tv:} \text{ Kronos (10913).} \\
\text{v:} & \text{ UC1041 (10913).}
\end{align*}
\]

\[
\begin{align*}
\text{Hyd-B1} & \{10913\}. \quad 2\text{BL} \{10913\}. \quad \text{tv:} \text{ Kronos (10913).} \\
\text{v:} & \text{ UC1041 (10913).}
\end{align*}
\]

\[
\begin{align*}
\text{Hyd-D1} & \{10913\}. \quad 2\text{DL} \{10913\}. \quad \text{tv:} \text{ Kronos (10913).} \\
\text{v:} & \text{ UC1041 (10913).}
\end{align*}
\]

\[
\begin{align*}
\text{Hyd-A2} & \{10913\}. \quad 5\text{AL} \{10913\}. \quad \text{tv:} \text{ Kronos (10913).} \\
\text{v:} & \text{ UC1041 (10913).}
\end{align*}
\]
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:
\[ \text{Glu-A3ax} \quad \{10116\} . \quad 6.1 \quad \{10116\} . \quad \text{tv: Buck Cristal} \quad \{10116\} . \]
The designation of this protein (subunit 6.1) as an allele of \( \text{Glu-A3} \) was deduced from its electrophoretic mobility and awaits confirmation through mapping studies.

Glu-B3.
Due to an error made in an earlier update, delete:
\[ \text{Glu-B3z} \quad \{10116\} . \quad 6.1 \quad \{10116\} . \quad \text{tv: Buck Cristal} \quad \{10116\} . \]

80.3.3. Other endosperm storage proteins
80.5.8. Puroindolines and grain softness protein
After the second last paragraph of notes starting ‘In \( T. \text{monococcum} \) 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
\( \text{Spa-A1} \quad \{10908\} . \quad 1\text{AL} \quad \{10909\} . \quad \text{v: Recital} \quad \{10909\} . \)
\( \text{Spa-B1} \quad \{10908\} . \quad 1\text{BL} \quad \{10909\} . \quad \text{v: Recital} \quad \{10908\} . \quad \text{ma: Glu-B1} - 1.3 \text{ cM} - \text{Spa-B1} \quad \{10909\} . \)
\( \text{Spa-B1a} \quad \{10908\} . \quad \text{v: Chinese Spring} \quad \{10909\} ; \text{Recital} \quad \{10908\} ; \text{Australian genotypes listed in} \quad \{10908\} . \)
\( \text{Spa-B1b} \quad \{10908\} . \quad \text{v: Renan} \quad \{10909\} ; \text{Australian genotypes listed in} \quad \{10908\} . \)
\( \text{Spa-D1} \quad \{10908\} . \quad 1\text{DL} \quad \{10909\} . \quad \text{v: Recital} \quad \{10909\} . \)

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 \( \text{Glu-B1} \) locus.

Pathogenic Disease/Pest Reaction

81. Reaction to Barley Yellow Dwarf Virus
\( \text{Bdv3} \). Add note:
Further translocations lines with \( \text{Bdv3} \) are described in \( \{10882\} . \)

82. Reaction to Bipolaris sorokiniana
\( \text{Sbl} \quad \{10855\} . \quad \text{Partial resistance.} \quad 7\text{DS} \quad \{10855,10856\} . \quad \text{i:} \quad \text{HUW234Ltn+} \quad \{10855\} . \quad \text{v:} \quad \text{Saar} \quad \{10856\} ; \text{Lines with} \quad \text{Lr34/Yr18/Pm38/Sr57} – \text{see Reaction to} \quad \text{Puccinia triticina}, \quad \text{Reaction to} \quad \text{Puccinia striiformis}, \quad \text{Reaction to} \quad \text{Blumeria graminis}, \quad \text{Reaction to} \quad \text{Puccinia graminis}, \quad \text{and Leaf tip necrosis.} \)
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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}.

ma: 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. PmHLYZ {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}.

bin: 7AL16 0.86-0.90.

tv: T. turgidum subsp. 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}.

bin: 2AL1 0.85.

ma: Xgwm372-2A – 5 cM – PmHNK54 – 6.0 cM – Xgwm312-2A {10897}.
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**MI3D32** (10892).

