CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2017 SUPPLEMENT

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The most recent version of the Catalogue, compiled for the 12th International Wheat Genetics Symposium held in Yokohama, Japan, is available on the Komugi and GrainGenes websites. Supplements 2013-2014 and 2015-2016 are also available at those sites.

Laboratory Designators

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Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

1.1 Squarehead/spelt

Add at the end of section:
A nucleotide change in the microRNA172 binding site of the Q locus played a critical role in wheat domestication and the origin of free-threshing modern wheats {11192}.

5. Anthocyanin Pigmentation

5.3. Red/purple coleoptiles.

***Rc-D1*.**

	***RcD1a*.**	**v:**	Add: Gaoyuan 115 {11160}.

	c:	*TaMYB-D1* isolated from Gaoyuan 115 was proposed as the candidate gene {11160}.

5.5. Purple grain/pericarp

At the end of section add:

A set of Saratovskaya 29 NILs is described in {11136}.

18. Dormancy

18.1 Germination index

TaSdr-A1 {11199}.	2A {11199}.		
	ma:	*Xgwm95-2A* – 1.4 cM – *TaSdr-A1* – 1.5 cM – *Xgwm372-2A* {11199}.	
	TaSdr-A1a {11199}.	v:	Yangxiaomai {11199}.
Associated with low germination index.			
	TaSdr-A1b {11199}.	**v:**	Zhongyou 9507 {11199}.
Associated with high germination index.			

Change present entry ***TaSdr*** to ***TaSdr-B1***

20. Earliness per se

***Eps-1A*^{m}.**	**ma:**	Add: The circadian clock gene *Elf3* was identified as a candidate gene for *Eps-A*^{m}*1* {11120}.	
Following the <u>*Eps-A1b* add:</u>			
Eps-D1 {111903}.	1DL {M11193}.		
	v:	Earliness allele: Cadenza and Spark {11193}. Lateness allele: Avalon and Rialto{11193}.	
	ma:	The earliness allele was associated with a subtelomeric deletion containing three candidate genes one of which was *TaELF-D1* {11193}. A QTL for heading date co-segregated with *TaELF3-1DL* in a RIL population derived from Gaocheng 8901 / Zhoumai 16 {11194}; a deletion of the *Eps-1D* region was associated with earlier flowering.	

29. Glaucousness (Waxiness/Glossiness)

29.2 Epistatic inhibitors of glaucousness

QTL

<u>Leaf glaucousness</u>

RAC875 (glaucous) / Kukri (non-glaucous). Several QTL affected leaf glaucousness, the strongest of which was *QW.aww-3A*; QTL of lesser effect *QW.aww-3B* and *QW.aww-3D* were detected at homoeologous regions on chromosomes 3B and 3D {11131}.

24. Flour Colour

Add to the present information:

Lutein is one of the carotenoids contributing to flour colour. Esterification of lutein contributes to its stability during storage. A locus controlling esterification was located in chromosome 7D.

Lutein esterification

Lute {11189}.	7DS {11189}.	**bin:**	7DS4-0.61-1.00.
	ma:	*Xwmc438-7D* – 15.1 cM – *Lute/XwPt-1163/XwPt-3727* – 17.7 cM – *Xbarc154-7* {11189}. Assigned to BAC TaBAC470M18 {11189}.	
	Alleles:	***Lute***	High lutein ester.
		v:	Indis {11189}; Sunco*2/Indus Der. DM5685*B12 {11189}. Most bread wheat accessions.
		lute	Low lutein ester.
		v:	Haruhikari {11189}.
Sunco is low lutein but high ester, whereas Haruhikari is low lutein and zero ester. Lutein esters were not detected in durum {11189}.			

33. Grain Traits

Variation in grain traits based on gene homology with other species

Insert above *TaSAP-A1*.

Tabas1-B1 {M11198}.	2BL {M11198}.		
	ma:	*Xbarc167-2B* – 10.38 cM – *Tabas1* – 5.23 cM – *Xcfa2278-2B* {11198}.	
	c:	BAS1is a type of 2-Cys peroxiredoxin in a large peroxidase family.	
	Tabas1-B1a {11198}.	**v:**	Jing 411 {M11198}.
Associated with higher TGW.			
	Tabas1-B1b {11198}.	**v:**	Hongmanchun 21 {11198}.
Associated with lower TGW.			

TaGW-A2 {11121,11122}	Orthologous to the rice RING-type E3 ubiquitin ligase *OsGW2* that functions as a negative regulator of grain weight		
	6A {11121}.	**ma:**	*TaGW2* was mapped on the Spark x Rialto DH population to chromosome 6A and linked to markers *BS000072146, BS000105973* and *CA643341* at 46.8 cM {11121}.
		c:	GenBank KP749901.1 {11122}.
A loss-of-function mutation in *TaGW2-A1* was associated with a 6.6% increase in grain weight in tetraploid and hexaploid wheat {11122}.			

