VI. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2008 SUPPLEMENT

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INTRODUCTION

9. Laboratory Designators

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Gene Symbol

Add to gene symbols list:

Vil. VIN3-like genes similar to Arabidopsis VIN3.

1. Gross Morphology: Spike characteristics

1.1. Squarehead/spelt

Q. **v:** Iranian spelts {0140}. **tv:** *T. turgidum* ssp. *carthlicum, durum* and *polonicum* {10457}.
ma: *Q* was cloned and shown to have similarity to *AtAP2* (APETALA 2) transcription factors {10457}, the *Q* allele was more abundantly transcribed than the *q* allele {10457}.

q. **v:** Insert 'European' in front of 'spelt' and add reference {10457}, i.e., 'European spelts {10457}'.
tv: *T. turgidum* ssp. *dicoccum, dicoccoides* {10457}.

4. Aluminium Tolerance

Insert before the QTL section:
Allelic variation at the promoter of *Almt-D1* is associated with differences in Al tolerance. Molecular and pedigree analysis suggest that Al resistance in modern wheat germ plasm is derived from several independent sources {10532}.

Add to QTL:
'Atlas 66 (insensitive)/Chisholm (sensitive)' RILs. One QTL, located in chromosome 4DL, corresponded to ALMT1 and accounted for 50% of the phenotypic variation {10483}. A second QTL was located on 3BL ($R^2 = 0.11$); nearest marker *Xbarc164-3B* {10483}. Both QTL were verified in 'Atlas/Century' {10483}.

5. Anthocyanin Pigmentation

5.3. Red/purple coleoptiles.

Rc-A1. Rc {10451}[3]. 7AS[3] {10451}. **dv:** PAU14087 {10451 }.
ma: *Xcfa2174-7AS* – 11.1 cM – *Rc-A1* – 4.3 cM – *Xgwm573-7AL/Xwmc17-7AL* { 10451}[3].

8. Blue Aleurone

Ba2. *Ba* {10451}. **dv:** PAU5088 = G2610 = PI 427389 {10451}.
ma: *Xcfd71-4A* – 10.3 cM – *Ba* – 16.5 cM – *Xcfa2173-4A* {0802}[3].

10. Boron Tolerance

Bo1. Add: 7BL {10460}. **v:** Carnamah {10460}**;** Frame {10460}; Krichauff {10460}; Yitpi {10460}.
ma: *Bo1* co-segregated with several STS-PCR markers, including *Xaww11-7BL*, falling within a 1.8 cM interval {10460}. The AWW7L7 (*Xaww11*) PCR marker allele was a good predictor of boron tolerance {10460}.

17. Dormancy (Seed)

Seed dormancy in wheat has several components, including factors associated with vivipary and red grain colour. Dormancy is an important component of resistance/tolerance to preharvest sprouting (PHS).

Vivipary: Othologues of maize viviparous 1 (*Vp-1*) are located in chromosomes 3AL, 3BL, and 3DL {9961} approximately 30 cM distal to the *R* loci. Variability at one or more of these loci may be related to germination index and hence to PHS {10468).

Three sequence variants of ***Vp-B1*** identified in {10468} were used to develop STS marker VpiB3 whose amplified products showed a significant, but not complete, association with germination index used as one measure of PHS.

Pre-harvest sprouting:

Phs1 {10500}. *Phs* {9960}. **i:** Haruyokoi*6 / Leader {10500}; Haruyokoi*6 / Os21-5 {10500}.
v: Leader {10500}; Os21-5 {10500}.
ma: *Xhbe03-4AL* – 0.5cM – *Phs1* – 2.1 cM – *Xbarc170-4AL* {10500}.
phs1. **v:** Haruyokoi {10500}.

QTL: As currently listed.

20. Flowering Time

Winter wheat cross 'Ernie (early)/MO94-317 (late)', days to anthesis (dta):
Qdta.umc-2D, linked to *Xbarc95-2D*, $R^2 = 0.74$ {10456}.

26. Glaucousness (Wasiness/Glossiness)

26.2. Epistatic inhibitors of glaucousness

Iw2. *Iw3672* {10510}. **v:** Synthetic hexaploid line 3672 {10510}.
ma: *Xbarc124-2D* – 0.9 cM – *Iw2* – 1.4 cM – *Xwe6* (*AL731727*) {10510}.

29. Grain Quality Parameters

29.2. Flour, semolina and pasta colour

Add at end of section:

QTL: Analysis of yellow flour pigment in an RIL population of 'PH82-2 (low)/Neixiang (high)' revealed major QTL on chromosomes 7A co-segegating with marker *YP7A* ($R^2 = 0.2 – 0.28$) (see Phytoene synthase 1), and 1B ($R^2 = 0.31 – 0.54$) probably contributed by 1RS {10501}.

29.8. Loaf volume

Add:

QTL: Loaf volume score consistent across three environments was scored in an RIL population 'Renan/Recital' and revealed major QTL on chromosomes 3A (flanking markers *Xfbb250-3A*, *Xgwm666-3A*, positive effect from Renan) and 7A (flanking markers *Xcfa2049-7A*, *Xbcd1930-7A*, positive effect from Recital) {10536}.

32. Hairy Leaf

Add note: A QTL analysis of the ITMI population identified loci determining hairiness of leaf margins and auricles in regions of chromosomes 4B and 4D orthologous to *Hl1*{10516}.

Hl1. **ma:** *Xgwm375-4B* - 12.1 cM - *Hl1* - 2.1 cM {10516}.

Hl2.

Add note following this entry:

The hairy leaf gene (Hl^{Aesp}) in *Ae. speltoides* introgression line 102/00^{I} was allelic with *Hl2* {10516}.

39. Height

39.1. Reduced Height: GA-insensitive

39.2. Reduced Height: GA-sensitive

***Rht8c*.v:** Add: Chuanmai 18 {10512}.

To the note following *Rht8c* add:

Although the 'diagnostic' association of *Rht8c* and $Xgwm261_{192}$ applied in many Strampelli derivatives and European wheats, there was no association between reduced height and this allele in Norin 10 and its derivatives {10512}. The pedigrees of a number of Chinese wheats postulated to have *Rht8c* on the basis of the marker trace to Italian sources {10515}.

