V. CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2018 SUPPLEMENT

R.A. McIntosh[1], J. Dubcovsky[2], W.J. Rogers[3], X.C. Xia[4], and W. J. Raupp[5].

[1]The University of Sydney, Plant Breeding Institute Cobbitty, PMB 4011, Narellen, NSW 2570, Australia. robert.mcintosh@sydney.edu.au.
[2]Department of Plant Sciences, University of California, Davis, CA 95616, USA. jdubcovsky@ucdavis.edu.
[3]Catedra de Genetica y Fitotecnia, DCBA y B, Facultad de Agronomia, CIISAS, CIC–BIOLAB AZUL, Universidad Nacional del Centro de la Provincia de Buenos Aires, Argentina; Av. Rep. Italia 780, CC47 73 Azul, Provincia de Buenos Aires, Argentina. CONICET–INBA–CEBB–MdP. rogers@faa.unicen.edu.ar.
[4]Institute of Crop Science, National Wheat Improvement Centre, Chinese Academy of Agricultural Sciences, 12 Zhongguancun South St, Beijing 100081, China. xiaxianchun@caas.cn.
[5]Department of Plant Pathology, Wheat Genetics Resource Center, Kansas State University, Manhattan, Kansas 66506, U.S.A. jraupp@k-state.edu.

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 2013–14, 2015–16, 2017 also are available at those sites.

The 13th International Wheat Genetics Symposium in 2017 adopted the resolution that genetic loci in wheat should be designated in uppercase italics, e.g., *RHT1*, *SR35*, and that alleles be designated with first letter in uppercase for dominant alleles, e.g., *Rht1*, *Sr35,* and all lowercase letters for recessive alleles, e.g., *rht1, sr35*. The same procedure can be used in the case of nomenclature based on homoeologous sets, e.g., *RHT-D1* for the locus and *Rht-D1a*, *Rht-D1b* for alleles.

Laboratory Designators

sicau	Triticeae Research Institute Sichuan Agricultural University Wenjiang, Chengdu Sichuan 611130 PR China
stars	Xiangyang Xu USDA–ARS, Wheat, Peanut, and Other Field Crop Research Unit 1301 N. Western Road Stillwater OK 74075 USA

Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

1.7. Multi-gynoecium

Pis1{10636}. **i:** Add: CM28TP {M10028}.

ma: Add: *KM69_132294739* – 3.5 cM – *KM70_136805221* – 3.0 cM – *Pis1* – 1.1 cM – *KM71_140258883* {11228}.

4. Aluminum Tolerance

Almt1. *TaALMT1* {11242}. 4DL {11242}.
v: CAR3911 {11242}.
ma: *Xwmc457-4D* – 4.0 cM – *Almt1* – 2.0 cM – *Xwmc331-4D* {11242}.

5. Anthocyanin Pigmentation

5.5. Purple grain/pericarp

The location the second complementary gene is confusing: all three group-7 homoeologues may be involved in different materials.

Pp1.
Pp-A1. 7AS **v:** Saratovskaya 29 (not purple) {11312}.
Pp-B1. 7BS Later renamed as *Pp3b*.
Pp-D1. *TaPpm1a* {11313}. 7DS {11312}.
v: Heixiaomai 76 *Pp3* {M1811}; Luozhen 1 *Pp3* {11313}.
c: GenBank KM382421, a purple pericarp MYB 1, is strongly expressed in the pericarp {11313}. GenBank MG066451 {11313}.

Pp3. *TaMyc1* {11312}, *TaPpb1a* {11313}. 2AS.
v: Heixiaomai 76 Pp3 {M1811}; Luozhen 1 Pp3 {11313}.
c: Encodes a protein with an anthocyanin bHLH regulatory factor {11313}. GenBank MG066455; has a 6x261 bp tandem repeat in the promoter {11313}. Specifically expressed in the seeds {11313}. The alternate allele has only a single 261-bp repeat {11313}.

Combinations of *Pp3* and one or other *Pp1* single purple allele gave light purple pericarp whereas combinations involving *Pp3* with multiple purple alleles gave a dark purple phenotype {11312}.

Add note at end of section: Transcription factor *TaMYB3* on chromosome 4BL bin 0.62-0.95 isolated from purple grained cv. Gy115 appeared to be involved in purple pericarp color, but was not the candidate gene for purple grain color {11285}. This may correspond to *TaPpm2* located on chromosome 4BL, one of three *Ppm* genes with no effect on purple pericarp {11313}.

2. Chlorophyll Abnormalities

2.4 Yellow-green

yg [{11238}]. Incompletely dominant. *y1718* {11238}. 2BS {11238}.
v: Xinong 1718 mutant {11238}.
ma: *Be498358* – 4.0 cM – *yg* – 1.7 cM – *Xwmc25-2B* {11238}.

The homozygous *ygyg* genotype is extremely yellow, stunted and sterile and the mutant is easily maintained as a heterozygote {11238}.

18. Dormancy (Seed)

18.3. Preharvest sprouting

Add at end of section:
QPhs.sicau-3B.1, distally located on chromosome 3B in '*T. aestivum* subsp. *spelta* CSSR6 (res) / Lang (sus)'; nearest marker *wPt-6157*; transferred to durum cv. Bellaroi using SCAR markers {11246}.

29. Glaucousness (Waxiness/Glossiness)

29.2 Epistatic inhibitors of glaucousness

W1. **bin:** 2BS-0.84-1.00. **v:** P86 {11247}.
ma: *Xgwm210-2B* – 0.77 cM – *XWGGC3197* – 0.81 cM – *W1* – 0.12 cM – *XWGGC2484* – 0.32 cM – *Xbarc35-2B* {11247}.
w1. **v:** J87 {11247}.
Iw1. **tvsu:** LDN$_{DIC521\text{-}2B}$ {11245}.
tv: *T. turgidum* subsp. *dicoccoides* PI 481521 {11245}.
ma: *Xgwm614-2B – Iw1/Xbarc35-2B/CD893659/CD927782/BQ788707/CD938589 – Be498111* {11245}.

Iw2. Add synonym *IwT* {11207}.

v: PBW114 /*Ae. tauschii* PAU14195 // 4*WH542 backcross selections {11207}.

dv: *Ae. tauschi* PAU14195 {11207}.

ma: *Xcau96-2D* – 1.6 cM – *LrT* (*Lr39*) – 0.6 cM – *Xbarc124-2D* – 0.3 cM – *Xte6-2D* – 2.5 cM – *IwT* – 4.1 cM – *Xgdm35-2D* {11207}.

30.2. Flour, semolina, and pasta color

Add at the end of section:

Three QTL for peroxidase activity in the grain identified in a 'Doumai (high POD activity) / Shi 4185 (low POD activity) 'cross were named as *QPod.caas-3AL QPod.caas-4BS,* and *QPod.caas-5AS* {11233}. Allelic variation was found at the *QPod.caas-3AL* locus {11233}.

TaPod-A1a {11233}. 3AL {11233}. **v:** Doumai {11233}.

TaPod-A1b {11233}. **v:** Shi 4185 {11233}.

There seemed to be no relationship to the *Per-* series identified by isozyme analyses and listed in the Protein section.

44. Height

44.2. Reduced Height: GA-sensitive

Rht14.

GA2oxA9 expression was higher in Castelporziano than in its tall parent Capelli – see *Rht18* {11301}.

Rht18. **matv:** *Xbarc118-6A* – 1.4 cM – *Rht18/TdGA2Ox-A9/S470865SSR4/Xbarc37-6A* – 0.4 cM – *IWA4371* – 0.4 cM - *Xgwm82.1-6A* {11295}.

Independent 'overgrowth' mutants isolated from Icaris contained changes in the *GA2oxA9* coding region; this gene is predicted to encode GA 2-oxidase that metabolizes GA biosynthetic intermediates into inactive products thus reducing bioactive GA_1 {11301}.

Rht24. *Rht24b* {11293, 11294}. **v:** Solotar {11294}.

ma: Excalibur_rep_c69275-346 {11294}.

Rht24 is occurs at relatively high frequencies in European and Chinese wheat cultivars, and maps in the same region as *Rht14, Rht16,* and *Rht18* {11293}.

Rht25 {11300}. *QHt.ucw-6AS* {11300}. 6AS {11300}.

bin: 6AS1-0.35-1.00.

v: UC1110 *Rht-D1b* {11300}.

ma: *QHt.ucw-6AS* was located in a 0.2 cM interval flanked by *6A13699/6A13791/6A14397* and *6A14825* {11300}.

Rht25 is proximal to *Rht14/Rht16/Rht18* {11300}.

44.3. Reduced height: temporary designations

Rht_NM9 {11273}. 2AS {11273}.

v: Induced mutant NM9 {11273}.

ma: *Xgwm122-2A* – 1.7 cM – *SNP34* – 1.9 cM – *Rht_NM9* – 1.9 cM – *SNP41* – 14 .0 cM – *Xwmc261-2A* {11273}.

46. Hybrid Weakness

46.6. Hybrid weakness type II

Add: A gene named *NetJingW176* (after *Ae. tauschii* accession Jing Y176) was located in chromosome 2DS – *Xgwm-102*-2D – 4.5 cM – *Nec2* – 3.8 cM – *Xgwm515-2D* {11307}.

48. Lack of Ligules

Add to the introductory paragraph:
A dominant mutant allele for liguleless phenotype is reported in *Ae. tauschii* – this locus is located in chromosome 2DL but is independent of *LG2*.

LG2. **bin:** C-2DL3-0.49.
ma: *Xbarc228-2D* – 12.7 cM – *Lg2/G3489_1DL12del/G3489_2DL11del* – 3.3 cM – *Xgdm6-2A* – 47.8 cM – *Xgwm301-2D* {11220}.

Following the *lg2* entry delete the sentence relating to diploid wheat.

LG^t {11220}. Dominant mutation to liguleless phenotype. **bin:** C-2DL9-0.75.
Lg2^t {11220}. **dv:** Liguleless mutants of Ae. tauschii accession KU20-9 {11220}.
ma: *Xgwm301-2DL*……… *Xbarc159-2D* – 9.3 cM – *LG*^{t} {11220}.

53. Male Sterility

53.1. Chromosomal

Ms1. 4BS. **ma:** Located in a 0.05 cM region between *X27140346* and *X12360198* {11269}.
c: Encodes a glycosylphosphatidylinositol-anchored lipid transfer protein that is essential for pollen exine production {11269}. GenBank KX447407.
ms1d. **c:** A G329A frameshift mutation in exon 1 {11269}.
ms1e. **c:** A C1435T + 16-bp deletion in exon 2 {11269}.
ms1f. **c:** A G155A frameshift mutation in exon 1 {11269}.
ms1g {619}. See ms5.
ms1h {11269}. **v:** Obtained in a TILLING population of QAL2000 {11269}.
c: A G178A frameshift mutation in exon 1 {11269}.

74. Stem solidness

Qsst.msub-3BL. **bin:** 3BL11-0.81-1.00.
v: Add: Fortuna {11230}; Genou {11230}; Judee {11230}; Rescue {11230}; S-615 {11230}; Vida {11230};

Add note before the present note: Haplotype analyses in a range of hexaploid and tetraploid accessions suggested the possibility of multiple alleles or loci in the QTL region {11230, 11239}. Conan with an intermediate level of stem solidness, represent, a different haplotype from other North American cultivars {11230}.