- **bin:** 5BL 0.59-0.76.
- **tv:** *T. turgidum* subsp. *dicoecoides* I22 (10892).
- **ma:** Xwmc415-5B – 1.3 cM – MI3D32 – 3.3 cM – CJ832481 (10892).
- **v:** 3D232 (10892).
- **ml3d32:** 5BL 0.59-0.76.

**MIAB10** (10873).

- **bin:** 2BL 0.89-1.00.
- **tv:** NC97BGTAB10 PI 604036 (10873).
- **ma:** Xwmc445-2B – 7 cM – MIAB10 (10873).
- **v:** NC97BGTAB10 PI 604036 {10873}.
- **tv:** *T. turgidum* subsp. *dicoccoides* PI 471746 (10873).
- **ma:** Xwmc445-2B – 7 cM – MIAB10 (10873).

**New: Reaction to Cephalosporium gramineum**

**Disease: Cephalosporium stripe**

**QTL:**

‘Coda (more resistant) / Brundage (less resistant)’; RIL population: seven QTL 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 Xgwm639-5A, R^2 = 0.12) and **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).
- **bin:** 4BL 0.86-1.00.
- **i:** ‘Mianyang 99-323*4/Nanda 2419/Wangshibai’ (10885).
- **v:** ‘Wangshuibai Fhb5’ (10884).
- **ma:** Located in a 1.7-cM segment flanked by Xhbg226-4B and Xgwm149/Xmag4580-4B (10883).
- **Fhb5** (10896).

- **Qfhi.nau-5A** (10282).
- **bin:** 5AS 0.75.
- **i:** Mianyang 99-323 and PH691 backcross derivatives selected for **Qfhi.nau-5A** (10896).
- **v:** ‘Wangshuibai Fhb4’ (10896).
- **ma:** Mapped to a 0.3-cM interval between Xbarc117/Xbarc358/gwm293/Xgwm304-5A and Xgwm415-5A (10896).

Although plants with *Fhb4* were taller than the recurrent parent, the height difference was not associated with the *Rht-B1* locus (10885).

‘Ernie (I) / MO 94-317 (S)’: RIL population: three QTL 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 nine NIL pairs made by MAS for Xgwm0181-3B earlier located near a FCR QTL on 3BL.

‘Grandin (S) / PI 277012 (I)’: DH population: Two QTL, **Qfhhwbw-5A.1** on 5AS (R^2 = 0.06-0.2) and **Qfhhwbw-5A.2** on 5AL (R^2 = 0.12–0.20) 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 Type IV resistance add:

Backcross-derived NILs with **Qfhhwbw-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 QTL, **Qfhrwgl-7D** (syn. *Qhb.hyz-7D*), nearest marker Xwmc121-7D, R^2 = 0.16–0.20), **Qfhrwgl-6B.1** *(Qhb.hyz-6B.1)*, R^2 = 0.4), **Qfhrwgl-6B.2** *(Qhb.hyz-6B.2)*, R^2 = 0.07), and **Qfhrwgl-5A** *(Qhb.hyz-5A)*, R^2 = 0.04–0.07) were from Haiyanzhong, and **Qfhrwgl-1A** *(Qfhrwgl-1A)*, R^2 = 0.05) was from Wheaton (10837).
To the paragraph beginning: In a reciprocal backcross 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 QTL for seedling resistance, viz. *QCr.usq-1D.1*, and a weaker QTL on chromosome 7A from 2-49 and *QCr.usq-3B.1* (R² = 0.41) from W22MMT70 {10883}.