41. Hybrid Weakness

41.4. Apical lethality

Apical lethality is caused by complementary recessive genes and is characterized by stunting and tiller death at the 4–5 leaf stage. The lethal genotype was designated *apd1 apd1 apd2 apd2* {10492}.

Apd1 {10492}. **v:** WR95 = Kalyansona / Gigas // HD1999 / Sonalika /3/ *T. turgidum* subsp. *carthlicum* {10492}.

apd2 {10492}. **v:** HD2009 {10492}; HW2041 {10492}; Lok-1 {10492}; others {10492}.

***Apd1 Apd2*.** **v:** Atila {10492}; Kalyansona {10492}; others {10492}.

apd1apd2 Lethal genotype.

Uniculm plants occurred as heterozygous segregates among progenies, but homozygous uniculm lines could not be established {10492}.

57. Polyphenol Oxidase (PPO) Activity

QTL: Chara (medium high PPO) / WW2449 (low PPO): one QTL was located on chromosome 2A. Two markers (one SNP, one CAPS) based on BQ161439 were polymorphic between the parents and showed linkage or allelism with PPO loci *Xtc1* and *XPPO-LDOPA*.

Xtc1 – 0.6 cM – *XPPO-LDOPA*/*XPPO18*/*BQ161439* {10484}.

59. Reaction to Black-Point of Grain

QTL: Add to the paragraph starting with 'Sunco/Tasman': Markers *Xgwm319-2B* and *Xgwm048-4AS* were confirmed in a 'Batavia/Pelsart (resistant)' DH population {10494}.

60. Response to Photoperiod

Insert following the current *Ppd-B1* entry:

Ppd-D1. Comparative mapping showed that *Ppd-D1* was co-linear with barley *Ppd-H1* – a member of the pseudo-response regulator (PRR) gene family {10466}. Stocks with *Ppd-D1a* had a 2,089bp deletion upstream of the coding region leading to misexpression of the 2D PRR gene {10466}.

Ppd-D1a. **v:** Add: Festival {10466}; Kavkaz {0917}; Orqual {10466}; Recital {10466}; Saitama 27 {10466}; Sideral {10466}; Soissons {10466}; Talent {10466}; Texel {10466}.
ma: Stocks with *Ppd-D1a* had a 2,089-bp deletion upstream of the coding region leading to mis-expression of the 2D PRR gene {10466}.

61. Response to Salinity

61.1. K+/Na+ discrimination

Kna1.

Add note: *Kna1* is a possible othologue of *Nax2* and is the Na^+ transporter *TaHKT1;5-D* {10455}.

6.1.2 Sodium exclusion

Nax1 {10452}. 2AL {10452}. **i:** Tamaroi*6/Line 149 = P06306 {10453}.
tv: Line 149 *Nax2* = 126775b {10452}.
dv: AUS 90382 *Nax2* = C68.101{10455} = JIC *T. aegilopoides* no. 3.

ma: *Nax1* was mapped as a QTL in the region *Xpsr102-2A* – 5.4 cM – *Xwmc170 -2A* – 0.9 cM – *Xksud22-2A/Xksu16-2A* – 0.8 cM – *Xgwm312-2A* with R^2 = 0.38 in 'Tamaroi/Line 149' {10452}. *TmHKT7-A2* was identified as a putative candidate Na^+ transporter{10454}.
Nax1 promotes withdrawal of Na^+ from xylem in leaf bases and roots {10453}.

Nax2 {10453}. 5AL {10455}. **i:** Tamaroi*6/Line 149 = P05603 {10453}.
tv: Line 149 *Nax1* = 126775b {10452, 10453}.
dv: AUS 90382 *Nax1* = C68.101{10455} = JIC *T. aegilopoides* no. 3.

ma: Co-segregation with *Xgwm291-5A/Xgwm140-5A/Xgpw2181-5A* {10455}. *TmHKT1;5-A* was identified as a candidate for *Nax2* {10455}.
Nax2 is a likely orthologue of *Kna1* {10455}.

63. Response to Vernalization

Add to the comment following *Vrn3* entries:
……… to Arabidopsis *FLOWERING LOCUS T* (*FT*) {10421}. Polymorphisms in the A and D genome copies of *TaFT* are associated with variation of earliness components in hexaploid wheat {10533}.

Add as a comment at the end of the section:
Three genes up-regulated by vernalization were cloned from *T. monococcum* subsp. *monococcum* {10531}. These were VIN3-like genes similar to Arabidopsis VIN3.

Vil-1{10531}. GenBank DQ886919 {10531}. **ma:** *T. monococcum* subsp. *monococcum* chromosome $5A^m$ {10531}.
Vil-2{10531}. GenBank DQ886917 {10531}. **ma:** *T. monococcum* subsp. *monococcum* chromosome $6A^m$ {10531}.
Vil-3{10531}. GenBank DQ886918 {10531}. **ma:** *T. monococcum* subsp. *monococcum* chromosome $1A^m$ {10531}.

71. Tenacious Glumes

Tg1. **ma:** Placed in a 12 cM interval between *Xwmc112-2D* and *Xbarc168-2D* {10497}.

Add below *Tg2*:
A QTL analysis of the relationship of glume tenacity (*Gt*) with threshability (*Ft*) and the size of the glume base scar (*Gba*) after glume detachment in two crosses, viz. the ITMI population and CS* /CS (*Ae. tauschii* 2D), was undertaken {10497}. In the first cross *QFt.orst-2D.1* and *QGt.orst-2D.1* were closely associated with *Xgwm261-2D*, and *XFt.orst-2D.2* and *XGt.orst-2D* were associated with *Xgwm455-2D*; in the second population only the first pair along with *XGba.orst-2D* were detected; these appeared to correspond with *Tg1* {10497}.

75.9. Grain yield

Add:

<u>Grain yield under drought stress</u>

QTL: 'Dharwar Dry (drought tolerant)/Sitta': SSR locus *Xwmc89-4AL* was the marker most closely associated with with QTL for grain yield, grain fill rate, spike density, grains/m^2, biomass, and drought susceptibility index covering a genetic distance of 7.7 cM {10488}.