Pathogenic Disease/Pest Reaction

89. Reaction to *Bipolaris sorokiniana*

Sb2 {11255}. *QSb.bhu-5B* {10709} 5BL {11255}.
bin: 5BL1-0.55-0.75. **v:** YS116 {11255}.
ma: Tightly linked to *Xgwm639-5B* and *Xgwm1043-5B* {11255}.
Sb3 {11256}. 3BS {11256}. **bin:** 3BS8-0.78 -1.00.
v: Line 621-7-1 {11256}.
ma: *Sb3/XWGGC3959* were mapped to a 2.2-cM interval between *Xbarc133/Xbarc147/Xcfp30-3B/XWGGC5911* and *XWGGC4320* {11255}; *XWGGC12798* – 0.08 cM – *SB3XWGGC9893/XWGGC10235* – 0.07 cM – *XWGGC6119* {11255}.

90. Reaction to *Blumeria graminis* DC.

90.1. Designated genes for resistance

Pm2a. **c:** NBS–LRR structure {11270}. GenBank CZT14023.1.

Pm4b. **i:** ‘VPM1 / 7*Bainong 3217’ {11287}.
ma: *Xics13* – 1.3 cM – *Pm4b* – 1.7 cM – *Xics43* covering a 6.7 Mb physical region {11287}.

Pm4e {M11317}. 2AL {M11317}. **v:** D29 {M11317}.
ma: *Xgdm93-2A* – 4.9 cM – *Pm4e/Xsts_bcd1231* – 1.8 cM – *Xhbg327-2A* {113017}.

Pm8. **c:** Ortholog of *Pm3* with 81% homology with *Pm2a* at the nucleotide level {11276}. GenBank AGY30894.1.

Pm21. **v:** Add: A derivative named HP33 was described as a 'cryptic' translocation {11275}.
c: Add: NLR-V1, one of two NLR-V genes in HP33, was identified as the candidate for *Pm21* {11275}. GenBank MF716955. Silencing of *NLR-V1* compromised *Pm21* resistance in the T6AL·6VS lines described below and decreased the level of resistance in the T6DL6VS lines described below {11275}.

Secondary recombinants 6AS$_{10:6}$ and 6AS$_{16:6}$ are reported in {11305}.

Pm58. **v:** U6714-A-011, PI 682090 {11320}; U6714-B-056, PI682089 {11320}.

Pm59 {11214}. *Pm181356* {11214}. **bin:** 7AL15-0.00-1.00.
v: PI 181356 {11214}.
ma: *Xwmc525-7A* – 1.8 cM – *Xmag1759* – 0.5 cM – *Pm18156* – 5.7 cM – *Xmag1714* – 20.0 cM – *Xcfa2257-7A* {11214}.

Pm60 {11250}. *PmR2* {M1800}. 7AL {11250}. **bin:** 7AL16-0.86-1.00.
dv: PI 428196 {11250}; PI 428210 {11250}; PI 428215{11250}; PI 428306 {11250}; PI 428309 {11250}; PI 428310 {11250}; PI 538737 {11250}; PI 538751 {11250}.
ma: *Xwmc273.3-7A* – 3.9 cM – *scaf10-5.13* – 2.0 cM – *scaf14-17.9* – 0.3 cM – *Pm60/scaf13-6.30* – 0.7 cM – *scaf45-5.24* {11250}.
c: NBS–LRR; the sequence in PI 428309 (GenBank MF996807) is 4,365 bp. The sequence of PI 428215 (GenBank MF996808) has a 240-bp insertion relative to PI 428309 whereas PI 428210 (GenBank MF996806) lacks the same sequence, which corresponds to two LRRs {11250}.

pm60. **dv:** G1812 {11250}.

Pm61 {11290}. 4AL {11290}. **bin:** 4AL4-0.8-1.00.
v: Xuxusanyuehuang {11290}.
ma: *Xgwm160-4A* – 0.23 cM – *Pm61* – 0.23 cM – *Xicsx79* {11290}.

This gene was considered to be at a different locus to MlIW30, a dominant gene in *T. turgidum* subsp. *dicoccoides* accession IW30 and its hexaploid derivative Line 2L6 {11289}.

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

MlIW30 {11289}. MLIW30 [{11289}]. 4AL {11289}.
bin: 4AL4-0.8-1.00
v: Line 2L6 {11289}.
tv: *T. turgidum* subsp. *dicoccoides* IW30 {11289}.
ma: *Xbarc78-4A* – 1.00 cM – *XB1g2020.2* – 0.1 cM – *MlIw30* – 0.1 cM – *XB1g2000.2* – 2.6 cM – *Xgwm350-4A* {11289}.

MlHLT {18057}. 1DS {11257}. **v:** Hulutou {11257}.
ma: *Xgwm-1D* – 1.7 cM – *Xwggc3026* – 1.5 cM – *MlHLT* – 2.1 cM – *Xwggc3148* – 4.0 cM – *Xcfd83-1D* {11257}.

MlUM15 {11216}. Derived from *Aegilops neglecta*. 7AL {11216}.
bin: 7AL15-0.99-1.00.
v: NC09BGTUM15 {11216}.
al: *Ae. neglecta* TTCC 223 {11216}.
ma: *Xwmc525-7A/IWA8057* – 0.7 cM – *Xcfa2257-7A* – 0.4 cM – *MlUM15* – 0.8 cM – *Xcfa2240-7A* – 2.8 cM – *Xmag2185* – 3.4 cM – *IWA29295* – 4.0 cM – *IWA4434* {11216}.

PmAF7DS {11291}. 7DS {M10891}. **v:** Arina {11291}.
ma: *Xpsr160-7D* – 1.3 cM – *Xgwm350a-7D* – 4.7 cM – *PmAF7DS* – 9.9 cM – *Xbarc184/Xgwm111-7D* {11291}.

Three of 61 Israeli *Bgt* isolates were avirulent: all three isolates were from tetraploid wheat accessions. It is possible that the gene may be present in many common wheat accessions.

PmG3M {M10102}. 6BL {11302}. **bin:** 6BL-0.7-1.00.
tv: *T. turgidum* subsp. *dicoccoides* G-305-3M {11302}.
ma: *Xgpw-6B* – 13.6 cM – *PmG3M* – 3.5 cM – *Xuhw213-6B* – 5.7 cM – *Xedm149-6B* {11302}.

PmU {11251}. 7AL {11251}. **dv:** UR206 {11251}.
ma: *Xwmc273-7A* – 2.2 cM – *PmU* – 3.8 cM – *Xpsp3003-7A* {11251}.

PmU was transferred to, and was effective in, common wheat.

PmX [{11215}]. *pmX* {11215}. 2AL {11215}.
bin: 2AL1-0.85-1.00.
v: Xiaohongpi {11215}.
ma: *Xhbg327-2A* – 0.6 cM – *PmX/Xsts-bcd1231* – 8.9 cM – *Xgpw4456-2A* {11215}.

95. Reaction to *Diuraphis noxia*

DN1. **bin:** 7DS-0.36-0.73 {11225}.
Dn1. Add note: Tests of allelism indicated that *Dn1*, *Dn2*, *Dn5*, *Dn6*, and *Dnx* and four uncharacterized lines were identical or closely linked {11225}.

Dn4. Following the {863}. Add: ', 1DS {11225}'.
Add note: *Dn4* and an uncharacterized gene in PI 151918 were allelic or tightly linked {11225}.

Dn6. 7DS {0352, 18025}.
ma: Xgwm44-7D – 11.6 cM – Xgwm111-7D – 3.0 cM – Dn6 {11225}.

Dn10 {11211}. 7DL {11211}. **bin:** 7DL-0.1-077.
v: PI 682675 {11211}.
ma: *Xcfd14-7D* – 2.3 cM – *Xgwm437-7D* – 9.0 cM – *Dn10* – 29.1 cM – *Xwmc488-7D* {11211}; *Xcfd14-7D* – 3.6 cM – *Xgwm437-7D* – 11.3 cM – *Dn10* – 35 cM – *Xwmc488-7D* {11211}; *Dn626580* – 2.0 cM – *Dn2401* – 8.4 cM – *Dn624151* {11211}.

Dn2401. **bin:** 7DS-0.37-0.61 {11211}.

Dn100695 {11226}. 7DS M19026}. **v:** IG 100695 {11226}.
ma: *Xgwm44-7D* – 13.0 cM – *Xcfd14-7D* – 15.7 cM – *Dn100695*.

Dn626580 {11227}. 7DS {11227}. **v:** PI 626580 {11227}.
ma: *Xgwm473-7D* – 3.2 cM – *Xbarc214-7D* – 1.8 cM – *Dn626580* {11227}.

96. Reaction to *Eurygaster Integriceps*

Sunn pest

Ei1 {11201}. 4BS {11201}. **bin:** 4BS4-C-0.27.
v: IG139431 {11201}; IG139883 {11201}.
ma: *IWB73001 – Ei1/BS00022785 – IWB9610* {11201}.

97. Reaction to *Fusarium* spp.

97.1. Disease: Fusarium head scab, scab

Fhb1. Modify or add:
v2: Alsen *Fhb5* {11071, 11237}; Carberry *Fhb5* {11237}; ND744 *Fhb5* {11237}; ND3085 *Fhb5* {11237}; Sumai 5 *Fhb2 Fhb5* {10314, 11237}.
ma: *Xgwm389-3B* – 3.0 cM – *Sr2/csr2* – 0.4 cM – *Xgwm389-3B* – 2.0 cM – *Fhb1/UMN10/UMN*$_{v2}$ (coupling) {11210}. *Xgwm493-3B* and *Xgwm533-3B* were confirmed as useful markers {11237}.
c: A pore-forming toxin-like gene product encodes a chimeric lectin with two agglutinin domains and an ETX/MTXZ toxin domain {11205}.

Fhb5. *Qfhs.ifa-5A* {10076}.
v2: Modify or add: Alsen *Fhb1* {11237}; Carberry *Fhb1* {11237}; ND744 *Fhb1* {11237}; ND3085 *Fhb1* {11237}; Sumai 5 *Fhb1 Fhb2* {10314, 11237}.
ma: *Xgwm150-5A*, *Xgwm304-5A*, and *Xgwm595-5A* confirmed as useful markers.

97.2. Disease: Crown rot

Three crosses involving EGA Wylie: *Qcrs.cpi-5Ds* ($R^2 = 0.31$) and *Qcrs.cpi-2DL* ($R^2 = 0.221$). Two additional QTL on chromosome 4BS were associated with plant height {11243}.

Nine NIL sets derived from three crosses of Australian wheat cultivars and *T. spelta* CSCR6: *Qcrs.cpi* was flanked by *Xcfp1822-3B* and *Xgwm181-3B* {11244}.

98. Reaction to *Heterodera avenae* Woll., *H. filipjeva* (Madzhidov) Stelter, add: ***H. latipons* Franklin**

At end of section:
For review {11309}.

99 Reaction to *Magnaporthe grisea* (Herbert) Barr Add: **Syn. *Pyricularia oryzae***

99.1 Current *Mg* list.

99.2 Reaction to *Magnaporthe oryzae*.

Rmg8.

Add note: *Rmg8* also confers resistance to the wheat form of the pathogen. Its response is not sufficiently effective when present alone, but is enhanced in the presence of *RmgGR119* {11263}.

AVR-Rmg8 was isolated and shown to be a small protein with a putative signal peptide. This protein was recognized by both *Rmg8* and *Rmg7* {11272}.

RmgGR119 {11263}. **v:** GR119 {11263}.