Following the entry ‘Lang (S) / CSCR6’ add: Six of nine 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 QTL for seedling resistance, viz. *QCr.usq-1D.1* and *QCr.usq.4B.1* (R² = 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: *Xrws10-3D* – 0.5 cM – *H32/Xrws11-3D* – 0.5 cM – *Xrws12-3D* {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}.


*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, R² = 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, R² = 0.12–0.32 {10879}.

*Stb18* {10827}.

6DS {10827}.

Confers resistance to IPO0323, IPO98022, IPO98046 {10827}.

v2: Balanced *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 QTL 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}.

93.1. 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: |

95. Reaction to *Puccinia graminis* Pers.

**Sr6.**
| ma:  | Add: Xgwm102-2D – 0.9 cM – Xgwpw4049-2D – 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. | Add: Millenium {10845}. |

**Sr30.**
| ma:  | Xcfij12-5D – 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_{286} {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 = T2BL-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 {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}. 5BL {10856,10851}.
bin: 5BL16.
v: AF533 {10851}.
v2: Arina Sr48 AUS 91457 {10138}.
ma: Xgwm118-5BL – 13.6 cM – wPt9116 – 12.5 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 Pm/Lr34/Yr18, see Reaction to Blumeria graminis, 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}.

Sr1RSamigo {10845}. 1AS (T1AL·1RS) {389,1624}.
v2: Amigo Sr24 {1464,10845}.
ma: Xscm09-1R224 {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}. 5AL {10679}.

bin: 5BS5-0.71 - 0.81.

v: AU528183 = V336 {10679}; AU528187 {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}.

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/BE44456-5AL/Xcfa2149-5AL/ Xgwp2181a-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}.

v: Line 5515 AUS 91456 {10850}.

ma: *wPt4478* – 9.8 cM – *Yr51* – 4.4 cM – *wPt0763* – 7.9 cM – *Xgwm160-4B* {10850}.

**Yr52** {10852}. Adult-plant resistance.

7BL {10852}.

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}.

v: ‘Avocet S / PI 480148’ F5-128 {10854}.

ma: *Xwmc441-2B* – 5.6 cM – *Yr53* – 2.7 cM – *XLRRrev/NLRRrev*_{150} – 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’ F3-4-14 {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’ F3-4-30 {10829}.
\[ v2: \] Xiaoyan 54 Yrxy1 {10829}.
\[ ma: \] Xwmc794-2AS – 4.0 cM – Yrxy2 – 6.4 cM – Xbarc5-2AL {10829}.

96.3. Stripe rust QTL
‘Pioneer 26R61 (R) / AGS2000 (S)’: RIL populations: Two QTL, QYr.uga-2AS (R² = 0.56) flanked by Xbarc124-2A and Xgwm359-2A (also named YrR61) and QYr.uga-6AS (R² = 0.06) {10914}. Minor QTL were also on other chromosomes.

‘UC1110 (MR) / PI 610750 (MR)’: RIL population: Qyr.ucw-3BS ex UC1110, R² = 0.22, associated with Xgwm522-3B.1. This marker differs from Xgwm533-3B.2 that is associated with Yr30 {10705}; Qyr.ucw-2BS, R² = 0.045, ex UC1110, located in the centromeric region near Xwmc474-2BS {10705}; and Qyr.ucw-2AS, R² = 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 // RIS713 / 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.  
\[ v: \] Postrock {10830}.

Lr42.  
\[ v: \] 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.  
\[ ma: \] Xwmc175-2B – 10.3 cM – Lr48 – 2.5 cM – Xwmc332-2B {10842}.  
Centromere – 27.5 cM – Lr48 (est.) {10842}.