Proteins

77. Proteins

77.2.6. Endopeptidase

Ep-D1b.

Add comment after the present entry: Assuming that *Ep-D1* encoded an oligopeptidase G, comarative genetics were applied to develop a STS marker for identifying resistance gene *Pch1*{10513} (see Reaction to *Tapesia yallundae*).

77.2.29. Starch branching enzyme

Insert headings:

Starch Branching Enzyme I

Present entries are in this section.

Starch Branching Enzyme II

SbeII

Suppression of SBEIIb expression alone had no effect on amylose content; however, suppression of both SBEIIa and SBEIIb expression resulted in wheat starch containing >70% amylose {10534}.

77.2.32.1 Phytoene synthase 1

Add introduction: Phytoene synthase is involved in the carotenoid biosynthetic pathway and influences yellow pigment content in grain (See Flour colour and Grain quality parameters: Flour, semolina and pasta colour). The gene *Psy-A1* was cloned and a functional marker developed from the sequence distinguishing Chinese common wheats with high and low pigment contents {10501}. Most hexaploid wheat culitvars have a 676-bp insertion in intron four that is absent in Australian cultivars Dundee, Raven, and Aroona with high yellow pigment. The *Psy-B1b* allele from tetraploid wheat Kofa is the result of a B–A intergenomic conversion event that probably occurred in Cappelli *ph1c* mutant l {10530}. An EMS mutation in the *Psy-E1* gene is associated with whiter endosperm in lines carrying the *Th. elongatum* 7EL translocation.

Psy-A1

Psy-A1a {10501}. GenBankEF600063 {10501}. No 37-bp insertion in intron 2 (194-bp fragment for marker *Yp7A*) {10501}. 676-bp insertion in intron 4 {10530}.
v: Chinese common wheats with high pigment content: CA9648 {10501}; Neixiang 188 {10501}.
ma: *Xwmc809* – 5.8 cM – *Yp7A* {10501}.

Psy-A1b {10501}. GenBank EF6000644 {10501}. 37-bp insertion intron 2 (231 bp fragment for marker *Yp7A*) {10501}. 676-bp insertion in intron 4 {10530}.
v: Chinese common wheats with low yellow pigment content {10501}. Ph82-2 {10501}; Xinong 336 {10501}.

Psy-A1c {10530}. Hexaploid wheats with no 37-bp insertion in intron 2 and no 676-bp insertion in intron 4 {10530}.
v: High yellow pigment cultivars: Aroona (PI 464647) {10530}; Dundee (PI 89424, PI106125) {10530}; Raven (PI 303633, PI 330959) {10530}.

Psy-A1d {10530}. GenBank EU096090 {10530}.
tv: Kofa {10530}; UC1113 {10530}.

Psy-B1

Psy-B1a {10530}. GenBank EU096093 {10530}.
tv: UC1113 {10530}.

Psy-B1b {10530}. GenBank EU096092 {10530}.
tv: Kofa {10530}.

Psy-E1
Psy-E1a {10530}. GenBank EU096095 {10530}.
v: Agatha (7EL translocation) {10530}.
Psy-E1b {10530}. = EU096095 with P to L mutation at amino acid 422 {10530}.
v: EMS mutant Agatha-28-4 (10530); Wheatear {10530}.

7.2.34. Polyphenol oxidase

Add as intoductory statement: High PPO activity in kernels and flour leads to a time-dependent discolouration of end products such as noodles, pasta and breads.

Primers different from those in {10386) were developed in {10504}, but their ability to distinguish phenotypic groupings (alleles) were similar. A null allele of *Ppo-D1* was identified for this locus using primer pair WP3-2 {10504}.

Ppo-A1.
Ppo-A1a. **v:** Add reference ',10504' to existing reference panels, i.e., {10385, 10386, 10504} and {10386, 10504}.
Ppo-A1b. **v:** Nongda 183 {10504}. Add reference ',10504' to 'others'.

Ppo-D1.
Ppo-D1a. **v:** Add reference ',10504' to existing reference panels.
Ppo-D1b. **v:** Nongda 183 {10504}. Add reference ',10504' to others.

Ppo-D1c [{10504}]. *Ppo-D1null* {10504}. **v:** Gaiyuerui {10504}; Xiaobingmai {10504}; Zm2851 {10504}; XM 2855 {10504}; 9114 {10504}.
ma: Wheats with this allele tend to have lower PPO activity {10504}.

Endosperm Storage Proteins
77.3.1. Glutenins
77.3.1.1. Glu-1
Glu-A1
Add:
Glu-A1y [{10535}]. 2·· {10535}. **v:** 211.12014 {10535}.

Glu-A1-1
In the following entries that appear in the 2006 Supplement:
Glu-A1v {10327}. 2.1* {10327}. **v:** KU-1094, KU-1026, KU-1086, Grado, KU-1139 {10327}.
Glu-A1w [{10327}]. 2' {10327}. **v:** TRI14165/91 {10327}.

replace '***Glu-A1v***' and '***Glu-A1w***' with '***Glu-A1-1v***' and '***Glu-A1-1w***', respectively.

Add:
Glu-A1-1x [{10535}]. 2·· {10535}. **v:** 211.12014 {10535}.

77.5.8. Puroindolines and grain softness protein

Under the preamble, add:
Recent reviews {10522, 10523} provide comprehensive descriptions of the molecular genetics and regulation of puroindolines. Morris and Bhave {10524} reconciled the D-genome puroindoline alleles with DNA sequence data. Bonafede et al. {10525, 10526} developed a CS line (PI 651012) carrying a T5A^{m}S·5AS translocation from *T. monococcum* subsp. *monococcum*; the translocated chromatin carries A-genome *Pina, Pinb*, and *Gsp-1* alleles that confer softer kernel texture.

Pina-D1b
i: Add: Near-isogenic pairs were developed in McNeal, Outlook, Hank, Scholar, and Explorer {10527}.
v: add: This BAC clone also contains *Pinb-D1a* {10431}.
Pina-D1m. Add: **v:** Hongheshang, (GenBank EF620907) {10208}.
Pina-D1n. Add: **v:** Xianmai GenBank EF620908) {10208}.