RmgGR119 confers resistance to the wheat form of the pathogen and its response is enhanced in combination with *Rmg8* {11263}.

Add Note: Near-isogenic lines with the T2A–2NS translocation from *Ae. ventricosa* displayed reduced levels of spike blast, but there was little effect on seedling leaf blast response {11265}: **v:** Milan; VPM1.

100. Reaction to *Mayetiola destructor* (Say)

H26. **ma:** *Xrwgs-3D* – 3.2 cM – *H26/Xrwgs11-3D* – 1.0 cM – *Xrwgs12-3D* {M11318}.

101. Reaction to *Meloidogyne* spp.

Rkn3. Reference {11264} added to reference {10801} for this gene.

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

Snn5 {11203}. 4BL {11203}. **bin:** 4BL5-0.85-1.00.
tv2: Lebsock *Tsn1 Snn3-B1* {11203}.
ma: *Xbarc163/Xcfd22-4B* – 13.3 cM – *Snn5* – 2.8 cM – *Xwmc349-4B* {11203}.

snn5. **tv2:** PI 94749 {11203}.

Snn6 {11206}. 6AL {11206}. **v:** Opata 85 {11206}; RIL ITMI137 {11206}.

snn6. **v:** Synthetic W-7984 {11206}.
ma: Flanked by XBE424987 and XBE403326 {11206}.

Snn7 {11292}. Sensitive to SnTox7. 2DL {11292}.
bin: 2DL-9-0.75-1.00.
s: CS(Timstein 2D) {11292}.
v: Timstein {11292}.
ma: *Xcdf267-2D* – 2.3 cM – *Xgdm6-2D* – 0.9 cM – *Snn7/Xcfd44-2D* – 1.8 cM – *Xgwm349-2D* – 11.3 cM – *Xgwm311-2D* {11292}.

106. Reaction to *Puccinia graminis* Pers.

Sr2. **ma:** *Xgwm389-3B* – 3.0 cM – *Sr2/csr2* – 0.4 cM – *Xgwm389-3B* – 2.0 cM – *Fhb1/UMN10/*UMN_{v2} (coupling) {11210}.

Sr5. **ma:** Flanked by *Xbarc183-6D* and *wPt3879* {11232}.

SR13. Revised listing.
Sr13 {674}. 6AL {929}. **bin:** 6AL-8
ma: *Xwmc59-6A* – 5.7 cM – *Sr13* {10607}; *CD926040* – *Sr13* – *BE471213* {10777}.
c: *Sr13* was identified as a CC–NBS–LRR gene with three haplotypes in two specificities {11217}.

Sr13a {674, 11217}.
i: Khapstein /9^{*}LMPG {685, 11217}; Khapstein / 10^{*}Marquis Sr7b {686}.
v: Machete {10607}.
v2: Khapstein *Sr7a Sr14* {674}.
tv: Kronos PI 576168 {11217}; Langdon {11217}; Maier {11217}; Renville {11217}; ST464-C1 {10473}.
tv2: Khapli *Sr14* {674}.

Sr13b {11217}. **tv:** D99656 {11217}; Kofa PI 584336 {10777; 11217}; Medora PI496260 {10777, 11217}; Sceptre {10777}.

Haplotypes of other germplasm previously listed are unknown.
v2: French Peace *Sr7a Sr9a* {680}.
tv2: Arrivato *Sr8b Sr9e* {10607}; ST464 *Sr9e* {10473}.

Unspecified allele. **tv:** PI534304 {11280}.

A resistance gene in 'Khapstein / 9*LMPG' and believed to be *Sr13* was mapped in chromosome 6AL by Admassu et al. {10778}. However, the map location was more than 50 cM proximal to that reported in {10777}. It was resolved in {10779} that the resistance locus mapped in {10778} could not be *SR13*.

Sr21. **v:** CSSr21 {M10115}.
madv: *CJ961291* – 0.02 cM – *Sr21* – 0.04 cM – NLR pseudo-gene cluster {11315}; A diagnostic marker was developed from the cloned gene {11315}.
c: *Sr21* is a CC–NBS–LRR gene of 4,872 bp; 44 diploid accessions with *Sr21* were classified as five haplotypes – i.e., Haplotype R1, MG582649, 28 accessions including DV92 (and CSSr21); Hap R2, GenBank MG601519, six accessions; Hap R3, MG601520, one accession; Hap R4, MG601521, six accessions; and Hap R5, MG601522, three accessions {11315}.

***Sr22*.** **c:** *Sr22* has CC–NBS–LRR structure: NCBI LN883743 {11213}.

Sr25. **v:** Misr 1 (Oasis/Skauz//4*BCN/3/2*Pastor) {11260}.

***Sr33*.** **c:** GenBank KF031291; 4,639 bp; protein CUM44200.1.

***Sr35*.**

Add note: *Sr35* was postulated in 21 accessions of *T. monococcum* subsp. *monococcum* {11288}.

Sr45. **c:** *Sr45* has CC–NBS–LRR structure: NCBI LN883757 {11213}.

Sr46. **bin:** 2DS5-0.47-1.00.
dv: *Ae. tauschii* var. *meyeri* AUS18913 {10538} = CIae 25 {11268}; *Ae. tauschii* TA1703 {11268}.
ma: *Xgwm210-2D* – 3.9 cM – *Sr46* – 5.6 cM – *Xcfd36-2D* – 0.3 cM – <u>*Xwmc111-2D*</u> {11268}.

Add note:
Sr46 was more effective at higher temperatures in laboratory tests {11268}.

Sr47. Modify: 2B = T2BL–2SL–2BL·2BS.
tv: RWG35 {10872}; RWG36 {10872}; RWG37 {10872}.

Add note immediately following the **ma:** entry:
Further markers were used to identify the introgressions in RWG25, RWG26, and RWG27 {10872}. STS marker *Xrwgs38* was diagnostic for the *Sr47* segment in DAS35 and DAS36 {11319}.

Sr50. **v:** T1DL1RS–DR.A1 {11316}.
c: *Sr50* is a CC–NBS–LRR gene homologous to barley *Mla* {11316}. GenBank KT725812, 3,508 bp.

Sr60 {11208}. 5A^{m}S {11208}. **dv2:** PI 306540 *Sr21 SrTm4 SrTm5* {11208}.
ma: *Pinb-5A^{m}S……GH724575/DK22976/CA5012332* – 0.25 cM – *Sr60/LRRK123.1* – 0.19 cM – *CJ942731/CJ884584* {11208}; *GH724575* – 1.56 cM – *Sr60/LRRK123*.1 – 0.52 cM – *FD475316* {11208}.

SrTm5 (11208}. 7A^{m}L {M11208}.
dv: *T. monococcum* subsp. *monococcum* PI 277131-2 {11208}.
dv2: *T. monococcum* subsp. *monococcum* PI 306540 *Sr21 Sr60 SrTm4* {11208}.
ma: *SrTm5/IWB25012/IWB44281/IWB405527/Sr22GMF/GMR* – 0.8 cM – *IWB6942* {11208}.

May be allelic with <u>*Sr22*</u> {112308}.

Sr10526 {11249}. 6DS {11249}. **v:** CItr 105026 {11249}.
ma: *IWB36391*/*IWB34477* – 2.9 cM – *Sr15026* – 3.0 cM – *IWA4000* {11249}; *IWB36391* – 0.4 cM – *IWB262* – 2.6 cM – *Sr15026* – 1.3 cM – *IWB49086* {11249}.

Sr150026 was detected with races QFCSC and TTTTF. When the same DH and RIL populations were tested with race TRTTF, there was evidence for complementary resistance genes on chromosomes 6DS and 6AS, one of which was *Sr10526*. When the populations were tested in the field in Kenya with Ug99 races *QSr.abr-6AS.1* (R^2 = 0.1–0.3) was detected.

Add note at the end of the section: Consensus maps of many reported genes and QTL for stem rust resistance are provided in {11202}.

QTL:
'Spark / Rialto' DH population: *Sr5* and *Sr31* were derived from Rialto and *QDr.sun-3BS* (*Xgwm1034-3B – BS00010945* region and *QSR.sun-5A* (*Xgwm445-5A – Xgwm205-5A* region) were derived from Spark {11231}.

106.1. Designated genes for resistance to stripe rust
Yr3a. After '1B {185, 184}' add:, revised to 5BL {11235}. 2B.

Yr5. **ma:** Add: Accurate prediction of *Yr5* was achieved with markers *IWA4096, IWA 6121* and *IWA7850* for which primer sequences are available in Cereals DB 11286}.

Yr10. **v:** Crest {11304}; 10 Chinese cultivars {11304}.
ma: *Yr10*/*Xsdauw79* – 0.2 cM – *Xsdauw78* – 1.0 cM – *Yr10*$_{CG}$ – 2.1 cM – *Xsdauw75* – 0.5 cM – *Xpsp3000-1B* {11304}.
c: AF149112 (*Yr10*$_{CG}$) shown not to be the candidate gene {11304}.

Yr15. **v:** Add: Ochre {11240}.
ma: Add: *Xbarc8-1B* – 0.26 cM – *R11*/*R5* – 0.51 cM – *Yr15* – 0.26 cM – *Xgwm413-1B*/*R8* {11240}.

Yr17. *YrHy1* {11308}, *YrMm58* {11308}.
v: Huaiyang 1 {11308}; Kochu {11267}; Mengmai 58 {11308}; Milan {11267}; Mutus {11267}.

Add note at the end of section: Although *Yr17* was reported as a seedling-effective gene {62} some researchers report problems in obtaining repeatable seedling responses and prefer to treat this gene as conferring adult-plant resistance {11221}.

Yr18.
Add at end of section: *Yr18* conferred seedling resistance to leaf rust when transformed into durum wheat {M10114}.

Yr24. **v:** Neimai 836 {11259}.

Yr29. **v2:** Add: Druchamp {11235}.

Yr34. Add: Syn. *Yr48* {11266}.
v: UC1110/PI610750 RIL#143 {11266}.
ma: *Xgwm291-5A* – 0.5 cM – *B1* – 1.5 cM – *Yr34*/*Xgwm410.2-5A*/*Xcfa2149-5A*/*KASP_109*/*KASP_6988*/etc. {11266}; *Xgwm291-5A* – 2.3 cM – *B1* – 0.7 cM – *Yr34*/*Xgwm410.2-5A*/*Xcfa2149-5A*/*KASP_109*/*KASP_6988*/etc. {11266}.

Yr34 is <1 cM from the awn inhibitor *B2* {11266}.

Yr36. **v:** Add: Shumai 1701 {11258}.
tv: Add: *T. turgidum* subsp. *dicoccum* PI 415152 {M10058}.

Add note: Although originally described as conferring high-temperature, adult-plant resistance, this gene confers partial resistance in both juvenile and adult plants at temperatures less than 18°C {11277}.

Yr46. **v:** Add: Kundan {M0848}.

Yr48. Add: Syn. *Yr34* {11266}.
v: UC1110/PI610750 RIL#143 {11266}.

Yr79 {11222}. 7BS {11222}. **bin:** 7BL-0.40-0.45.
v: PI 182103 {11222}; PI 679609, Avocet S / PI 679609 RIL#195 {11222}.
ma: *IWA220* – 2.9 cM – *Yr79* – *Xwmc335-7B* – 0.9 cM – *Xbarc72-7B* – 1.7 cM – *Xgwm297-7B* – 1.6 cM – *Xgwm333* {11222}.
Yr80 {11261}. Adult-plant resistance. *YrAW11* {11261}.
3BL {11261}. **bin:** 3BL2-C-0.22.
v: AUS27284 {11261}.
ma: *Xgwm3763B* – 15.2 cM – *KASP_5392*/*KASP_65624* – 3.0 cM – *Yr80* – 4.9 cM – *KASP_53113* {11261}.

