V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2019 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 13Th International Wheat Genetics Symposium held in Yokohama, Japan, is available on 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. Supplements 2014, 2015, 2016, 2017, and 2018 also are available at those sites.

Suggestions of information, preferably in suitable format, for listing in the Wheat Gene Catalogue can be submitted to the curators. Publication details on papers listed as 'Draft Manuscript' or 'In press' also would be helpful.

Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

1.1. Squarehead/spelt

Q. Add synonym '*Ap2-5A*'.
c: Move the last sentence under **ma:** to a new section **c:** and Add: GenBank AY02956.1.

Add note: The pleiotropic features of the *Q* locus include effects on glume toughness, threshability, rachis fragility, spike length, flowering time, and plant height {11342}.

At the end of section: add two references, i.e., '{11192, 11344}. Final spike and reproductive morphology is affected by the *Q*/*q* sequence and its regulation by miR172 {11344} along with direct or indirect interaction with the homoeologues {11344}.

Homoeologues of *Q* were described in {11192}. Both have miRNA172 target sites close to the 3' ends of the coding region. These genes were referred to as *Ap2-5B*, a transcriptionally active pseudogene, and *Ap2-5D,* that encodes a functional protein that contributes to suppression of the speltoid phenotype {11342}. Reduced height gene *Rht23*, a mutationally derived allele in NAUH164, was caused by a SNP (G3147A, Ala416Thr) within the miR172 target site in 5Dq that permitted up-regulation of *Ap2-5D* due to down-regulation of miR172 in leaves, stems and spikes {11345}.

17. Crossability with Rye and *Hordeum* and *Aegilops* spp.

kr5 [{11387}]. *skr* {11352}, {11352}. 5BS {11352}.
su: Courtot (Fukuhokomugi 5B) {11352}.
v: Balthazar-crossable {11352}; Deucendeu {11352}; Ornicar-crossable {11352}.
Balthazar-crossable and Ornicar-crossable probably also carry *kr1* {11352}.

44. Height

44.2. Reduced Height: GA-sensitive

***Rht-B1c*.** **c:** *Rht-B1c* carries a 2,026-bp insertion of a *terminal repeat transposons in miniature* (TRIM) insertion at position 147 bp relative to *Rht-B1a*; this leads to an additional 30 amino acids in the DEELLA domain affecting affinity between GID1 and Della {11390}. Genbank JN857970 (gDNA), JN859791 (cDNA) {11390}.

***Rht14*.** **ma:** Add: Mapped to genomic region 383–422 Mb flanked by *GA20xA9* and *Xwmc753-6A* {11372}.

***Rht25*.** Add synonym: *5Dq* {11345}.
c: NAUH164 has a G3147A (Ala416Thr) SNP mutation relative to its Sumai 3 parent, AP2-D is the likely candidate for *Rht23* {11345}.

46. Hybrid Weakness

46.1. Hybrid necrosis

***Ne1*.** **ma:** *Ne1* – 11 cM – *Xgwm639-5B* {11343}.

***Ne2*.** **ma:** *Xbarc7-2B* – 3 cM – *Ne2* – 6 cM – *Xwmc344-2B* {11343}.

49. Leaf Characteristics

Re-organization

49.1. Leaf erectness	Currently: 49. Leaf Erectness
49.2. Leaf tip necrosis	Currently: 50. Leaf Tip Necrosis
49.3. Seedling leaf chlorosis	Currently: 64. Seedling leaf chlorosis

NEW:

49.4. Early leaf senescence

els1 {11326}. 2BS {11326}.
v: ZK331 / Xiangmai 99171 // 2*Lumai 30 Line 114 {11326}.
ma: *WGGB305* – 0.3 cM – *els1*/*WGGB302* – 1.2 cM – *WGGB303*/*WGGB304*/*WGGB306* – 0.6 cM – *Xbarc92-2B* {11326}.

The *els1* 'mutant' was detected in an F_4 population. Because the parents had a normal phenotype, complementary genes were likely involved. The similar location of *ELS1* to the *NE1* locus in chromosome 2BS and similar phenotype suggests that this gene may be *Ne2*. See 49. Hybrid Weakness; 49.1. Hybrid necrosis

53. Male Sterility

53.1. Chromosomal

***ms2*.** **ma:** Mapped to a 0.05-cM region flanked by *Xsauw27-4D* and *Xsdauw29-4D* {11388}.
c: *Ms2* has a long terminal-repeat in miniature (TRIM) transposon at position –314 to –310 {11388}. Genbank KX585234 {11388}.