Correct:

Pinb-D1p {10121}. **v:** Nongda 3213 {10121}; Nongda 3395 {10121}.
Pinb-D1u. **v:** Tiekmai, add: (GenBank EF620911) {10427}.

Delete existing information and relace with:

Pinb-D1x {10528}. **v:** Kashibaipi (GenBank AM909618) {10528}.
Pinb-D1ab **v:** Add: Tuokexunyihao {10528}.

Pathogenic Disease/Pest Reaction

78. Reaction to Barley Yellow Dwarf Virus

Bdv2. 7D = T7DS-7Ai#1S7Ai#1L group: **v:** Glover (with TC6) {10491}.

79. Reaction to *Blumeria tritici*

79.1. Designated genes for resistance

Pm12. **ma:** Add: Secondary recombination analysis indicated that *Pm12* was located in the long arm of 6S between *Xwmc105* and *Xcau127* {10517}.

Pm21. **ma:** Add: Marker NAU/Xibao15, developed from a serine/threonine gene upregulated by powdery mildew infection, acts as a co-dominant marker for lines carrying *Pm21* {10519}.

Pm37. **v:** List as: PI 615588 = NC99BgTAG11 = Saluda*3/PI 615588 {10372}.
ma: Add: *Xgwm332-7A* – 0.5 cM – *Pm37* – 0.5 cM – *Xwmc790-7A* – 15.5 cM – *Pm1* {10372}.

Pm39 {10481}. Adult-plant resistance. 1BL {10480, 10481}.
i: Avocet-R+*Lr46*/*Yr29* = Avocet-R*3//Lalb mono 1B*4/Pavon 76 {10480}. Genotypes with *Lr46*/*Yr29*; see Reaction to *Puccinia triticina*, Reaction to *P. striiformis*.
v: Saar (CID: 160299, SID: 188) *Pm38* {10481}.
ma: *Xwmc719-1BL* – 4.3 cM – *Lr46/Yr29/Pm39* – 2.5 cM – *Xhbe248-1BL* {10481}.

To the paragraph following the last named *Pm* gene and beginning; 'Single resistance genes……' add: A further gene derived from *T. monococcum* PI 427772 was identified in BCBGT96A = PI 599036 = Saluda*3 / PI427772 {10479}.

79.2. Suppressors of *Pm*

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

PmLK906 {10476}. Resistance is recessive (10476, 0928}. 2AL {10476,10477}.
v: Lankao 90(6)21-12 {10476}; Zhengzhou 9754 {10476}.
ma: *TacsAetPR5-2A/Pm4* – 3.9 cM – *Xgwm265-2A* – 3.72 cM – *Pm39* – 6.15 cM – *Xgdm93-2A* {10476, 10477}. *TacsAetPR5-2A* was converted to a STS marker {10477}.

79.4. QTL for resistance to *Blumeria graminis*

At the end of the paragraph ending with ' ….. Becker / Massey {0284}.' Add: These QTL were confirmed by the addition of extra markers to the 'Becker/Massey' map and in a separate analysis of 'USG 3209 (A Massey derivative)/Jaypee (susceptible)' {10505}. USG 3209 possessed *Pm8* (T1BL·1RS) and an unknown specific resistance factor and their combination had a positive effect on APR even though neither was effective against the races used to identify the QTL {10505}.

81. Reaction to *Diuraphis noxia*

Dn7. *Dn2414* {10478}. **v:** ST-ARS 02RWA2414-11 {10474}.
ma: *Xhor2-1R* – 1.7 cM – *Dn7* – 1.0 cM – *Xscb241-1R* {10474}. Marker *Xrems1303*$_{320}$ was amplified only in genotypes resistant to biotype 3 and presumably possessing *Dn7* {10474}.

82. Change to: Reaction to *Fusarium* spp.

82.1. Disease: Fusarium head scab, scab

Insert as an introductory statement before listing the first gene:

Whereas much of the recent genetic work involved FHB caused by *F. graminearum*, according to {10514} *F. culmorum* is more damaging than *F. graminearum* in terms of FHB severity, kernel damage, yield reduction, and DON/NIV contamination.

Fhb3 {10529}. 7D = T7AL·7Lr#1S {10529}. **v:** TA 5608 (10529).
al: *Leymus racemosus* {10529}.
The level of type-2 resistance conferred by *Fhb3* was similar to that of Sumai 3 {10529}.

***QFhs.ndsu-3AS*.ma:** Add: *Qfhs.ndsu-3AS* was placed within a 11.5-cM region flanked by TRAP marker loci *Xfcp401-3A* and *Xfcp397.2-3A* {10482}. This gene is unlikely to be a homoeologue of *Qfhs.ndsu-3BS* = *Fhb1* {10482}.

QFhs.pur-7El {10489}. 7el$_2$ {10489}, T7DS·7DL-7el$_2$ {10489}. **su:** K2630 {10489}.
v: K11695 = T7DS·7DL-7el$_2$ {10489}; KS10-2 = T7el$_2$S·7el$_2$L-7DL {10489}; KS24-1 and KS24-2 = T7DS·7el$_2$ {10489}.
ma: *Qfhs.pur-7el$_2$* was flanked by *BE445653* and *Xcfa2270-7D* {10489}. These markers also were present in KS10-2 {10489}.

QTL: Add after 'Chokwang/Clark':
'Ernie (Resistant)/MO94-317 (Susceptible)': 243 F$_8$ RIL population. Four QTL from Ernie detected as follows:
Qfhs.umc-2B, linked to *Xgwm278-2BS*, R^2 = 0.04 {10456}.
Qfhs.umc-3B, linked to *Xgwm285-3BS*, R^2 = 0.13 {10456}.
Qfhs.umc-4B, linked to *Xgwm495-4BL*, R^2 = 0.09 {10456}.
Qfhs.umc-5A, Linked to *Xgwm165-5A*, R^2 = 0.17 {10456}.
Evidence was provided to suggest the QTL acted additively {10456}.