Yr81 {11262}. *YrAW5* {11262}. 6AS {11262}
v: AUS27430/AvS RIL#16 {11262}.
v2: AUS27430 Yr18 {11262}.
ma: *Xgwm459-6A* – 19.0 cM – *KASP_3077* – 4.4 cM – *Yr81* – 2.8 cM – *KASP_79351* {11262}

107.2. Temporarily designated gene for resistance to stripe rust

YrF {11218}. 2B {11218}, 2BS {11219}.
v2: Francolin#1 *Yr29* {11218, 11219}.
ma: *Xgwm374-2B* – 2.0 cM – *YrF* – 1.8 cM – *Xwmc474-2B* {11219}.

YrHu {11229}. Derived from *Psathyrostachys huashanica*. 3AS {11229}.
bin: 3AS4-0.45-1.00.
v: H9020-17-25-6-4 {11229}.
ma: *Xcfd79-3A* – 7.2 cM – *YrHu* – 0.7 cM – *BG604577* {11229}.

GISH failed to detect foreign chromatin {11229}.

YrH62 {11303}. 1B {11303}.
v: Line 03031-1-5 (ex CIMMYT) {11303}.
ma: *Xgwm273-1B* – 3.7 cM – *Ax-109871410*/*Ax-109472792*/*Ax109352427* – 0.3 cM – *YrH62* – 0.8 cM – *Ax-109862469* – 2.1 cM – *Xbarc137-1B* {11303}.

YrLk {11252}. 7BL {11252}.
v: Lankao 5 {11252}.
ma: *Xbrac267-7B* – 4.4 cM – *YrLk* – 3.3 cM – *Xwmc396-7B* {11252}.

YrLM168a {11284}. Adult-plant resistance. 6BL {11284}
v: LM16a {11284}; LM16b {11284}.
ma: *Xwmc756-6B* – 4.6 cM – *YrLM168a* – 4.6 cM – *Xbarc146-6B* {11284}.

LM168a and LM168b are derivatives of Milan {11284}.

YrMY37 {11282}. *yrMY37* {11282}. Recessive.
7BL {11282} **v:** Mianmai 37 {11282}.
ma: *Xwmc476-7B* – 1.57 cM – *Xgwm297-7B* – 0.79 cM – *YrMY37* – 0.38 cM – *Xbarc267-7B* {11282}.

YrMY41 {11271}. 1B {11271}. **v:** Mianmai 41 {11271}.

A cross with AvS+*Yr26* failed to segregate. Although claimed to be a possible allele of *Yr24*/*Yr26*, the gene identified is likely to be the same.

107.3. Stripe rust QTL

'Avocet (S) / Kundan (R)': *Yr46* plus *QYr.com-2AL* flanked by *3064488_30:T>G* (R^2 = 0.05–0.09), *QYr.cim-3DS* flanked by *3021242* and *224356* (R^2 = 0.04) and *QYr.cim-5AS* flanked by *3025355_10:T>C* and *1067590* (R^2 = 0.04–0.05) {11248}.

'Avocet S (S) / Napo 63 (R)': *Qyrnap.nwafu-2BS* (11283}. 2BS {11283}.
bin: 2BS-1-0.53. **ma:** Mapped to a 5.46 cM interval flanked by KASP markers *90K-AN34* and *90K-AN36*; and by *Xbarc55-2B* and *Xgwm374-2B* {11283 }.

'Avocet R (S) / Chilero': *Lr46*/*Yr29*, *QLr.cim-5DS*/*QYr.cim-5DS*, *QYr.cim.6BS* and *QYr.cim-7BL* from Chilero, and *QLR.cim-1DL*/*QYr.cim-1DL* from Avocet R {11306}.

'Druchamp (R) / Michigan Amber (S)': Eight QTL for high-temperature, adult-plant resistance: QTL in chromosomes 1BL (nearest marker *Xgwm131-1B*), 2BL (*IWA7583*) and 5BL (2, *IWA2558* and *IWA6383*) were stable across environments, whereas genes in chromosomes 1BL (*IWA8581*, probably *Yr29*), 1DS (*IWA22668*), 3AL (*IWA6834*), and 6BL (*IWA6420*) were not {11284}. In addition, three QTL for all-stage resistance were detected on chromosomes 5B (probably *Yr3*, *IWA6271*), 5DL (*IWA8331*), and 6BL (*IWA3297*).

'Kariega / Avocet S' DH population: Add to existing entry:
These locations were confirmed in a subsequent study; *QYr.sgi-2B.1a* was located within the *wPt5556 – wPt6278* segment {11232}.

'Mingxian (S) / P1057' RIL population, and 'Avocet S (S) / P10057' and 'Zhengmai 9023 (S) / P10057' F_2:F_3 populations: Two strong QTL located in clustered QTL regions: *Qlrlov.nwafu-2BS* identified by *IAW5377, IWA2674, IWA5830*, and *Qyrlov.nwafu-3BS* identified by *IWB57990* and *IWB6491* {11279}.

'Yaco S (R) / Mingxian 169 (R)': Adult-plant resistance. *Qyryac.nwafu-2BS* located within a 1.3-cM region flanked by KASP markers *BS00022657_51* and *IACX6411.BobWhite_22503_605* within the 10.4 cM *Xgwm148-2B – Xbarc55-2B* region {11241}.

Add at end of section: Markers associated with many stripe rust resistance genes are summarized in {11254}.

108. Reaction to *Puccinia triticina*

108.1. Genes for resistance

Lr15. **bin:** 2DS1-0.33-0.47.
ma: *Xgwm4562-2D* – 3.1 cM – *Lr15* – 9.3 cM – *Xgwm102-2D* {11234}.

Lr16. **v2:** Francolin#1 Lr46 {11219}; Waxwing {11267}
ma: *Xwmc764-2B* – 9.4 cM – *Lr16* – 1.4 cM – *Xwmc661-2B* {11219}.

Lr21. **ma:** Add: *Lr21*-mediated resistance requires expression of *RAR1*, *SGT1*, and *HSP90* {11274}.

Lr22a. **i:** CH Campala Lr22a {11209}.
v: Line 98B34-T4B {10467}.
ma: *Xgwm455-2D* – 0.39 cM – *Lr22a* – 1.1 cM – *Xgwm296-2D* {11209}.
c: GenBank KY064064; NBS–LRR structure encoding an intracellular immune receptor homologous to the *Arabidopsis thaliana* RPM1 protein {11209}.

Lr29. **v:** Add: Kundan {11248}.

Lr34. Add at end of section

Lr34 conferred seedling resistance to leaf rust when transformed into durum wheat {11314}.

Lr36. **v:** Add: CDC Bounty {11253}.

Lr39. Add: synonym *LrT* {11207}.

v: 'PBW114 / *Ae. tauschii* PAU14195 // 4*WH542' backcross selections {11207}.
dv: *Ae. tauschii* PAU14195 {11207}.
ma: *Xcau96-2D* – 1.6 cM – *LrT* (*Lr39*) – 0.6 cM – *Xbarc124-2D* – 0.3 cM – *Xte6-2D* – *IwT* – 4.1 cM – *Xgdm35-2D* {11207}.

Lr61 {11224}. *LrAW2* {11223}. 6BS {11223}.

tv: AUS 26579 {11224}; PI 244061 {11280}.
tv2: AUS 26582 Lr79 {11224}.
ma: *sun682* – 0.7 cM – *Lr61*/*sun683*/*sun684* – 0.2 cM – *sunKASP_60* {11223}; *sun682* – 0.6 cM – *Lr61*/*sun684* – 0.6 cm – *sunKASP_59* {11223}.

Lr67. **c:** GenBank: coding sequence KR604817.2, 1,545 bp; protein sequence ALL26331.2, 514 amino acids.

Lr74. Add note:

'Tc*3 / Caldwell' population: a gene for adult-plant resistance derived from Caldwell was identified with closest marker *Xcfb5006-3B*; the 'Tc*2 / Caldwell 24-1' parent shared the same T allele at KASP marker IWB44132 as Spark and BT-Schomburgk Selection {11281}.

Lr78 {11212}. *QLr.cdl.5D* {11212}. 5DS {11212}.

v: 'Tc*3 / Toropi 4A212A' {11212}.
v2: Toropi (actual accession source not available) {11212}.
ma: *Lr70* – 5.6 cM – *Xbarc130-5D* – 1.8 cM – *Xwmc233-5D* ………*Xcfd189-5D* – 13.2 cM – *IWA2689* – 2.2 cM – *Lr78* – 8.0 cM – *Xcfa2104-5D* {11212}.

According to Somers et al. (2004) *Xbarc130* is in bin 5DS2-0.78-1.00 and *Xcfd189* in in bin 5DS1-C-0.63.

Lr79 {11224}. LrAW3 {11224}. 3BL {11224}. **bin:** 3BL-0.63-0.90.

tv: 242/Bansi#149, C18.1 {11224}.
tv2: AUS26582 *Lr61* {11223, 11224}.
ma: *KASP_31457* – 8.1 cM – *sun770* – 2.9 cM – *Lr79* – 1.8 cM – *sun786* {11224}.

Lr79 conferred resistance to Australian common wheat Pt races, but not to durum-specific Ethiopian and Californian races {11224}.

LrPI244061 {11280}. 2BS {11280}. **tv:** PI 244061 {11280}.

ma: *LrPI144061* – 11.5 cM – *KASP_2BS_IWB6117* {11280}.

Add note: This gene may be *Lr13* {11280}.

LrPI287263 {11280}. 6BL {11280} **tv:** PI 287263 {11280}.

ma: *LrPI287263* – 2.8 cM – *KASP_6BL_IWB44753* – 2.8 cM – *Xdupw217* {11280}.

LrPI209274 {11218}. 6BS {11280}. **tv:** PI 209274 {11280}.

ma: *KASP_6BS_IWB39456* – 3.7 cM – *LrPI209274* – 1.0 cM – *KASP_6BS_IWB6117* – 8.1 cM – *Xdupw217-2B* {11280}.

This gene may be *Lr53* {11280}.

108.3. QTL for reaction to *P. triticina*

'Avocet / Kundan' RIL population: *Lr29* (flanked by *10902272* and *02414*, $R^2 = 0.5–0.65$), *QLR.cim-2BL* flanked by *1237388* and *1081780_35C>T* from Avocet and *QLr.cim-2DS* flanked by *1237388* and *1081780_35C>T* from Kundan {11248}.

'Avocet R (S) / Chilero': *Lr46/Yr29* and *QLr.cim-5DS/QYr.cim-5DS* from Chilero and *QLR.cim-1DL/QYr.cim-1DL* from Avocet R {11306}.

'CI 13227 (R) / Lakin (MS)' DH population: Adult-plant resistance conferred by *QLR.hwwg-2DS* ($R^2 = 0.11–0.26$), *QLr,hwwg-7BL* ($R^2 = 0.08–0.19$, likely *Lr68*) and *QLr.hwwg-7AL* from CI 13227, and *QLr.hwwg-3BS* from Lakin {11311}.