The TRIM element acts as an enhancer that activates anther-specific transcription of the *Ms2* allele {11388, 11389}. *Ms2* induced male sterility in barley and *Brachypodium* {11388} as well as triticale {597, 11388}.

57. Meiotic Characters

57.2 Pairing homoeologous

***Ph1b*.** **ma:** Dualplex marker *Xwgc2111* + *Xwgc2049* behaves like a co-dominant marker {11359}.

Add note: The *Ph1b* deletion involves a region of at least 60,014,523 bp {11359}.

57.4 Asynapsis/desynapsis

A putative gene for desynapsis designated *Ddes2* was placed between *Xwmc325-3B* and *wPt-8983* in deletion bin 3BL7-0.63-1.00 by mapping of deletion hybrids {11339}. There is no mutant stock to represent this gene first reported in CS nullisomic 3B by Sears {1293}.

70. Response to Vernalization

Insert above *Vrn-B3*:

Vrn-A3. 7AS.

An earlier variant of *T. turgidum* subps. *dicoccum* line TN28 was caused by a novel allele. Line TN26 lacked a 7-bp insertion, including a cis-element GATA box, in the *Vrn-A3* promoter region {11370}.

80. Yield and Yield Components

80.7. Spikelet number/ear

WAPO1 {11383}. *Wheat Ortholog of APO1.*
 WAPO-A1 {11383}. *TraesCS7A02G481600.* 7AL {11383}
  ma: IWGSC RefSeq v1.0 coordinates 674,081,462 – 674,082,918.
  Wapo-A1a {11383}. Low number of spikelets per spike (115-bp deletion in promoter and D384N amino acid change) {11383}.
   v: RAC875 {11383}.
   tv: Kronos {11383}.
  Wapo-A1b {11383}. High number of spikelets per spike (C47F amino acid change) {11383}.
   v: Berkut {11383}; Chinese Spring {11383}.
  Wapo-A1c {11383}. Low number of spikelets per spike (115-bp deletion in promoter and D384N amino acid change) {11383}.
   v: AGS2000 {11383}; LA95135 {11383}.
   tv: PI 519639 {11383}.
  Wapo-A1d {11383}. Low number of spikelets per spike {11383}.
   tv: Langdon {11383}; Rusty {11383}.

Ful2 {11384}.

Loss of function mutation in gene *FUL-A2* (Kronos mutant T4-837) and *FUL-B2* (Kronos mutant T4-2911) resulted in significant increases in spikelet number {11384}.

Vrn1 {11384}. Loss of function mutation in gene *VRN-A1* (Kronos mutant T4-2268) and *VRN-B2* (Kronos mutant T4-2619) resulted in significant increases in spikelet number {11384}.

Pathogenic Disease/Pest Reaction

89. Reaction to *Bipolaris sorokiniana*

Add note at the beginning of section: This pathogen likely harbours Tox A in common with *Parastagonospora nodurum*, *Parastagonospora avenaria tritici,* and *Pyrenophora tritici-repentis* {11375}.

Sb2 {11375}. *QSb.bhu-5B* {11375} 5BL {11375}.
 bin: 5BL1-0.55-0.75.
 v: Ning 8201 {11375}; Yangmai 6 {11375}; YS116 {11375}.
 ma: *Xgwm639-5B* – 1.4 cM – *Sb2* – 0.06 cM – *Xgwm1043-5B* {11375}.
sb2. *Tsn1* {11376}. **v:** Duster {11376}; Sonalika {11375}. Presumably all genotypes with *Snb1*.

90. Reaction to *Blumeria graminis* DC.

90.1. Designated genes for resistance

Pm4e. **ma:** Add: *Xwgrc763-2A* – 0.13 cM – *Pm4e/Xwgrc872-2A/Xwgrc869-2A* – 0.58 cM – *Xwgrc982-2A*, a region of about 6.1 Mb {11335}.
Pm8. **ma:** An STS marker distinguished *Pm8* from *Pm17* {0186}. *Pm8* is located between *Gli/Glu3* and rust resistance genes *Sr31, Lr26* and *Yr9* {11354}.
 c: *Pm8* is an orthologue of *Pm3* and an allele of *Pm8* in the rye genome {11354}. GenBank KF572030.

Delete the final sentence of comments: 'A STS marker…'.