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\textbf{Lr52.} \hspace{1cm} \textbf{v:} Add: AUS28183 = V336 \{10679\}; AUS18187 \{10679\}.
\textbf{ma:} Add: Xgwm234-5B – 10.9 cM – Lr52 – 4.1 cM – Yr47 – 9.6 cM – Xcgb309-5B \{10679\}; Xgwm234-5B – 10.2 cM – Lr52 – 3.3 cM – Yr47 – 8.2 cM – Xcgb309-5B \{10679\}.

\textbf{Lr58.} \hspace{1cm} \textbf{ma:} A codominant STS marker Xncw-Lr58-1 was based on the sequence of XksuH16 \{10819\}.

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

\textbf{Lr65 \{10848\}.} \hspace{1cm} \textbf{LrAlt \{10739\}.} \hspace{1cm} \textbf{2AS \{10739,10848\}.} \hspace{1cm} \textbf{v:} Selection ARK 0; \{10848\}; \textit{T. aestivum} subsp. \textit{spelta} Altgold Rotkorn \{10739,10848\}.
\textbf{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\}.

Some plants of Altgold Rotkorn possess a second gene conferring IT 12C \{10848\}.

\textbf{Lr67.} Correct chromosome location to 4DL \{10675\}.
\textbf{bin:} C-0.53 \{10675\}; Distal to 0.56 \{10678\}.
\textbf{ma:} Replace first sentence with: ‘Xcfd71-4D – 1.5 cM – Lr67 \{10675\}.

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

\textbf{Lr69 \{10903\}.} \hspace{1cm} \textbf{3DL \{10903\}.} \hspace{1cm} \textbf{v:} Toropi-6.3 \{10903\}.

\textbf{Lr70 \{10904\}.} \hspace{1cm} \textbf{5DS \{10904\}.} \hspace{1cm} \textbf{v:} Yet to be named selection of cross or backcross to Tc \{10904\}.
\textbf{v2:} KU3198 LrXX \{108221\}. \hspace{1cm} \textbf{ma:} \textit{Lr70} – \textit{Xgwm190-5D} \{10904\}.

\textit{LrXX} is believed to be a known gene for resistance.

\textbf{Lr71 \{10911\}.} \hspace{1cm} \textbf{LrARK12c \{10910\}.} \hspace{1cm} \textbf{1B centromere region not resolved \{10911\}.} \hspace{1cm} \textbf{v:} LrARK12c = \textit{T. aestivum} subsp. \textit{spelta} Altgold Rotkorn selection \{10910\}. Common wheat reference line under increase \{10911\}.
\textbf{ma:} Xgwm11-1B – 3.3 cM – Xgwm18-1B – 1.0 cM – Lr71 – 1.3 cM – Xbarc187-1B – 0.5 cM – Xbarc137-1B \{10911\}.

\textbf{LrAlt.} \hspace{1cm} \textbf{Delete this section.}

\textbf{98. Reaction to \textit{Pyrenophora tritici-repentis} (anomorph: \textit{Drechlera tritici-repentis})}

\textbf{98.2. Insensitivity to tan spot toxin (chlorosis)}

\textbf{Tsc2.} \hspace{1cm} \textbf{v:} Add: Katepwa \{10871\}. \hspace{1cm} \textbf{bin:} 2BS3 0.84-1.00.
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.
Sal1 \{(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.

107. Reaction to Wheat Streak Mosaic Virus

Wsm2 \{10802,10898\}.

References

Updates


10673. Theoretical and Applied Genetics 121: 195-204.


10816. Hiebert C 2011 Personal communication.


10834. Schnurbusch T, Langridge P & Sutton T 2008 The BoI-specific PCR marker AWWSL7 is predictive of boron tolerance status in a range of exotic durum and bread wheats. Genome 51: 963-971.


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10861. Singh RP et al. Lr34/Yr18/Pm38/Ltn1 confers slow rusting, adult plant resistance to Puccinia graminis f.sp. tritici. Manuscript in preparation.


A n n u a l  W h e a t  N e w s l e t t e r  V o l .  5 8


10913. Dubcovsky JD 2012 Personal communication.