'Ning7840 / Clark' RIL population: *QLr.hwwg-5AS* from Ning 7840; *QLr.hwwg-6AS* from Clark, flanked by *barc23-6A* and *IWA3321*; *Qlr.hwwg3BS.1* from Clark, flanked by *IWA4654* and *IWA1702*, possibly *Lr74*; and *QLr.hwwg-7DS/Lr34* from Ning 7840 {11278}.

'Thatcher*3/Americano 44d' RIL population: QTL for adult-plant resistance identified on chromosomes 3AS (*QLr.cdl-3A*), 3DS (*QLr.cdl-3DS*), and 6DS (*QLr.cdl-6D*); both the 3AS and 3DS QTL were required for expression of resistance {11296}.

Genotype lists: To Chinese cultivars: add reference {', 11310'}.

Add at end of section: See {18053} for historical review of leaf rust work in Canada.

109. Reaction to *Pyrenophora tritici-repentis*

109.1. Insensitivity to tanspot toxin (necrosis)

Tsn1.Insert at the end of the section, but before 'A review…..':
Tsn–ToxA interaction has a major role in SNB development in both common and durum wheat whereas it has a variable role in tanspot development in bread wheat and is not a significant factor for tanspot development in durum wheat {M18004}.

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

Bt9. 6DL {11299}. **v:** PI 554099 {11299}.

Bt10. *QCbt.spa-6D* {M118098}. **v:** PI 554118 {11299}.

Bt11. 3B {11297}.
ma: May be associated with *Xbarc180*, *Xwmc623*, *Xwmc808*, and *Xgwm285* {11297}.

QTL:
'Carberry / AC Cadillac': AC Cadillac contributed QTL *QCbt.spa-6D* (*Bt10*) on chromosome 6D (markers *XwPt-1695*, *XwPt-672044*, and *XwPt-5114*). Carberry contributed *QCbt.spa-1B* (*XwPt743523*), *QCbt.spa-4B* (*XwPt 744434-Xwmc617*), *QCbt.spa-4D* (*XwPt-9747*), *QCbt.spa-5B* (*XtPt-3719*), and *QCbt.spa-7D* (*Xwmc273-7D*) {11298}.
At end of section: Additional QTL are listed in {18099}.

References.

Updates

10446. 115: 877-884.
10549. Faris JD, Xu SS, Cai XW, Friesen TL and Jin Y 2008 Molecular and cytogenetic characterization of a durum wheat-*Aegilops speltoides* chromosome translocation conferring resistance to stem rust. Chromosome research 16: 1097-1105. DOI: 10.1007/s10577-008-1261-3.
10964. Chhetri M, Bariana H, Kandiah P and Bansal U 2016 *Yr58*: A new stripe rust resistance gene and its interaction with *Yr46* for enhanced resistance. Phytopathology 106: 1530-1534. DOI: 10.1094/PHYTO-04-16-0182-R.

10970. Zhou XL, Han DJ, Chen XM, Gou HL, Guo SJ, Rong L, Wang QL, Huang LL and Kang ZS 2014 Characterization and molecular mapping of stripe rust resistance gene *Yr61* in winter wheat cultivar Pindong 34. Theoretical and Applied Genetics 127: 2349-2358. DOI: 10.1007/s00122-014-2381-0.

11045. 2015 Mapping of powdery mildew resistance gene *Pm53* introgressed from *Aegilops speltoides* into soft red winter wheat. Theoretical and Applied Genetics 128: 303-312. DOI: 10.1007/s00122-014-2430-8.

11052. Hou LY, Jia JQ, ZhangXJ, Li X, Yang ZJ, Ma J, Guo HJ, Zhan HX, Qiao LY and Chang ZJ 2016 Molecular mapping of the stripe rust resistance gene *Yr69* on wheat chromosome 2AS. Plant Disease 100: 1717-1724. DOI: 10.1094/PDIS-05-15-05550-RE.

11056. Bariana H, Forrest K, Qureshi N, Miah H, Hayden M and Bansal U 2016 Adult plant stripe rust resistance gene *Yr71* maps close to *Lr24* in chromosome 3D of common wheat. Molecular Breeding 36, 98. DOI: 10.1007/s11032-016-0528-1.

11066. Rahmatov M, Rouse MN, Nirmala J, Danilova T, Friebe B, Steffenson BJ and Johannson E 2016 A new 2DS·2RL Robertsonian translocation transfers stem rust resistance gene *Sr59* into wheat. Theoretical and Applied Genetics 129: 1383-1392. DOI: 10.1007/s00122-016-2710-6.

11067. Phytopathology 106: 1186-1193. DOI: 10.1094/PHYTO-01-16-0045-F1.

11164. Kolmer JA, Su ZQ, Bernardo A, Bai GH and Chao SM 2018 Mapping and characterization of the new adult plant leaf rust resistance gene *Lr77* derived from Santa Fe winter wheat. Theoretical and Applied Genetics 131:1553-1560. DOI: 10.1007/s00122-018-3097-3.

11171. Change 'PmTA1662' to '*Pm58*'.

11174. DOI: 10.1007/s00122-017-2946-9.

11185. Tian X, Wen W, Xie L, Fu L, Xu D, Fu C, Wang D, Chen X, Xia X, Chen Q, He Z and Cao S 2017 Fontiers in Plant Science 8, 1379. DOI: 10.3389/fpls.2017.01379.

New

11201. Emebiri LC, Tan M-K, El-Bouhssini M, Wildman O, Jighly A, Tadesse W and Ogbonnaya FC 2017 QTL mapping identifies a major locus for resistance in wheat to Sunn pest (*Eurygaster Integriceps*) feeding at the vegetative growth stage. Theoretical and Applied Genetics 130: 309-318. DOI: 10/1007s00122-016-2812-1.

11202. Yu L, Barbier H, Rouse MN, Singh S, Singh RP, Bhavani S, Huerta-Espino J and Sorrells M 2014 A consensus map for UG99 stem rust resistance loci in wheat. Theoretical and Applied Genetics 127: 1561-1581. DOI 10.1007/s00122-014-2326-7.

11203. Friesen TL, Chu CG, Xu SS and Faris JD 2012. Tox5-*Snn5*: a novel *Stagonospora nodorum* effector-wheat gene interaction and its relationship with SnToxA-*Tsn1* and SnTox3-*Snn3-B1* interactions. Molecular Plant Pathology 13: 1101-1109. DOI: 10.1111/J.1364-3703.2012.00819.X.

11204. Virdi S, Liu ZH, Overlander ME, Zhang ZC, Xu SS, Friesen TL and Faris JD 2016 New insights into the roles of host gene-necrotrophic effector interactions in governing susceptibility of durum wheat to tan spot and Septoria nodorum blotch. Genes, Genomes, Genetics (G3) 6: 4139-4150. DOI: 10.1534/g3.116.036525/-/DC1.

11205. Rawat N, Pumphrey MO, Liu SX, Zhang XF, Tiwari VK, Ando K, Trick HN, Bockus WW, Akhunov E, Anderson JA and Gill BS 2017 Wheat *Fhb1* encodes a chimeric lectin with agglutinin domains and a pore-forming toxin-like domain conferring resistance to Fusarium head blight. Nature Genetics 48: 1576-1580. DOI: 10.1038/ng.3706.

11206. Gao Y, Faris JD, Liu Z, Kim YM, Syme RA, Oliver RP, Xu SS and Friesen TL 2015 Identification and characterization of the SnTox6-*Snn6* interaction in the *Parastagonospora nodorum*-wheat pathosystem. Molecular Plant Microbe Interactions 28: 615-625. DOI: 10.1094/MPMI-12-14-0396-R.

11207. Saluja M, Kaur S, Bansal U, Bhardwaj SC and Chhuneja P 2017 Molecular mapping of linked leaf rust resistance and non-glaucousness gene introgressed from *Aegilops tauschii* Coss. in hexaploid wheat *Triticum aestivum* L. Plant Genetic Resources 1-7. DOI: 10.1017/S1479262116000240.

11208. Chen SS, Guo Y, Briggs J, Dubach F, Chao SM, Zhang WJ, Rouse MN and Dubcovsky J 2018 Mapping and characterization of wheat stem rust resistance genes *SrTm5* and *Sr60* from *Triticum monococcum* Theoretical and Applied Genetics 131: 625-635. DOI: 10.1007/s00122-017-3024-z.

11209. Thind AK, Wick WE, Sinkova H, Fossati D, Moullet O, Brabent C, Vrana J, Dolezel J and Krattinger SG 2017 Rapid cloning of genes in hexaploid wheat using cultivar-specific long-range assembly. Nature Biotechnology DOI: 10.1038/nbt/3877.

11210. Zhang ZF, Rouse MN, Nava IC, Jin Y and Anderson JA 2016 Development and verification of wheat germplasm containing both *Sr2* and *Fhb1*. Molecular Breeding 36, 85. DOI: 10.1007/s11032-016-0502-Y.

11211. Li GQ, Xu XY, Carver BF, Guo PG and Puterka 2018 *Dn10*, a new gene conferring resistance to Russian wheat aphid biotype 2 in Iranian wheat landrace PI 682675. Crop Science 58: 1219-1225. DOI: 10.2135/cropsci2017.10.0649.

11212. Kolmer JA 2017 Personal communication.

11213. Steuernagel B, Periyannan S, Hernandez-Pinzon I, Witek K, Rouse MN, Yu GT, Hatta A, Ayliffe M, Bariana H, Jones JDG, Ladudah ES and Wulff BH 2016 Rapid cloning of disease-resistance genes in plants using mutagenesis and sequence capture. Nature Biotechnology 34: 652-655. DOI 10.1038/nbt.3543.

11214. Tan CC, Li CQ, Cowger C, Carver BF, and Xu XY 2018 Characterization of *Pm59*, a novel powdery mildew resistance gene in Afghanistan wheat landrace PI 181356. Theoretical and Applied Genetics 131: 1145-1152. DOI: 10.1007/s00122-018-3067-9.

11215. Fu BH, Chen Y, Li N, Ma HQ, Kong ZX, Zhang LX, Jia HY and Ma ZQ 2013 *pmX*: a recessive powdery mildew resistance gene at the *Pm4* locus identified in wheat landrace Xiaohongpi. Theoretical and Applied Genetics 126: 913-921. DOI 10.1007/s00122-012-2025-1.

11216. Worthington M, Lyerly J, Petersen S, Brown-Guidera G, Marshall D, Cowger C, Parks R and Murphy JP 2015 MlUM15: an *Aegilops neglecta*-derived powdery mildew resistance gene in common wheat. Crop Science 54: 1397-1406. DOI 102125/cropsci2013.09.0634.

11217. Zhang WJ, Chen SS, Abate Z, Nirmala J, Rouse MN and Dubcovsky 2017 Identification and characterization of *Sr13,* a tetraploid wheat gene that confers resistance to the Ug99 stem rust race group. Proceedings of the National Academy of the United States of America, Early Edition. DOI: 10.1073/pnas.1706277114.

11218. Lan CX, Singh RP, Huerta-Espino J, Calvo-Salazar V and Herrera-Foessel SA 2014 Genetic analysis of resistance to leaf rust and stripe rust in wheat cultivar Francolin#1. Plant Disease 98: 1227-1234. DOI: 10.1094/PDIS-07-13-1717-RE

11219. Lan CX, Rosewarne GM, Singh RP, Herrera-Foessel SA, Huerta-Espino J, Basnet BR, Zhang YL and Yang EN 2019 QTL characterization of resistance to leaf rust and stripe rust in the spring wheat Francolin#1. Molecular Breeding 34: 789-803. DOI 10.1007/s11032-014-0075-6.