Pm17. **v:** Add: Embrapa 16 {11355}; Hugenoot {11355}; TXGH13622 {11355}.
 c: *Pm17* shares 96% nucleotide identity with *Pm8* (83% at the protein level) and low but significant identity with *Pm3CS* {11355}. GenBank MH0779.

Pm21. **v:** Yangmai 18 {11352}.
ma: Genetic mapping in a 'resistant × susceptible' *D. villosum* cross identified two RGA candidate loci (markers 6VS-09.4 and 6VS.09.4b) co-segregating with *Pm21* and overlapped by an EMS-induced, susceptible mutation {11352}.
c: Add: Marker 6VS-09.4 but not marker 6VS-09.4b was deleted in a susceptible mutant indicating that the former was *Pm21* – the protein product had a CC–NBS –LRR structure – GenBank MF370199 {11353}. This gene was different from *Stpk-V* {11275} but was quite similar to *NLR-V1* {11353}.

Pm57. Correction: '…..2BL (T2BS·2BL-2S^S#1)…'.
ad: Add: BCS+2S^S#1 TA3581 {11159}.

Pm62 {11321}. Adult-plant reaction. *Pm2VL* {11321}. T2BS·2VL#5 {11321}.
v: NAU1823 {11321}.
ma: *X2L4g9P4/Hae111* {11159}.

Pm63 {11331}. *Pm628024* {11331}. 2BL {11331}.
bin: 2BL6-0.89-1.00.
v: PI 628024 {11331}.
ma: *Xwmc175-2B* – 1.7 cM – *Xstars419-2B* – 0.6 cM – *Pm63* – 1.1 cM – *Xbcd135.2 – 2B*; 7103 – 7234 in the CS Reference Assembly {11331}.

Pm64 {11346}. *PmWE35* {11346}. 2BL {11346}.
bin: 2BL4-0.5-0.89.
v: WE35 {11346}.
tv: *T. turgidum* subps. *dicoccoides* G-573-1 {11346}.
ma: *Xwmc175-2B* – 1.12 cM – *Pm64/Xgwm47-2B* – 2.18 cM – *Xwmc332-2B* {11346}. Complete repulsion linkage with *Yr5* in 644 F_3 lines {11346}.

Pm65 {11356}. *PmXM208* {11356}. 2AL {11356}.
v: Xinmai 208 {11356}.
ma: *Xhbg327-2A* – 4.4 cM – *XresPm4/XTaAetPR5* – 0.6 cM – *PmXM208* – 1.6 cM – *Xbarc122-2A* {11356}. An allelism test of *Pm65* and *Pm4a* showed a recombination value of 10.3 cM based on the frequency of susceptible F_2 plants {11356}.

Pm66 {11364}. 4BS (T4BL·4S^l#7S) {11364}.
v: TA3465 {11364}.
al: *Ae. longissima* (unknown accession).
ma: 4S^lS markers developed in {11364}.

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

Insert at the beginning of the *Pm* series:

Pm10V-2 {11380}. 5DS {11380}.
bin: 5DS-0-0.63.
v: 10V-2 {11380}.
ma: *Xbwm25-5D/Xswgi066-5D* – 1.2 cM – *Pm10V-2*/several markers – 1.2 cM – *Xcfd-5D* {11380}.

The complex nature of temporarily named powdery mildew resistance genes in the *Pm2* region is discussed in {11380}.

Insert alphabetically:

PmTx45 {11374}. Recessive. 4BL {11374}.
bin: 4BL5-0.85-1.00. **v:** Tian Xuan 45 {11374}
ma: *Ax-110673642* – 3.0 cM – *PmTx45* – 2.6 cM – *ILP4B01G266900* {11374}.

95. Reaction to *Diuraphis noxia*

Dn1. Add note at end of section:

'VIGS silencing of *5AL-B4* on chromosome 5A compromised resistance conferred by *Dn1* suggesting a decoy role {11333}.'

96. Reaction to *Fusarium* spp.

96.1. Disease: Add: Fusarium head scab, scab

***QFhs.ndsu-3A*.** Add: This gene was transferred to durum cultivars using the closely linked marker *Xgwm2-3A* {11367}.

Luke (S) / AQ24788-83 (R): RIL population: *QFhb.cau-7DL* near marker *Xgwm428-7DL* was equally effective as *Fhb1* {11358}.

Under the heading 'Tetraploid wheat' add:
Ben*2 / Tunisian 108 BIL population: nine QTL for FHB resistance of which new QTL *Qfhb.ndsu-2B* and *Qfhb.ndsu-3BL* and *Qfhb.ndsu-5A* and *Qfhb.ndsu-7BL* were the most important {11382}.