Add after 'Arina/Forno':
'Arina/Riband' DH lines: QTL affecting AUDPC were identified in 1BL (2), 2B, 4DS, 6BL, and 7AL (Arina), and 7AL and 7BL (Riband). The most effective was the 4DS QTL that appeared to be an effect of *Rht-D1a* rather than height *per se* {10464}.

'Cansas (moderately resistant)/Ritmo (susceptible)' : Map-based analysis across environments revealed seven QTL, *QFhs.whs-1BS* (1RS), *QFfhs.whs-3B* (not *Fhb1*), *QFhs.whs-3DL, QFhs.whs-5BL, QFhs.whs-7AL*, and *QFhs.whs-7BL* (cumultatively, R^2 = 0.56). The chromosome 1D gene was primarily involved in resistance to fungal penetration and the others in resistance to spread {10503}. There were significant correlations of FHB response with height and heading date {10503}.

Add above 'Frontana/Remus' entry:
'Veery (susceptible)/CJ 9306 (resistant)': Four QTL, *QFhs.ndsu-3BS* (*Xgwm533b* – Xgwm493), *QFhs.nau-2DL* (*Xgwm157* – *Xwmc-041*), *QFhs.nau-1AS* (*Xwmc024* – *Xbarc148*), and *QFhs.nau-7BS* (*Xgwm400* – *gwm573*) accounted for 31, 16, 10, and 7%, respectively, of the average phenotypic variation over three years {10490}.

Continue under 'Dream/Lynx': 'Dream*4/Lynx' lines were developed by selection of QTL on chromosomes 6AL, 7BS, and 2BL. Lines carrying *QFhs.lfl-6AL* and *QFhs.lfl-7BS* were more resistant than lines lacking them; the 2BL QTL effect was not verified {10470}.

Change the heading 'DON accumulation' to 'Resistance to DON accumulation'
Add:
'Veery/CJ 9306 (resistant)': Four QTL contributed to resistance; *QFhs.ndsu-3BS*, nearest marker *Xgwm533b* (R^2 = 0.23), *QFhs.nau-2DL, Xgwm539* (R^2 = 0.2), *QFhs.nau-1AS, Xbarc148* (R^2 = 0.05) and *QFhs.nau-5AS, Xgwm425* (R^2 = 0.05) {10496}.

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

83.Reaction to *Heterodera avenae* Woll.

CreX {10486}. Derived from *Ae. variabilis*. 2AS or 2DS {10486}. **ad:** Line M {10487}.
v: Line D {10486}.
ma: RAPD markers OP02$_{1000}$, OpR4$_{1600}$, OpV3$_{450}$ {10486}.
CreY {10486}. Derived from *Ae. variabilis*. 3BL {590}. **v:** Line X {10487}.
ma: Co-segregation with RAPD OpY16$_{1065}$ {0103} which was converted to SCAR16 {10486}.
May be the same gene as *Rkn-mn1* (see reaction to *Meloidogyne naasi*).

84. Reaction to *Magnaporthe grisea* (Herbert) Barr

Rmg1 {10462}. 1D {10462}. **s:** CS (Cheyenne 1D) {10462}.
v: Cheyenne (10462}; Norin 26 {10462}; Shin-chunaga {10462}.
Rmg2 {10461}. 7A {10461}. **i:** CS (Thatcher 7A) {10461}.
v2: Thatcher *Rmg3* {10461}.
Rmg3 {10461}. 6B {10461}. **i:** CS (Thatcher 6B) {10461}.
v2: Thatcher *Rmg2* {10461}.

86. Reaction to *Meloidogyne* spp.

Rkn-mn1. **ma:** After RAPD Op$_{1065}$ insert: (converted to SCAR Y16 {10486}). May be the same as *CreY* (see reaction to *Heterodera avenae*).

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

Stb6. **v:** Add: Bezostaya 1 {10495}.

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

Disease: Septoria nodorum blotch, Stagonospra nodorum blotch.
This entire section has been revised

89.1. Genes for resistance

Snb1 {856}. 3AL {856}. **v:** Red Chief {856}.
v2: EE8 *Snb2* {856}.
Snb2 {856}. 2AL {856}. **v2:** EE8 *Snb1* {856}.
Snb3 {1594}. 5DL {1594}. **s:** CS*/Synthetic 5D {1594}.
v: Synthetic {1594}.
dv: *Ae. tauschii* {1594}.
SnbTM {856, 857}. 3A {857}, 3AL {856}.
v: Coker {10210}; Hadden {10210}; Missouri {10210}; Red Chief {10210}; 811WWMN 2095 {10210}; 86ISMN 2137 {10210}.
tv: *T. timopheevii* subsp. *timopeevii*/2*Wakooma {856}; *T. timopheevii* subsp. *timopeevii* PI 290518. *T. timopheevii* subsp. *timopeevii* derivatives: S3-6 {857}; S9-10 {857}; S12-1 {857}.
ma: *UBC521*$_{650}$ - 15 cM - *SnbTM* - 13.1 cM - *RC37*$_{510}${0212}. *UBC521*$_{650}$ was converted to a SCAR marker {0212}.

Allelism of the hexaploid wheat gene and the *T. timopheevii SnbTM* was suspected. but not confirmed.

QTL

A QTL analysis of SNB response in the ITMI population found significant effects associated with chromosome 1B (probably *Snn1*) and 4BL, with an interactive effect involving the 1BS region and a marker on chromosome 2B {10009}. An additional QTL on 7BL was effective at a later stage of disease development {10009}.

Four QTL, on chromosomes 2B (proximal part of long arm), 3B (distal part of short arm), 5B. and 5D, were mapped in a 'Liwilla/Begra' DH population. Longer incubation period and lower disease intensity were contributed by Liwilla {10045}.

Two QTL for glume blotch resistance under natural infection were identified on chromosomes 3BS and 4BL in 'Arina/Forno' RILs {10065}. The 3BL QTL, designated *QSng.sfr-3BS*, was associated with marker *Xgwm389-3B* and explained 31.2% of the variation. The resistance was contributed by Arina {10065}. The 4BL QTL, *QSng.sfr-4BL*, was associated with *Xgwm251-4B* and explained 19.1% of the variation. Resistance was contributed by Forno {10065}. A QTL on 5BL, *QSng.sfr-5BL*, overlapped with QTL for plant height and heading time {10065}. *QSng.sfr-3BS* peaked 0.6 cm proximal to *Xsun2-3B* {10465}. Association mapping involving 44 modern European cultivars indicated that the association was retained in a significant proportion of genotypes {10465}.