11220. Amagai Y, Kuboyama T and Watanabe N 2017 Genetic mapping of diagnostic markers for the *Lg2* locus conferring ligules in *Triticum aestivum* L. and derived from *Aegilops tauschii* Coss. Euphytica 213, 59. DOI: 10.1007/s10681-o17-1852-1.

11221. Sthapit J, Gbur EE, Brown-Guidira G, Marshall DS and Milus EA 2012 Characterization of resistance to stripe rust in contemporary cultivars and lines of winter wheat from the Eastern United States. Plant Disease 96: 737-745. DOI: 10.1094/PDIS-07-11-0612.

11222. Feng JY, Wang MN, See DR, Chao SM, Zheng YL, Chen XM 2018 Characterization of novel gene *Yr79* and four additional QTL for all-stage and high-temperature adult-plant resistance to stripe rust in spring wheat PI 182103. Phtopathology 108: 731-747. DOI: 10.1094/PHYTO-11-17-0375-R.

11223. Qureshi N, Bariana H, Kolmer JA, Miah H and Bansal U 2017 Genetic and molecular characterization of leaf rust resistance in two durum wheat landraces. Phytopathology 107: 1381-1387. DOI: 10.1094/PHYTO-01-17-0005-R.

11224. Qureshi N, Bariana H, Kumran VV, Muruga S, Forrest KL, Hayden M and Bansal U 2017 A new leaf rust resistance gene *Lr79* mapped in chromosome 3BL from the durum wheat landrace Aus26582. Theoretical and Applied Genetics 131: 1091-1098. DOI: 10.1007/s00122-018-3060-3.

11225. Liu XM, Smith CM, Friebe BR and Gill BS 2005 Molecular mapping and allelic relationships of Russian wheat aphid–resistance genes. Crop Science 45:2273–2280. DOI: 10.2135/cropsci2004.0704.

11226. Tonk FA, Istipliler D, V Tosun, Ilbi H and Cakir M 2016 Genetic mapping and inheritance of Russian wheat aphid resistance gene in accession IG 100695. Plant Breeding 135: 21-25. DOI: 10.1111/pbr.12339.

11227. Valdez VA, Byrne PF, Lapitan NLV, Peairs FB, Bernardo A, Bai GH and Haley SD 2012 Inheritance and genetic mapping of Russian wheat aphid resistance in Iranian wheat landrace accession PI 626580. Crop Science 52: 676–682. DOI: 10.2135/cropsci2011.06.0331.

11228. Yang ZJ, Chen ZY, Peng ZS, Yu Y, Liao ML and Wei SH 2017 Development of a high-density linkage map and mapping of the three-pistil gene (*Pis1*) in wheat using GBS markers. BMC Genomics 18, 567. DOI 10.1186/s12864-017-3960-7.

11229. Ma DF, Fang ZW, Yin JL, Chao KX, Jing JX, Li Q and Wang BT 2016 Molecular mapping of stripe rust resistance gene *YrHu* derived from *Psathyrostachys huashanica*. Molecular Breeding 36, 64. DOI: 10.1007/s11032-016-0487-6.

11230. Cook JP, Blake NK, Heo H-Y, Martin JM, Waver DK and Talbert LE 2017 Phenotypic and haplotype diversity among tetraploid and hexaploid wheat accessions with potentially novel insect resistance genes for wheat stem sawfly. Plant Genome 10: DOI: 10.3835/plantgenome2016.03.0026.

11231. Getie B, Singh D, Bansal U, Simmonds J, Uauy C and Park RF 2015 Identification and mapping of resistance to stem rust in the European winter wheat cultivars Spark and Rialto. Molecular Breeding 36, 114. DOI: 10.1007/s11032-016-0537-0.

11232. Prins R, Pretorius ZA, Bender CM and Lehmensiek A 2011 QTL mapping of stripe, leaf and stem rust resistance genes in a Kariega × Avocet S doubled haploid wheat population. Molecular Breeding 27: 259-270. DOI10.1007s11032-010-9428-y.

11233. Wei JX, Geng HW, Zhang Y, Liu JD, Wen WI, Zhang Y, Xia XC, Chen XM and He ZH 2015 Mapping quantitative trait loci for peroxidase activity and developing gene-specific markers for *TaPod*-A1 on wheat chromosome 3AL. Theoretical and Applied Genetics 128: 2067-2076. DOI: 10.1007/s00122-015-2567-0

11234. Dholakia BB, Rajwade AV, Hosmani P, Khan RR, Chavan S, Reddy DMR, Lagu MD, Bansal UK, Saini RG and Gupta VS. 2013 Molecular mapping of leaf rust resistance gene *Lr15* in hexaploid wheat. Molecular Breeding 341: 743-747. DOI: 10.1007/s11032-012-9813-9.

11235. Hou L, Chen XM, Wang M, See DR, Chao SM, Bulli P and Jing JX 2015 Mapping a large number of QTL for durable resistance to stripe rust in winter wheat Druchamp using SSR and SNP markers. PLoS One 10e0126794. DOI: 10.1371/journal.pone.0126794.

11236. Klindworth DL, Saini J, Long YM, Rouse MN, Faris JD, Jin Y and Xu SS 2017 Physical mapping of DNA markers linked to stem rust resistance gene *Sr47* in durum wheat. Theoretical and Applied Genetics 130: 1135-1154. DOI: 10.1007/s00122-017-2875-7.

11237. Bokore FE, Knox RE, DePauw RM, Clarke F, Cuthbert RD, Campbell HL, Brule-Babel AL, Gilbert J and Ruan Y 2017 Validation of molecular markers for use with adapted sources of Fusarium blight resistance in wheat. Plant Disease 101: 1292-1299. DOI: 10.1094/PDIS-10-16-1421-RE.

11238. Zhang LL, Liu C, An XY, Wu HY, Feng Y, Wang H and Sun DJ 2017 Identification and genetic mapping of a novel incompletely dominant yellow leaf color gene, *Y1718*, on chromosome 2BS in wheat. Euphytica 213, 141. DOI: 10.1007/s10681-017-1894-4.

11239. Varella AC, Weaver DK, Cook JP, Blake NK, Holland ML, Lamb PF and Talbert LE 2017 Characterization of resistance to the wheat stem sawfly in spring wheat landrace accessions from targeted geographic regions of the world. Euphytica 213, 153. DOI10.1007/s10681-017-1945-x.

11240. Ramirez-Gonzalez RH, Segovia V, Bird N, Fenwick P, Holdgate S, Berry S, Jack P, Caccamo M and Uauy C 2015 RNA-Seq bulked segregant analysis enables the identification of high-resolution genetic markers for breeding in hexaploid wheat. Plant Biotechnology Journal 13: 613-624. DOI: 10.1111/pbi.12281.

11241. Li HY, Wang QL, Xu LS, Mu JM, Wu JH, Zeng QD, Yu SZ, Huang LL and Kang ZS 2017 Rapid identification of a major effect QRL conferring adult plant resistance to stripe rust in wheat cultivar Yaco'S'. Euphytica 213, 124. DOI 10.1007/s10681-017-1912-6.

11242. Soto-Cerda BJ, Inostroza-Blancheteau C, Mathias M, Penaloza E, Zuniga J, Munoz G, Rengel Z and Salvo-Garrido H 2015 Marker-assisted breeding for *TaALMT1*, a major gene conferring aluminium tolerance to wheat. Biologia Plantarum 50: 83-91. DOI 10.1007/s.

11243. Zheng Z, Kilian A, Yan G and Liu C 2014 QTL conferring Fusarium crown rot resistance in the elite bread wheat variety EGA Wylie. PLoS One 9: e96011. DOI: 10.1371/journal.pone.0096011.

11244. Zheng Z, Ma J, Stiller J, Zhao QA, Fen Q, Choulet C, Feullet C, Zhang YL, Wei YM, Han B, Manners JM and Liu CL 2015 Fine mapping of a large-effect QTL conferring Fusarium crown rot resistance on the long arm of chromosome 3B in hexaploid wheat. BMC Genomics 16, 850. DOI: 10.1186/s12864-015-2105-0.

11245. Xu ZC, Yuan CL, Wang JR, Fu DL and WU JJ 2015 Mapping the glaucousness suppressor *Iw1* from wild emmer wheat "PI 481521". The Crop Journal 3: 37-45. DOI:1016/j.cj.2014.09.004.

11246. Liu YJ, Liu YX, Zhou Y, Wight C, Pu ZE, Qi PF, Jiang QT, Deng M, Wang ZX, Wei YM, Cao WG, Liu DC, Zheng YL, Liu CJ, Fregeau-Reid J and Wang JR 2017 Conferring resistance to pre-harvest sprouting in durum wheat by a QTL identified in *Triticum spelta*. Euphytica 213,19. DOI: 10.1007/s10681-016-1796-x.

11247. Lu P, Qin JX, Wang GX, Wang LL, Wang ZZ, Wu QH, Xie JH, Liang Y, Wang Y, Zhang DY, Sun QX and Liu ZY 2015 Comparative fine mapping of the waxy (*W1*) locus in hexaploid wheat. Theoretical and Applied Genetics 128: 1595-1603. DOI: 10.1007/s00122-015-2534-9.

11248. Ren Y, Singh RP, Basnet BR, Lan CX, Huerta-Espino J, Lagudah ES and Ponce-Molina LJ 2017 Identification and mapping of adult plant resistance loci to leaf rust and stripe rust in common wheat cultivar Kundan. Plant Disease 101: 456-463. DOI: 10.1094/PDIS-06-0890-RE.

11249. Babiker EM, Gordon TC, Bonman JM, Chao S, Rouse MN, Jin Y, Newcomb M, Wanyera R and Bhavani S 2017 Genetic loci conditioning adult plant resistance to the Ug99 race group and seedling resistance to races TRTTF and TTTTF of the stem rust pathogen in wheat landrace CItr 15026. Plant Disease 101: 496-501. DOI: 10.1094/PDIS-10-16-1447-RE.

11250. Zou SH, Wang HA, Li YW, Kong ZS and Tang DZ 2017 The NB-LRR gene *PmR2* confers powdery mildew resistance in diploid wheat. New Phytologist 218: 298-309. DOI: 10.111/nph.14964.

11251. Qiu YC, Zhou RH, Kong XY, Zhang SS and Jia JZ 2005 Microsatellite mapping of a *Triticum urartu* Tum. derived powdery mildew resistance gene transferred to common wheat (*Triticum aestivum* L). Theoretical and Applied Genetics 111: 1524-1531. DOI: 10.1007/s00122-005-0081-5.

11252. Yao Q, He MM, Hou L, Han JH, Guo, Jing JX and Kang ZS 2017 Genetic analysis and molecular mapping of stripe rust resistance genes in Chinese native wheat (*Triticum aestivum*) Lankao 5. Australasian Plant Pathology 46: 213-221. DOI: 10.1007/s13313-017-0478-z.

11253. McCallum, BD, Hiebert CW, Cloutier S, Bakkeren G, Rosa SB, Humphreys DG, Marais GF, McCartney CA, Panwar V, Rampitsch C, Saville BJ and Wang XB 2016 A review of wheat leaf rust research and the development of resistant cultivars in Canada. Canadian Journal of Plant Pathology 38: 1-18. DOI: 10.1080/07060661.2016.1145508.

11254. Zhang SG, Li YF, Lu L, Liu ZH, Zhang CH, Ao DH, Li LR, Zhang CY, Liu R, Luo CP, Wu Y and Zhang L 2017 Evaluating the contribution of genes to stripe rust resistance breeding through marker-assisted detection in wheat. Euphytica 213, 50. DOI 10: 1007/s10681-016-1826-6.