Insert after *TaSAP-A1*.

TaTGW6-A1 {11196}.	3AL {11196}.		
	ma:	*Gene-3665_61* – 2 cM – *TaTGW-A1* – 18 cM – *BobWhite_c47304_56* {M11196}.	
	c:	TGW6 in rice encodes an indole-3-acetic acid -glucose hydrolase [{11196}].	
	TaTGW-A1a {11196}.	**v:**	Doumai {11196}; Zhou 8425B {11196}.
Associated with higher TKW.			
	TaTGW-A1b {11196}.	**v:**	Chinese Spring {11196}.
Associated with lower TKW.			

TaTGW-B1 {11196}.	3BL {11196}.
TaTGW-D1 {11196}.	3DL {11196}.

TaTGW-7A {11197}.		7AS {11197}.	**Bin:**	C-7AS8-0-0.45.
	ma:	*SLAF49035* – 3.02 cM – *TaTGW7A/TG* – 9.19 cM – *Xbarc-7A* {M11197}.		
	c:	Traes–7AS_378A12AA9.1. *GW2* in rice encodes an E3 ubiquitin ligase [{11197}].		
	TaTGW-7Aa {11197}.	**v:**	Jing 411 {M11197}.	
Associated with higher TGW.				
	TaTGW-7Ab {11197}.	**v:**	Hongmanchun 21 {11197}.	
Associated with lower grain weight.				

44. Height

44.2. Reduced height: GA-sensitive

Rht24. {11185}.	*QTL_height_6A_1* {11183}; *QPH.caas-6A* {11184}.	6AL {11185}.
v:	Aikang 58 {11185}.	
ma:	*Xwmc256-6A* – 2.71 cM – *TaGa3* – 7.05 cM – *TaAP2* – 0.24 cM – *Rht24* – 1.61 cM – *TaFAR* – 13.87 cM – *Xbarc103-6A* {11185}.	
Rht24 was identified in many Chinese cultivars and a low number of European wheats based on flanking markers designed from *TaAP2* and *TaFAR* {11185}.		

46. Hybrid Weakness

46.5 Hybrid necrosis type III

Nec1 {11158}.	7DS {11158}.	
v:	(*T. durum* cv. Langdon × *Ae. tauschii* KU-2828) amphiploid {11158}.	
al:	*Ae. tauschii* KU-2828 {11158}.	
ma:	*Xbarc352-7D* – 5.3 cM – *Lr34* – *Xgwm295-7D* – 4.0 cM – *Xbarc154-7D* – 1.7 cM – *Nec1* – 13.2 cm – *Xcfd-7D* {11158}.	

Although this form of hybrid necrosis is caused by complementary genes mapping of *Nec1* was based on a cross of necrotic and non-necrotic Langdon × *Ae. tauschii* amphiploids. Consequently only *Nec1* was mapped {11158}.

53. Male Sterility

53.3 Photoperiod and/or temperature-sensitive male sterility (PTGMS)

List as the first entry:

tmsBS20T {11157}.	2BL {11157}.	**v:**	BS20-T {11157}.
ma:	*Xgwm403-2B* – 2.2 cM – *tmsBS20T* – 4.5 cM – *Xgwm374-2B* {11157}.		

wptms1. Add note:
Chromosome 5B was also implicated in spontaneous mutant line Xinong 291S: a second gene was not located {11143}.

70. Response to Vernalization

Immediately above the ***Vrn-1*** heading continue the existing paragraph with: ‘The *Vrn-D4* locus in TDF includes a duplication of ~290 kb region from chromosome arm 5AL inserted into the proximal region of chromosome arm 5DS. This translocated segment includes a functional copy of *VRN-A1* that carries distinctive mutations in its coding and regulatory regions {11123}.

Vrn-2. Continue the current introductory paragraph with: ‘A triple *Vrn2* mutant (PI 676269, synthetic *vrn2-null*) is available in hexaploid wheat combining the non-functional *vrn-A2* allele present in most polyploid wheats with a *Vrn-B2* deletion from tetraploid wheat, and a non-functional *vrn-D2* allele from *Aegilops tauschii* {11124}.’

Vrn-B2. 4BL {11163}.
A study of winter wheats 2174 and Jagger showed that 2174 has a tandom repeat of *Vrn-B2* whereas Jagger has a deletion of this gene {11163}. Identical apparently functional sequences of *Vrn-B2* were found in contig sequences of Chinese Spring obtained from chromosomes 4BS, 2BS and 5DL {11163}.

Vrn-D2. 4DL {11163}.