A QTL, *QSnl.ihar-6AL*, identified in DH lines of 'Alba (resistant)/Begra (susceptible)' accounted for 36% of the phenotypic variance in disease severity and 14% of the variance in incubation period {10143}.

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

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

'Br34/Grandin': Three QTL with resistance effects from BR34; *Qsnb.fcu-5BL.1* (*Tsn1*), $R^2 = 0.63$, *Qsnb.fcu-5BL.2*, $R^2 = 0.06$, and *Qsnb.fcu-1BS* (vicinity of *Snn1*) $R^2 = 0.10$ (10458). QTL analysis of the RIL population with Culture *Sn6* revealed four QTL, *Qsnb.fcu-2DS* ($R^2 = 0.3 – 0.49$) associated with *Snn2*, *Qsnb.fcu-5BL* ($R^2 = 0.14 – 0.2$) associated with *Tsn1*, *Qsnb.fcu-5AL* ($R^2 = 0 – 0.13$) associated with *Xfcp13-5A*, and *Qsnb.fcu-1BS* ($R^2 = 0 - 0.11$) associated with *Xgdm125-1BS* {10507}.

'P91193D1 (partially resistant)/P92201D5 (partially resistant)' RIL populations were tested in India and Western Australia for glume resistance. Two QTL were idientified: *Qng.pur-2DL.1* from P91193D1 ($R^2 = 12.3$ in Indiana and 38.1% in WA, respectively; *Xgwm526.1-2D – Xcfd50.2-2D*) and *QSng.pur-2DL.2* from P99201D5 ($R^2 = 6.9\%$ and 11.2%, respectively; *Xcfd50.3-2D – wPT9848*) {10471}.

89.2. Sensitivity to SNB toxins

Tsn1 {10458, 346, 10207}. Sensitive to SnToxA which is functionally identical to Ptr ToxA {10459}.
v: See reaction to *Pyrenophora tritici repentis* {10458}. Cheyenne {0007}; Hope {0007}; Jagger {0007}; Kulm {346,10030, 10458}; ND495 {0007}; Timstein {0007}; Trenton {0315}.
tv: Langdon {10458}.

tsn1 {346,10207}. Insensitivity (disease resistance) is recessive {346}. 5BL {346}.
v: AC Barrie {10153}; AC Cadillac {10153}; AC Elsa {10153}; BR34 {0007}; CEP17 {0007}; Chinese Spring {0007}; Erik {0007,10030}; Hadden {10155}; Laura {10153}; Line 6B-365 {10155}; Red Chief {10155}; 1A807 {0007}; 1A905 {0007}; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. squarrosa* C122.
tv: Altar 84 {0007}; D87450 {0007}; *T. turgidum* subsp. *dicoccoides* Israel A {10506}.
ma: *Xbcd1030-5B* – 5.7 cM – *tsn1* – 16.5 cM – *Xwg583-5B* {346}; *tsn1* – 3.7 cM – *Xbcd1030-5B* {0007}; *Xfgcg7-5B* – 0.4 cM – *Tsn1*/*Xfcg17-5B* – 0.2 cM – *Xfcg9-5B* {10207}; *Xfcg17-5B* – 0.2 cM – *Tsn1* – 0.6 cM – *Xfcg9-5B* {10207}; *Xfcp1-5B* and *Xfcp2-5B* delineated *Tsn1* to an interval of about 1 cM {10337}. *Tsn1* was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1*/*XBE425878*/*Xfcc*/*XBE443610* {10413}.

snn1 tsn1. Atlas 66 {10458}; BR34 {10458}; Erik {10458}; Opata 85 {10458}; ND688 {10458}.

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

snn2. **v:** Br34 {10507}.

Snn2 {10507}. Sensitivity to SnTox2 is dominant {10507}. 2DS {10507}.
v: BG223 {10507}. **v2:** Grandin *Tsn1Tsn* {10507}.
ma: *Xgwm614-2D* – 7.6 cM – *Snn2* – 5.9 cM – *Xbarc95-2D* {10507}.

90. Reaction to *Puccinia graminis*

Sr9a. **ma:** *Xbarc101-2B*/*Xgwm12-2B* – 2.7 cM – *Xgwm47-2B* – 0.9 cM – *Sr9a*/*Xwmc175-2B* {10472}.
Sr8b. **tv:** According to Luig {841} one of the genes in Leeds is *Sr8b*. This could be the gene located on chromosome 6A in ST464-A1 {10473} and one of the genes present in ST464, a parent of Leeds.
Sr9e. **tv:** ST464-A2 {10473}. **tv2:** ST464 *Sr13* {10473}.
Sr13. **tv:** ST464-C1 {10473}. **tv2:** ST-464 *Sr9e* {10473}.
Genotype lists: add: {10511}.

Sr46 {10538}. 2DS {10538}. **v:** L-18913 / Meering selections R9.3 {10538}; R11.4 {10538}; R14.2 {10538}.
v2: L-18913 = Synthetic, Langdon / *Ae. tauschii* var. *meyeri* AUS 18913 *Sr9e* {10538}.
ma: Co-segregation with RFLP *Xpsr649-2DS* at both the diploid and hexaploid levels {10538}. A PCR-based marker, *csSC46*, was developed from a BAC clone containing *Xpsr649* {10538}.

91. Reaction to *Puccinia striiformis*

91.1. Designated genes for resistance to stripe rust

Yr21. After 1B add reference: {',10450'}.

A closely linked gene, also in Lemhi, conferred resistance to *P. s. hordei* {10450}. Both genes were mapped relative to RGAP markers. *Yr21 – YrRpsLem,* 0.3 cM {10450}.

Yr41 {10502}. ***YrCN19***{10228}. 2BS {10228, 10502}. **v:** AIM {10228}; AIM6 {10228}; Chuannong 19 {10228, 10502}.
ma: Complete linkage to a 391-bp allele of *Xgwm410-2BS* {10228}. *Xgwm410-2B* – 0.3 cM – *Yr41* {10502}.