99. Reaction to *Mayetiola destructor*

Add at end of section:
Jagger (S) / 2174 9 (R): RIL population: *QHf.osu-1A* (Syn. *Qhf.osu*^{74} ($R^2 = 0.70$) and *QHf.osu-2A* ($R^2 = 0.18$) {11325}. The QTL in chromosome 1A appeared to be co-linear with several previously named *H* genes in tetraploid wheat; the gene in 2A was in repulsion with the 2N segment present in Jagger {11325}.

Duster (R) / Billings: DH population: *QHf.osu.1A.2* (Syn. *QHf.osu-1A*^{d}), $R^2 = 0.88$, delimited to a 2.7 cM region flanked by *GBS07851* and *GBS10205* {11324}. This was a distinct locus 11.2 cM proximal to *QHf.osu.1A*.

Mayetiola-destructor susceptibility gene-1
Mds-1A [*Mds-1*] {11327}. 3AS {11327}.
v: No allelic variation demonstrated.
c: EST CD453475, GenBank JN162442; *Mds-1A* encodes a 151 amino-acid protein with 96% identity with HSP16.9 {11327}. Homoeologues are present in chromosomes 3B and 3D. Silencing of *Mds-1* expression caused immunity in otherwise FHB-susceptible genotypes {11327}.

101. Reaction to *Mycosphaerella graminicola* (Fuckel) Schroeter, *Zymoseptoria tritici*

Stb19 {11360}. 1DS {11360}. **v:** Lorikeet {11360}.
ma: KASP markers snp_4909967 and snp_1218021 {11360}.
The source of *Stb19* was a synthetic wheat {11360}.
Add at end of section:
'See {11332, 11361} for reviews.'.

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

102.2 Sensitivity to SNB toxins (necrotrophic effectors)

***Snn1*.** Synonym: *TaWAK* {11341}.
c: *Snn1* encodes a wall-associated kinase (WAK) {11341}. GenBank: KP091701.
Snn1 was present in some *T. turgidum* subsp. *dicoccum* accessions, 73% of durum accessions and 16% of common wheat accessions {11341}.
***snn1*.** **s:** CS/Hope 1B {11341}.

105. Reaction to *Puccinia graminis* Pers.

***Sr26*.** **ma:** Add: Four KASP markers were developed for the original translocation (FL 0.85). WA-1 (AUS91435) a derivative with a shortened 6Ae#1 segment (FL 0.32), amplified only *sunKASP_224* and *sunKASP_225* {11336}. The latter was diagnostic for accession AGG91586WHEA *SrB*, a derivative of line WA-5 (AUS91436) {11338}. PCR markers based on NLR genes in homoeologous group 6 chromosomes were used to confirm that WA-2 Type 1 was the smallest secondary translocation carrying *Sr26* {11357}.
***Sr60*.** **c:** Cloning of *Sr60* from *T. monococcum* PI 306540 revealed a protein with two putative kinase domains designated Wheat Tandem Kinase 2 (WTK2) {11386}.

SrB {11337}. 6A = T6AS.6AL-6Ae#1-6Ae#3 {19018}.

v: AGG91586WHEA Sr26 {19018}.

ma: *SrB* was recombined with a 6Ae#1 segment possessing *Sr26*. Marker *sunKASP_225* {11336} was diagnostic for the recombined line AGG91586WHEA {11338}.

6Ae#3 {11338}. **su:** W3757 {11337}, a (6Ae#3(6D) line {11338}.

Complex genotypes:
Add:
PI 362698: *Sr5*, *Sr8a*, *Sr12*, *Sr15*?, *Sr16* {11347}.

106. Reaction to *Puccinia striiformis* Westend.

106.1. Designated genes for resistance to stripe rust

YR5. Add to introductory sentence: ', but cloning indicated that *Yr7* is not allelic with *Yr5* and *YrSP* {11351}.

Yr5a [{11397}]. *Yr5*.

c: *Yr5* (GenBank MN275771) along with *Yr7* and *YrSP* has a BED–LRR structure lacking a CC-domain {11351}.

Yr5b [{11397}]. See *YrSP*, *YrSp*

c: (GenBank MN273772) along with *Yr5* and *Yr7* has a BED–LRR structure lacking a CC-domain {11351}. *YrSp* is a truncated form of *Yr5* but confers a different specificity {11351}.