11255. Kumar S, Roder MS, Bhushan S, Tripathi SB, Kumar S, Chand R, Joshi AK and Kumar U 2015 Mendelization and fine mapping of a bread wheat spot blotch resistance QTL. Molecular Breeding 35, 218. DOI: 10.1007/s11032-015-0411-5.

11256. Lu P, Liang Y, Li DL, Wang ZZ, Li WB, Wang GX, Wang Y, Zhou SH, Wu QH, Xie JZ, Zhang DY, Chen YX, Li MM, Zhang Y, Sun QX and Liu ZY 2015 Fine genetic mapping of spot blotch resistance gene *Sb3* in wheat (*Triticum* aestivum). Theoretical and Applied Genetics 128: 577-589. DOI: 10.1007/s00122-015-2649-z.

11257. Wang ZZ, Li HW, Zhang DY, Guo L, Chen JJ, Chen YX, Wu QH, Xie JZ, Zhang Y, Sun QX, Dvorak J, Luo M-C & Liu ZY 2015 Genetic and physical mapping of powdery mildew resistance gene *MlHLT* in Chinese wheat landrace Hulutou. Theoretical and Applied Genetics 128: 365-373. DOI: 10.1007/s00122-014-2436-2.

11258. Liu DC, Zhang LQ, Hao M, Ning SZ, Yuan ZW, Dai SF, Huang L, Wu BH, Yan ZH, Lan XJ and Zheng YL 2018 Wheat breeding in the hometown of Chinese Spring. The Crop Journal 6: 82-90. DOI: 10.1016/j/cj.2017.08.009.

11259. Huerta-Espino J and Singh RP 2017 First detection of virulence in *Puccinia striiformis* f. sp. *tritici* to wheat resistance genes *Yr10* and *Yr24* (=*Yr26*) in Mexico. Plant Disease 101: 1676. DOI :10.1094/PDIS-04-17-0532-PDN.

11260. Patpour M, Hovmoller MS and Hodson D 2017 First report of virulence to *Sr25* in race TKTTF of *Puccinia graminis* f. sp. *tritici* causing stem rust on wheat. Plant Disease 101: 1678. DOI: 10.10904.PDIS-11-16-1666-PDN.

11261. Nsabiyera V, Bariana HS, Qureshi N, Wong D, Hayden MJ and Bansal UK 2018 Characterization and mapping of adult plant stripe rust resistance in wheat accession AUS27284. Theoretical and Applied Genetics. DOI: 10.1007/s00122-018-3090-x.

11262. MK Gessese, Bansal U, et al. 2017 Molecular mapping of stripe rust resistance genes in Aus27430, a common wheat landrace. Draft manuscript.

11263. Wang SZ, Asuke S, Vy TTP, Inoue Y, Chuma I, Kato K, Fujita M and Tosa Y 2017 *Rmg9*, a new gene for resistance to *Triticum* isolates of *Pyricularia oryzae* is combined with *Rmg8* in a common wheat landrace. Manuscript.

11264. Williamson VM, Thomas V, Ferris H and Dubcovsky J 2013 An *Aegilops ventricosa* translocation confers resistance against root-knot nematodes to common wheat. Crop Science 53: 1412-1418. DOI: 10:2135/cropsci2013.120681.

11265. Cruz CD Peterson GL, Bockus WW, Kankanala P, Dubcovsky J, Jordan KW, Akhunov E, Chumley F, Baldelomar FD and Valent B 2016 The 2NS translocation from *Aegilops ventricosa* confers resistance to the *Triticum* pathotype of *Magnaporthe oryzae*. Crop Science 56: 990-1000. DOI: 10.2135/cropsci2015.07.0410.

11266. Qureshi N, Bariana HS, Zhang P, McIntosh RA, Bansal UK, Wong D, Hayden MJ, Dubcovsky J and Shankar M 2018 Genetic relationship of stripe rust resistance genes *Yr34* and *Yr48* in wheat and identification of linked KASP markers. Plant Disease 102: 443-420. DOI: 10.1094/PDIS-08-17-1144-RE.

11267. Juliana P, Singh RP, Singh PK, Crossa J, Huerta-Espino J, Lan CX, Bhavani S, Rutkovski JE, Poland JA, Bergstrom GC and Sorrells ME 2017 Genomic and pedigree-based prediction for leaf, stem, and stripe rust resistance in wheat. Theoretical and Applied Genetics 130: 1415-1430. DOI: 10.1007/s00122-017-2897-1.

11268. Yu GT, Zhang QJ, Friesen TL, Rouse MN, Jin Y, Zhong SB, Rasmussen, Lagudah ES and Xu SS 2015 Identification and mapping of *Sr46* from *Aegilops tauschii* accession CIae 25 conferring resistance to race TTKSK (Ug99) of wheat stem rust pathogen. Theoretical and Applied Genetics 128: 431-443. DOI: 10.1007/s00122-014-2442-4.

11269. Tucker EJ, Baumann u, Kouidri A, Suchecki R, Baes M, Garcia M, Okada T, Dong CM, Wu YZ, Sandhu A, Singh M, Langridge P, Wolters P, Albertsen MC, Cigan AM and Whitford R 2017 Molecular identification of the wheat male fertility gene *Ms1* and its prospects for hybrid breeding. Nature Communications 18: 869. DOI: 10.1038/s41467-017-00945-2.

11270. Sanchez-Martin J, Steurnagel B, Ghosh S, Herren G, Hurni G, Adamski N, Vrana J, Kublakova M, Krattinger SG, Wicker T, Dolezel J, Keller B and Wulff BH 2016 Rapid gene isolation in barley and wheat by mutant chromosome sequencing. Genome Biology 17, 221. DOI: 10.1186/s13059-016-1082-1.

11271. Ren Y, Li SR, Wei YM, Zhou Q, Du XY, He YJ and Zheng YL 2015 Molecular mapping of a stripe rust resistance gene in Chinese wheat cultivar Mianmai 41. Journal of Integrative Agriculture 14: 295-304. DOI: 10.1016/S2095-3119(14)60781-4.

11272. Anh VL, Inou Y, Asuke S, Vy TTP, Anh NT, Wang SZ, Izumi C and Tosa Y 2017 *Rmg8* and *Rmg7*, wheat genes for resistance to the wheat blast fungus, recognize the same avirulence gene *AVR-Rmg8*. Molecular Plant Pathology 19: 1252-1256. DOI: 10.1111/mpp.12609.

11273. Lu Y, Xing LP, Xing SJ, Hu P, Cui CF, Zhang MY, Xiao J, Wang HY, Zhang RQ, Wang X Chen PD and Cao AZ 2015 Characterization of a putative new semi-dominant reduced height gene *Rht_Nm9*, in wheat (*Triticum aestivum* L.). Journal of Genetics and Genomics 42: 685-698. DOI: 10.1016/j.jgg.2015.08.007.

11274. Scofield SR, Huang L, Brandt AS and Gill BS 2005 Development of a virus-induced gene silencing system for hexaploid wheat and its use in functional analysis of the *Lr21*-mediated leaf rust resistance pathway. Plant Physiology 138: 2165-2173. DOI: 10/1104/pp.105.061861.

11275. Xing LP, Hu P, Liu JQ, Cui CF, Wang H, Di ZC, Zhou SA, Xu JF, Huang ZP and Cao AZ 2017 *NLR1-V*, a CC-NBS-LRR encoding gene is a potential candidate gene of the wheat powdery mildew resistance gene *Pm21*. BioRxiv preprint: DOI: http://dx.doi.org/10.1101/114058.

11276. Hurni S, Brunner S, Buchmann G, Herren G, Jordan T, Krukowski P, Wicker T, Yahoaoui N, Mago and Keller B 2013 Rye *Pm8* and wheat *Pm3* are orthologous genes and show evolutionary conservation of resistance function against powdery mildew. The Plant Journal 76: 957-969. DOI: 10.1111/tpj.12345.

11277. Segovia V, Hubbard A, Craze M, Bowden S, Wallington E, Bryant R, Greenland A, Bayles R and Uauy 2014 Phytopathology 104: 871-878. DOI: org/10.1094/PHYTO-10-13-0295-R.

11278. Li Cl, Wang ZH, Bowden R, Bai GH, Li CX and Su ZQ 2017 Mapping of quantitative trait loci for leaf rust resistance in the wheat population Ning 7840 × Clark. Plant Disease 101: 1974-1979. DOI: 10.1094.PDIS-12-16-1743-RE.

11279. Wu Jh, Wang QL, Kang ZS, Liu SJ, Li HY, Mu JM, Dai MF, Han DJ, Zeng QD and Chen XM 2017 Development and validation of KASP-SNP markers for QTL underlying resistance to stripe rust in common wheat cultivar P10057. Plant Disease 101: 2079-2087. DOI: 10.1094.PDIS-04-14-0468-RE.

11280. Aoun M, Kolmer JA, Rouse MN, Chao SM, Bubula WD, Elias EM, Acevedo M 2017 Inheritance and bulked segregant analysis of leaf rust and stem rust resistance in durum wheat genotypes. Phytopathology 107: 1496-1506. DOI: 10.1094/PHYTO-12-16-0444-R.

11281. Kolmer JA, Chao S, Brown-Guedira G, Bansal U and Bariana H 2018 Adult plant leaf rust resistance derived from the soft winter wheat cultivar ‘Caldwell’ maps to chromosome 3BS. Crop Science 58: XXX. DOI: 10.2135/cropsci2017.05.0272.

11282. Ren Y, Li SR, Xia XC, Zhou QA, He YJ, Wei YM, Zheng YL and He ZH 2015 Molecular mapping of a recessive stripe rust resistance gene *YrMY37* in Chinese wheat cultivar Mianmai 37. Molecular Breeding 35, 97. DOI: 10.1007/s11032-015-0293-6.

11283. Wu JH, Wang QL, Liu SJ, Huang S, Mu JM, Zeng QD, Huang LL, Han DJ and Kang ZS 2017 Saturation mapping of a major effect QTL for stripe rust resistance on wheat chromosome 2B in cultivar Napo 63 using SNP genotyping arrays. Frontiers in Plant Science 6, 653. DOI: 10.3389.fpls.2017.00653.

11284. Feng JY, Chen GY, Wei YM, Liu YX, Jiang QT, Li W, Pu Z, Lan XJ, Dai SF, Zhang M and Zhenh YL 2015 Identification and mapping stripe rust resistance gene *YrLM168a* using extreme individuals and recessive phenotype class in a complicated genetic background. Molecular and General Genomics 290: 2271-2278. DOI: 10.1007/s00438-015-1077-8.

11285. Li N, Zong Y, Liu BL, Chen WJ and Zhang B 2017 *TaMYB3*, encoding a functional MYB transcriptor, isolated from the purple pericarp of *Triticum aestivum*. Cereal Research Communications 45: 368-380. DOI: 10.1556/0806.45.2017.027.

11286. Naruoka Y, Ando K, Bulli P, Muleta KT, Rynearson S and Pumphrey MO 2016 Identification and validation of SNP markers linked to the stripe rust resistance gene *Yr5* in wheat. Crop Science 56: 3055-3065. DOI: 10.2135/cropsci2016.03.0189.