91.2. Temporarily designated genes for resistance to stripe rust

YrCN19. This listing can be deleted.

91.3. Stripe rust QTL

Add at end of section: *T. monococcum* subsp. *monococcum* PAU14087 (resistant) / *T. monococcum* subsp. *aegilopoides* PAU5088 (resistant): RIL population: One adult-plant resistance QTL identified in each parent and named *QYrtm.pau-2A* (in a 3.6 cM interval between *Xwmc407-2A* and *Xwmc170-2A*; $R^2 = 0.14$) and *QYrtb.pau-5A* (in a 8.9 cM interval between *Xbarc151-5A* and *Xcfd12-5A*; $R^2 = 0.24$) {10518}.

92. Reaction to *Puccinia triticina*

92.1. Genes for resistance

Lr3.

At the end of the section add note: Durum cv. Storlom likely carries *Lr3a* or *Lr3b* {10469}. Cv. Camayo was considered to have a closely linked gene, or *Lr3* allele {10469}. Resistance in Storlom co-segregated with an STS derivative of *Xmwg798-6B* {10469}. All three Thatcher NILs with named *Lr3* alleles carried the STS marker {10469}.

Lr13. **ma:** *Lr13* – 10.7 and 10.3 cM – *Xgwm630-2BS* {10463}.
Lr14a. Add: *LrLla* {10520}. **tv:** Lloreta INIA {10520}; Somateria {10520}.
ma: *Xwmc273-7B* – 13 cM – *Lr14a* – 10 cM – *Xgwm344-7B* {10520}.
Lr22a. **i:** Neepawa*6/RL5404, RL4495 {10467}; Thatcher*7//Tetra-Canthatch/RL5271, RL6044 {10467}.
ma: *Xgwm455-2D* - 1.5 cM - *Lr22a* - 2.9 cM - *Xgwm296-2D* {10467}.
Lr34. **v2:** Mentana *Lr3b* {10493}.
ma: After the entry …csLV34a ……*Lr34* {10387}. Add: STS marker csLV34 was used to confirm or postulate the presence of *Lr34* in Australian culitvars {10493}.
Lr58. **ma:** After the third RFLP add: '..... and SSR marker *Xcfd50* …..'.
Lr61 {10485}. 6BS {10485}. **tv:** Guayacan 2 {10485}; Guayacan INIA {10485}.
ma: Closely linked and distal to 3 AFLP markers about 22 cM distal to SSR marker *Xwmc487-6B* {10485}.

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

This entire section has been revised. Disease: Tan spot, yellow leaf spot.

Virulence in the pathogen is mediated by host-specific toxins and host resistance is characterized at least in part by insensitivity to those toxins. Three toxins, Ptr ToxA, Ptr ToxB, and Ptr ToxC, have been identified (see {10153}). Toxin sensitivity determined by use of toxins extracted from pathogen strains and resistance determined by infection experiments are treated as different traits, although common genes may be involved.

93.1. Insensitivity to tan spot toxin (necrosis)

tsn1 {346, 10207}. Insensitivity (disease resistance) is recessive {346}. *Tsr1* {10508}, see Resistance to tanspot 5BL {346}.

v: AC Barrie {10153}; AC Cadillac{10153}; AC Elsa {10153}; Atlas 66 {10458}; BR34 {0007,10458}; CEP17 {0007}; Chinese Spring {0007,10458}; Erik{0007,10030,10458}; Laura {10153}; IA807 {0007}; IA905 {0007}; ND688 {10458}; Opata 85 {10458}; Synthetic W-7976 = Cando/R143/Mexicali 'S'/3/*Ae. tauschii* C122 {346,10207,10458}; Synthetic W-7984 = Altar 84/*Ae. tauschii* CI 18 {0007,10458}.

tv: Altar 84 {0007}; D87450 {0007}. *T. turgidum* subsp. *dicoccoides* Israel A {10506}.
ma: *Xbcd1030-5B* – 5.7 cM – *tsn1* – 16.5 cM – *Xwg583-5B* {346}; *tsn1* – 3.7 cM – *Xbcd1030-5B* {0007}; *Xfcg7-5B* – 0.4 cM – *Tsn1/Xfcg17-5B* – 0.2 cM – *Xfcg9-5B* {10207}; *Xfcg17-5B* – 0.2 cM – *Tsn1* – 0.6 cM – *Xfcg9-5B* {10207}; *Xfcp1-5B* and *Xfcp2-5B* delineated *Tsn1* to an interval of about 1 cM {10337}. *Tsn1* was placed in a 2.1 cM region spanned by *XBF483506* and *XBF138151.1/XBE425878/Xfcc1/XBE443610* {10413}.

Tsn1. Sensitive to Ptr ToxA.
v: Grandin {10458}; Bobwhite {10458}; Cheyenne {0007, 10458}; Glenlea {10458}; Hope {0007, 10458}; Jagger {0007}; Katepwa {10458}; ND2709 {10458}; ND495 {0007}; Sumai 3 {10458}; Timstein {0007, 10458}.
tv: Langdon {10458}.
v2: Kulm *Tsc1* {346,10030,10458}; Trenton *Tsc1* {0315}.

In Kulm/Erik, toxin response accounted for 24% of the variation in disease response, which was affected by 4–5 genes {10030}.
Ptr ToxA is functionally identical to *S. nodorum* ToxA but has two predicted amino acid differences {10459}. See Reaction to *Phaeosphaeria nodorum*.

93.2. Insensitivity to tan spot toxin (chlorosis)

tsc1 {344}. Insensitivity is recessive. *QTsc.ndsu-1A* {9924}.
v: Katepwa {0315}; Opata 85 {344}; Synthetic W-7984 {0315}.
Tsc1 {344}. Sensitivity to Ptr ToxC {344}. 1AS {344}.
v: 6B365 {0315}; Opata 85 {344}.
v2: Kulm *Tsn1* {0315}; Trenton *Tsn1* {0315}.
ma: *Gli-A1* – 5.7 cM – *Tsc1* – 11.7 cM *XksuD14-1A* {0315}.
According to {10376} the same allele, presumably *tsc1*, conferred resistance to chlorosis induced by races 1 and 3 in cultivars Erik, Hadden, Red Chief, Glenlea, and 86ISMN 2137 in crosses with 6B-365.
tsc2. Insensitivity allele {10015}. **v:** Opata 85 {0315,10015}.
Tsc2. Sensitive to Ptr ToxB {10015}. 2BS {10015}.
v: Synthetic W-7984 {10015}.