Yr7. Add to the introductory sentence: ', but cloning indicated that *Yr7* is not allelic with *Yr5* and *YrSP* {11351}.

v: Paragon {11351}.

c: *Yr7* (GenBank MN273773) along with *Yr5* and *YrSP* has a BED–LRR structure lacking a CC-domain {11351}.

Yr15. **v:** Add: Clearwhite 515 {11392} Expresso {11392}; Patwin 515 {11392}; Seahawk {11392}.

ma: *Xbarc-8-1B* – 4.2 cM – *Yr15* – 3.5 cM – *Xgwm413-1B* {11348}; *Xbarc8-1B* – 4.1 cM – *Yr15* – 2.5 cM – *Xuhw-1B* – 0.5 cM – *Xgwm413-1B* {11348}. *Yr15* is proximal to *Yr64*; recombinant lines are reported in {11349}; *Xwhu300-1B* – 0.013 cM – *Xwhu273-1B* {11392}.

c: Encodes a putative kinase-pseudokinase protein designated as wheat tandom kinase 1 (TPK1), g-DNA 4,655 bp, 665 amino acids. GenBank MG649384, MG674157 {11392}.

Yr17. **v:** Add a reference following Jagger, i.e. 'Jagger {10973, 19008}'.

Add note at end of *Yr17* section: 'Mundt {11340} noted that many genotypes containing *Yr17* continued to have adult-plant resistance to races virulent on the seedlings. These cultivars included Renan, Apache, Jagger, Bobtail, and Madsen. However, it was unclear as to whether this represented additional resistance gene(s) in the introduced segment or APR genes at other loci.'.

Yr24. Replace the final reference 939 in '{10339, 939}' with '{10339, 11391}'.

Yr26. **ma:** Add: *Xgwm11-1B* – 0.9 cM – *Yr26* – 6.3 cM – *Xbarc181* {11350}. Located between KASP markers *WRS435* and *WRS312* in an interval of 0.4 cM {11350}.

Replace the final references '{10339, 939}' with '{10339,11391}'.

Yr29. **ma:** *QYr.ucw-1BL* was mapped to a 0.24 cM region (332 kb IWGSC RefSeq v1.0 between *ucw.k31* and *csLV46G22* {11386}.

Yr64. **ma:** *Yr64* is distal to *Yr15*; recombinant lines are reported in {11349}.

Yr82 {11322}. **bin:** 3BL7-0.63-1.00.

v2: AUS27969 = JI 1190592 *Yr29* {11322}.

ma: *KASP_13376*/*sunKASP_301* – 0.4 cM – *sunKASP_300* – 2.0 cM – *Yr82* – 2.0 cM – *KASP_8775* {11322}.

106.2. Temporarily designated genes for resistance to stripe rust

YrM866-4 {11381}. 4AL {11381}. **bin:** 4AL13-0.59-0.66.

v: M8664-3 {11381}.

ma: *Xgpw2331-4A* – 2.8 cM – *Yr8664-3* – 8.1 cM – *Xgpw3224-4A* {11381}.

106.3. Stripe rust QTL

Avocet S / PI182103 RIL population: QTL detected on chromosomes 2AS and 3AL for seedling resistance and 4DL, 5BS, and 7BL for APR; *QyrPI182103.wgp-4DL* was designated as *Yr79* {11222}.

Avocet S (S) / Qinnong 142 (R): RIL population: Adult-plant resistance: *QYrqin.nwafu-1BL – AX-95133868 – AX-94522424*, R^2 = 0.16–0.20, likely *Yr29*; *QYrqin.nwafu-2AL*, *AX-94655393 – AX-9489521*, R^2 = 0.08–0.20; *QYrqin.nwafu-2BL*, *AX-94507002 – AX-94562871*, R^2 = 0.18–0.39; *QYrqin.nwafu-6BS* R^2 = 0.14–0.31 {11377}.
Seedling resistance in Qinnong 142 to race CYR23 was attributed to genes on chromosomes 1DS and 4AL {11377}.

Jagger (MR) / 2174 (MS): After {10973}. Add: According to {11356} *Qyr.osu-5A* is an orthologue of *OsXA21* and confers resistance to multiple pathogens/pests.

Luke (MR) / AQ24788-83 (APR): RIL population: *QYr.cau-2AL* near *IWB4475* (R^2 = 23–40%) from AQ24788-83 and *Yr18* (R^2 = 11.0–14.7%) from Luke (11366).