11287. Wu PP, Xie JZ, Hu JH, Qiu D, Liu ZY, Li JT, Li MM, Zhang Hj, Yang L, Zhou Y Zhang ZJ and Li HJ 2018 Development of molecular markers linked to powdery mildew resistance gene *Pm4b* by combining SNP discovery from transcriptome data with bulked segregant analysis (BSR-Seq) in wheat. Frontiers in Plant Science 9, 95. DOI: 10.3389.fpls.2018.00095.

11288. Rouse MN and Jin Y 2011 Stem rust resistance in A-genome diploid relatives of wheat. Plant Disease 95: 941-944. DOI: 10.1094/PDIS-04-10-0260.

11289. Geng MM, Zhang J, Peng FX, Liu X, Lv XD, Mi YY Li YH, Li F, Xie CJ and Sun QX 2016 Identification and mapping of *MLIW30*, a powdery mildew resistance gene derived from wild emmer wheat. Molecular Breeding 36, 130. DOI: 10/s11032-016-0553-0.

11290. Sun HG, Hu JH, Song W, Qiu D, Wu PP, Zhang HJ, Liu HW, Yang L, Qu YF, Li YH, Li T, Zhou Y, Liu ZY, Li JT and Li HJ 2018 Identification of recessive gene *PmXX* for resistance to powdery mildew on chromosome 4AL in wheat landrace Xuxusanyuehuang by comparative genomics analysis. Draft manuscript.

11291. Bheema Lingeswaara Reddy IN, Chandresekhar K, Zewdu Y, Dinoor A, Keller B and Ben-David R 2016 Identification and genetic mapping of *PmAF7DS* a powdery mildew resistance gene in bread wheat. Theoretical and Applied Genetics 129: 1127-1137. DOI: 10.1007/s00122-016-2688-0.

11292. Shi GJ, Friesen TL, Saini J, Xu SS, Rasmussen JB and Faris JD 2015 The wheat *Snn7* gene confers susceptibility on recognition of the *Parastagonospora nodorum* necrotrophic effector SnTox7. Plant Genome 8(2): DOI: 10.3835/plantgenome2015.02.0007.

11293. Wurschum T, Langer SM, Longin CF, Tucker MR and Leister WL 2017 A modern Green Revolution gene for reduced height in wheat. The Plant Journal 92: 892-903. DOI: 10.1111/tpj.13726.

11294. Herter CP, Ebmeyer E, Kollers S, Korzun V, Leister WL, Wurschum T and Miedaner T 2018 *Rht24* reduces height in the winter wheat population 'Solitar × Bussard' without adverse effects on Fusarium head blight infection. Theoretical and Applied Genetics 131: 1263-1272. DOI: 10.1007/s001222-018-3076-8

11295. Vikhe P, Patil R, Chavan A, Oak M and Tamhankar S 2017 Mapping gibberellin-sensitive dwarfing locus *Rht18* in durum wheat and development of SSR and SNP markers for selection in breeding. Molecular Breeding 37, 28. DOI 10.1007s11032-017-0641-9.

11296. Kolmer JA, Garvin DF, Hayden M and Speilmeyer W 2018 Adult plant leaf rust resistance derived from wheat landrace Americano 44d is conditioned by interaction of three QTL. Euphytica 214, 59. DOI: 10.1007/s10681-018-2141-3.

11297. Ciuca M 2011 A preliminary report on the identification of SSR markers for bunt (*Tilletia* sp.) resistance in wheat. Czech Journal of Plant Breeding (Special Issue) 47: S142-S145.

11298. Singh A, Knox RE, DePauw, Singh AK, Cuthbert RD, Kumar S and Campbell HL 2016 Genetic mapping of common bunt resistance and plant height QTL in wheat. Theoretical and Applied Genetics 129: 243-256. DOI: 10.1007/S00122-015-2624-8.

11299. Steffen PM, Torp AM, Bergen A, Backes G and Rasmussen SK 2017 Mapping of common bunt resistance gene *Bt9* in wheat. Theoretical and Applied Genetics 130: 1031-1040. DOI: 10.1008/s00122-017-2868-6.

11300. Mo YJ, Vanzetti L, Hale I, Spagnolo EJ, Guidobaldi G, Al-Obouchi, Odle N, Pearce S, Helguera M and Dubcovsky J 2018 Identification and characterization of *Rht25,* a locus on chromosome arm 6AS affecting wheat plant height, heading time and spike development. Theoretical and Applied Genetics In press.

11301. Ford BA, Foo E, Sharwood R, Karafaitova M, Vrana J, MacMillan C, Nichols DS, Steurnagel B, Uauy C, Dolezel Y, Chandler PM and Spielmeyer W 2018 *Rht18* semidwarfism in wheat is due to increased GA 2-oxidaseA9 expression and reduced GA content. Plant Physiology 177: 168-170. DOI: 10.1104/pp18.00023.

11302. Xie WL, Ben-David R, Zeng B, Distenfeld A, Roder MS, Dinoor A and Fahima T 2013 Identification and characterization of a novel powdery mildew resistance gene *PmG3m* derived from wild emmer wheat, *Triticum aestivum*. Theoretical and Applied Genetics 124: 911-922. DOI: 10.1007s/s00122-011-1756-8.

11303. Wu JH, Wang QL, Xu LS, Chen XM, Li B, Mu JM, Zeng QD, Huang LL, Han DJ and Kang ZS 2018 Combining single nucleotide polymorphism genotyping array with bulked segregant analysis to map a gene controlling adult plant resistance to stripe rust in wheat line 03031-1-5 H62. Phytopathology 108: 103-113. DOI: 10.1094/PHYTO-04-17-0153-R.

11304. Yuan CL, Wu JZ, Yan BQ, Hao QQ, Zhang CZ, Lyo B, Ni F, Caplan A, Wu JJ and Fu DL 2018 Remapping of the stripe rust resistance gene *Yr10* in common wheat. Theoretical and Applied Genetics 131: 1353-1262. DOI: 10.1007/s00122-018-3075-9.

11305. Lukaszewsky AJ and Cowger C 2017 Re-engineering of the *Pm21* transfer from *Haynaldia villosa* to bread wheat by induced homoeologous recombination. Crop Science 57: 2590-2594. DOI: 10.2135/cropsci2017.03.0192.

11306. Ponce-Molina LJ, Huerta-Espono L, Singh RP, Basnet BR, Alvarado G, Randhawa MS, Lan CX, Aguilar-Rincon VH, Lobata-Ortiz R and Garcia-Zavala JJ 2018 Characterization of leaf rust and stripe rust resistance in spring wheat 'Chilero'. Plant Disease 102: 421-427. DOI: 10.1094/PDIS-11-16-1545-RE.

11307. Xue FB, Guo J, Guan CY, Wang HW, Li AF and Kong LR 2015 Molecular mapping of the hybrid necrosis gene *NetJingY176* in *Aegilops tauschii* using microsatellite markers. The Crop Journal 3: 298-304. DOI: 10.1016/j.cj.2015.05.003.

11308. Wang Y, Zhang HZ, Xie JZ, Guo BM, Chen YX, Zhang HY, Lu P, Wu QH, Li MM, Zhang DY, Guo GH, Yang J, Zhang PP, Zhang Y, Wang XC, Zhao H and Cao TJ 2018 Mapping stripe rust resistance genes by BSR-Seq: *YrMM58* and *YrHy1* on chromosome 2AS in Chinese wheat lines Mengmai 58 and Huaiyang 1 are *Yr17*. The Crop Journal 6: 91-98. DOI: 10.1016/j/cj.2017.03.002.

11309. Smiley RW, Dababat AA, Iqbal S, Jones MGK, Maafi ZT, Peng DL, Subbotin SA and Waeyenberge L 2017 Cereal cyst nematodes: a complex and destructive group of *Heterodera* species. Plant Disease 101: 1692-1720. DOI: 10.1094/PDIS-03-017-0355-FE.

11310. Gabrewahid TW, Yao ZJ, Yan XC, Gao P and Li ZF 2017 Identification of leaf rust resistance genes in Chinese common wheat cultivars. Plant Disease 101: 1729-1737. DOI: 10.1094/PDIS-02-17-0247-RE.

11311. Lu Y, Bowden RL, Zhang GE, Xu XY, Fritz AK and Bai GH 2017 Quantitative trait loci for slow rusting resistance to leaf rust in doubled-haploid wheat population CI13227 × Lakin. Phtopathology 107: 1372-1380. DOI: 10.1094/PHYTO-09-16-0347-R.

11312. Shoeva OY, Gordeeva EI and Khlestkina EK 2014 The regulation of anthocyanin synthesis in wheat pericarp. Molecules 19: 20166-20279. DOI: 10.3390/molecules191220266.

11313. Jiang WH, Liu TX, Nan WZ, Jeewani DC, Niu YL, Li CL, Wang Y, Shi X, Wang C, Wang JH, Li Y, Gao X and Wang ZG 2018 Two transcription factors TaPpm1 and TaPpb1 co-regulate anthocyanin biosynthesis in purple pericarps of wheat. Journal of Experimental Botany 69: 2555-2567. DOI: 10.1093/jxb/ery101.

11314. Rinaldo A, Gilbert B, Boni R, Krattinger SG, Singh D, Park RF, Lagudah and Ayliffe M 2016 The *Lr34* adult plant rust resistance gene provides seedling resistance in durum wheat without senescence. Plant Biotechnology Journal 15: 894-905. DOI: 10.1111/pbi.12684.

11315. Chen SS, Zhang WJ, Bolus S, Rouse MN and Dubcovsky J 2018 Identification and characterization of wheat stem rust resistance gene *Sr21* effective against the UG99 race group at high temperature. PLoS Genetics 14(4):e1007287. DOI:10.137/journal.pgen.1007287.

11316. Mago R, Zhang P, Vautrin S, Šimková H, Bansal U, Luo M-C, Rouse M, Karaoglu H, Periyannan, Kolmer J, Jin Y, Ayliffe MA, Bariana H, Park RF, McIntosh R, Dolezel T, Berges H, Spielmeyer W, Lagudah ES, Ellis JG and Dodds PN 2015 The wheat *Sr50* gene reveals rich diversity at a cereal disease resistance locus. Nature Plants 15186. DOI: 10.1038/nplants.2015.186.

11317. Li N, Jia HY, Kong ZX, Tang WB, Ding YX, Liang JC, Ma HQ and Ma ZQ 2017 Identification and marker-assisted transfer of a new powdery mildew resistance gene at the *Pm4* locus in common wheat. Molecular Breeding 37, 79. DOI: 10.1007/s11032-017-0670-4.

11318. Yu GT, Cai XW, Harris MO, Gu YQ, Luo M-C and Xu SS 2009 Saturation and comparative mapping of the genomic region harboring Hessian fly resistance gene *H26* in wheat. Theoretical and Applied Genetics 118: 1589-1599. DOI: 10.1007/s00122-009-1006-5.

11319. Yu GT, Klindworth, DL, Friesen TL, Faris JD, Zhong SB, Rasmussen JB and Xu SS 2015 Development of a diagnostic co-dominant marker for stem rust resistance gene *Yr47* introgressed from *Aegilops speltoides* into durum wheat. Theoretical and Applied Genetics 118: 1589-1599. DOI: 10.1007/s00122-015-2590-1.

11320. Wiesma AT, Whetten RB, Zhang GR, Sehgal S, Kolb FL, Poland JA, Mason RE, Carter AH, Cowger C and Olson EL 2018 Registration of two wheat germplasm lines fixed for *Pm58*. Journal of Plant Registrations. DOI: 10.3198/jpr2017.06.0036crg.