93.3 Resistance to tanspot

Tsr1. [*tsn1* See: Insensitivity to tanspot toxin]. Resistance is recessive.
5BL **v:** Genetic stocks that do not have *Tsn1* and other genes that respond to toxins produced by the pathogen.
Tsr2. [*tsn2* {10344}]. Resistance is recessive. Confers resistance to race 3 {10344}. 3BL {10344}.
sutv: LDN (DIC-3B) {10344}.
tv: *T. turgidum* subsp. *dicoccoides* Israel-A {10344}.
tv2: *T. turgidum* subsp. *turgidum* no. 283, PI 352519 *Tsr5* {10344}.
ma: Identified as a QTL in region *Xgwm285-3B* – *Xwmc366.2-3B* ($R^2 = 91\%$) {10344}, also classified as a single gene: *Xgwm285-3B* – 2.1 cM – *tsn2* – 15.2 cM – *Xwmc366.2-3B* {10344}.
Tsr3. [*tsn3* [{10394}]. 3D {10394}, 3DS {10419}.
v: XX41 = [Langdon / *Ae. tauschii* CI 00017] {10394}; XX45 {10394}; XX110 {10394}.
dv: *Ae. tauschii* CI 00017 {10394}.
ma: *Xgwm2a* – *tsn3*, 15.3 cM, 14.4 cM, and 9.5 cM in 'CS/XX41', 'CS/XX45', and 'CS/XX110', respectively {10419}.
Resistances in XX41 and XX110 were recessive whereas that in XX45 was dominant – all three were hemizygous-effective {10394}. The genes were given different temporary designations {10394, 10419}, but all will be considered to have a common gene until they are shown to be different.

Tsr4. Resistance is recessive. [*tsn4* (10350)]. Resistance to race 1 (culture ASC1a) {10350}. 3A {10350}.
v: Salamouni {10350}.
Tsr5. *tsn* {10509} . 3BL {10509}.

tv2: *T. turgidum* subsp. *turgidum* no. 283, PI 352519 *Tsr2* {10509}.
ma: *Tsr5* – 8.3 cM – *Xgwm285-3B* – 2.7 cM – *Tsr2* {10509}.

QTL:

QTsc.ndsu-1A {9924}. Resistance is likely recessive {344}. [*Tsc1* {344}]. 1AS {344}. **v:** Synthetic W7984 {344}.**ma:** Association with *Gli-A1* {344, 0040, 0264}. *QTsc.ndsu-1A*, or a closely associated gene, confers insensitivity to Ptr ToxC, see {0315}. Inoculation with purified toxin Ptr ToxC was used to map this locus. *QTsc.ndsu-1A* confers resistance in both seedlings and adult plants.

QTsc.ndsu-4A. 4AL {0090}. **v:** Opata 85 / W-7984 (ITMI) RI mapping population; resistance was contributed by W-7984 {0090}; In W-7976 / Trenton resistance was contributed by W-7976 {0264}. **ma:** Association with *Xksu916(Oxo2)* - 4A and *Xksu915(14-3-3a)-4A* {0090}; In W-7976 / Trenton there was association with *Xwg622-4A* {0264}; Minor QTL in chromosomes 1AL, 7DS, 5AL and 3BL were associated with resistance in adult plants {0264}.

QTL: ITMI population: In addition to *tsc2* which accounted for 69% of the phenotypic variation in response to race 5, a QTL in chromosome 4AL (*Xksu916(Oxo)-4AS*, W-7948) accounted for 20% of the phenotypic variation {10015}. 'Grandin (susceptible)/BR34 (resistant)' RILs: QTL in 1BS, *QTs.fcu-1BS,* (13-29% of variation depending on race) and 3BL, *QTs.fcu-3BL*, (13-41%) were involved in resistance to 4 races. Five other QTL showed race specific responses {10248}.

Introgressions of genes for insensitivity to Ptr ToxA and Ptr ToxB are outlined in {10153}.

96. Reaction to Soil-Borne Cereal Mosaic

Add: **QTL:** *QSbv.ksu.5D* in interval *Xcfd86-5D – Xcfd10-5D* in 'TA 4152-4/Karl 92'. TA 4152-4 = '*T. turgidum* subps. durum Altar 84/*Ae. tauschii* WX193 {10521}'.

97. Reaction to *Tapesia yallundae*. (Anomorph: *Pseudocerosporella herpotrichoides*

Pch1. **v:** Add: Coda {10513}. **ma:** Add: Leonard et al. {10513} predicted that *Ep-D1* might encode an oligopeptidase B, and by comparative genetics, developed primers to a wheat oligopeptidase B-encoding wheat EST BU1003257. Complete linkage occurred for a derived STS marker *Xorw1* and *Pch1* in a Coda / Brundage RIL population and the marker identied the presence or absence of *Pch1* 44 among wheat accessions {10513}.

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

Bt10. **i:** BW553 = Neepawa*6 // Red Bobs / PI178383 (10475}.

99. Reaction to *Tilletia indica* Mitra

QTL:

Qkb.ksu-4BL.1. 'WL711/HD29 (resistant)' RILs: $R^2 = 0.25$, associated with *Xgwm538-4B* {10498}. 'WH542/W485 (resistant)' RILs: $R^2 = 0.15$, *Xgwm6-4BL – Xwmc349-4BL* interval {10499}.
Xkb.ksu-5BL.1. 'WH542/HD29 (resistant)' RILs: $R^2 = 0.19$, *Xgdm116-5BL – Xwmc235-5BL* {10499}.
Xkb.ksu-6BS.1. 'WH542/HD29 (resistant)' RILs: $R^2 = 0.13$, *Xwmc105-6BS – Xgwm88-6BS* {10499}.

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