Mingxian 169 (S) / Chakwal 86 (R): RIL population: QTL on chromosomes 1BL (*Yr29*), 3BS (not *Yr30*), and 6BS (*QYrcw.nwafu-6BS*) contributed to the high level of APR in Chakwal 86 {11371}.

Mingxian (S) / P9936 (R): RIL population: *QYr.nwafu-3BS* (probably *Yr30*) and *QYr.nwafu-7BL* flanked by *AX-108819274* and *AX*-11040708 (R^2 = 36.0–38.9%; a KASP marker was developed for the latter {11373}.

Mingxian 169 (S) / Qing Shumai (R): RIL population: APR QTL *QYr.cau.6DL*, *Xbarc1121-6D – Xgpw4005-6D* region: positive interaction with *Yr18* {11323}.

Mingxian 169 (S) / Centrum (R): RIL population: QTL detected on chromosomes 7BL (*QYrcen.nwafu-7BL*, R^2 = 23.4%, *AX-94556751 – AX-110366788*), 1AL (*QYrcen.nwafu-1AL* (R^2 = 11.2%, *AX-94488258 – AX-94458040*), and 4AL (*QYrcen.nwafu-4BL*, R^2 = 12.6%, *AX-94695204 – AX94996273* {11365}.

Mingxian 169 (S) / Toni (R): RIL population: *QYrto.swust-3AS*, *AX-95240 – AX-9482889091*, R^2 = 0.22–0.56: *QYrto.swust-3BS*, *AX-994509749 – AX-94998050*, R^2 = 0.23–0.55 {11379}.

Soru#1 (R) / Naxos (MR): RIL population: Seedling and field tests detected two moderately effective QTL that were likely *Yr24* and *Yr28* derived from Soru#1 {11368}. A KASP marker was developed for *Yr28*.

Thatcher (S) / Hong Qimai (APR) RIL population: *QYr.cau-2AL* near *Xgwm311-2A* and *IWB4475* (R^2 = 47–52%), *Qyr.cau-4AL* (R^2 = 5–7%) and *Qyr.cau-7AL* (R^2 = 9–10%) derived from Hong Mai {11366}.

107. Reaction to *Puccinia triticina*

107.1. Genes for resistance

***Lr17*.**
***Lr17a*.** **v2:** Jagger *Lr37* {11328}.
At the end of section add the following to the list of complex genotypes:
Duster: *Lr34 Lr46 Lr77* {11369}.

***LrSV2*.** Add note:
'According to {11334} *LrSV2* acted in a complementary way with *Lrc*-SV2 on chromosome 4BL. These complementary genes were closely linked to the locations of *Lr27* and *Lr31* but were considered to be different genes.'.

109. Reaction to *Pyrenophora tritici-repentis*

109.1. Resistance to tan spot

Tsr7 {11363}. Dominant. *QTs.zhl-3B* {11362}.
3BL {11362, 11363}. **v:** *Br34* {11363}; Penawawa {11363}.
sutv: LDN (*T. dic*. IsraelA 3B} {11363}.
ma: Linked STARP markers were developed {11363}.
Tsr7 conferred resistance to race 1 (isolate Pti2), race 2 (isolate 86-124), race 3 (isolate 331-9), and race 5 (isolate DW5) {11362}.

QTL
Louise / Penawawa RIL population: *QTs.zhl-1A*, located at interval 0–6.0 cM and likely *Tsc1*; *QTs.zhl-2D*, located at 144.0–152.0 cM; *QTs.zhl-3B*, located at 72.0–78.0; and *QTs.zhl-5A* located at 154–160 cM {11362}.

112. Reaction to *Schizaphis graminum*

Gb8 {11378}. *Gb595379-1* {11378}. 7DL {11378}.

bin: 7DL3-0.81-1.00. **v:** PI 595379-1 {11378}.

ma: *Xbarc11-7D* – 10.41 cM – *Gb8* – 7.4 cM – *Xwmc824-7D* – 4.8 cM – *Xgwm428-7D* {11378}. *Gb3* – *Gb8* 15 cM {11378}.

119. Reaction to Wheat Streak Mosaic Virus

Wsm2. **v:** Add: Clara CL PI 1665948 {11329}; Oakley CL PI 670190 {11329}.

ma: Eight SNP markers were mapped within 1 cM of *Wsm2* {11329}. KASP markers were developed from some of these SNP {11330}.

122. Reaction to Wheat Yellow Mosaic Virus

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