71. Restorers for Cytoplasmic Male Sterility

71.4 Restorers for temperature-sensitive *Aegilops kotchyi* cytoplasm

Two recessive genes for temperature-sensitive sterility as follows.			
rfv_1^{sp} {11151}.	1BS {11151}.	**v:**	MS line KTP116A rfv_2 {11151}.
	ma:	*Xgwm413-1B* – 8.9 cM – rfv_1^{sp} – 12 cM – *Xgwm11-1B* {11151}.	
rfv_2 {11151}.	2A {11151}.	**v:**	MS line KTP116A rfv_1^{sp} {11151}.
	ma:	*Xwmc474-2A* – 23.9 cM – *rfv2* – 13.7 cM – *Xwmc644-2A* {11151}.	

86. Proteins

86.2. Enzymes

86.2.30. Starch branching enzyme II

SbeII.
Continue the present text with: ‘Combined loss-of-function mutations in *SbeIIa-A*, *SbeIIa-B*, *SbeIIb-A*, and *SbeIIb-B* (PI 670160) increased amylose content by 66% and resistant starch by 753% relative to the control in tetraploid wheat cv. Kronos {11125}. Combination of these four mutations with mutations of *SbeIIa-D* in hexaploid wheat (PI 670160) increased amylose content by 63% and resistant starch by 1,057% in field experiments relative to the control {11126}.

86.3. Endosperm storage proteins

86.3.1.3. Glu-3

Add after the GLU3 description and immediately before listing *Glu-A3*:
‘Characterization of near isogenic lines for the different *Glu3* alleles provides a useful quantification of their contribution to bread making quality {11129}.’

Pathogenic Disease/Pest Reaction

90. Reaction to *Blumeria graminis* DC.

90.1. Designated genes for resistance

Pm2.

Add note at end of section:
Several alleles of *Pm2* with wheat and alien origins have been reported in Chinese genotypes – see temporary designations.

Pm56 {11155}.	Derived from *S. cereale.*	6AS (T6RS.6AL) {11155}.		
	v:	LM47-6 {11155}.	**al:**	*S. cereale* cv. Qinling {11155}.
Study of misdivision products from a double monosomic 6A, 6R located *Pm56* to the subterminal region of 6RS {17026}.				
Pm57 {11159}.	Derived from *Ae. searsii.*	2BL (T2BS·2BL-2S^S#1L) {11159}.		
	v:	Line 89-346, TA5108 {11159}; Line 89(5)69 TA5109 {11159}.		
Line 89-346 has a 28% distal *Ae. searsii* segment and line 89(5)69 has a 33% distal *Ae. searsii* segment {11159}.				
Pm58 {11171}.	*PmTA1662* {11171}.	Derived from *Ae. tauschii.*		
	2DS {11171}.	**v:**	Reference line to be chosen and accessioned {11171}.	
	dv:	*Ae. tauschii* TA1662 {11171}.		
	ma:	Co-segregation with KASP™ markers *K-TP331370, K-TP338253, K-Tp15990* and *K-Tp313873* {11171}.		

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

PmHo {11176}.	2AL {11176}.	**v:**	Mv Hombar {11176}.
	ma:	*XwPt-665330* – 0.3 cM – *PmHo* – 0.1 cM – *XwPt-3114* {11176}.	
PmLX66 {11162}.	5DS {11162}.	**v:**	Liangxing 66 {11162}.
PmLX66 was allelic with *Pm2* {11162}.			
PmTb7A.1 {11130}.	7AL {11130}.	**bin:**	7AL18-0.90-1.00.
	dv:	*T. boeoticum* PAU5088 *PmTb7A.2* {11130}. **ma:** Mapped to a 4.3 region flanked by *wPt4553* and *Xcfa2019-7A* {11130}. Estimated to be 46 cM proximal to *Pm1* {11130}.	
PmTb7A.2 {11130}.	7AL {11130}.		
	dv:	*T. boeoticum* PAU5088 *PmTb7A.1* {11130}.	
	ma:	Mapped to a 0.8 cM region flanked by *MAG1759* and *MAG2185b* {11130} in the region of *Pm1* {11130}.	

PmW14 {11162}.	5DS {11162}.	**v:**	Wennong 14 {11162}.	
PmWE14 was allelic with *Pm2* {11162}.				
PmWE99 {11166}.	Derived from *Thinopyrum intermedium*.	2BS {11166}.		
	bin:	2BS-0.84-1.00.	**v:**	WE99 {M18037}.
	ma:	*Pmw99* – 10.4 cM – *Xgwm148-2B* – 3.1 cM – *Xbarc55-2B* {11166}.		
GISH failed to detect alien chromatin.				
Mlm2033.	Please correct the earlier entry listed as *Mlm3033*.			
	ma:	*Xwgrc353/Xwggc4659* – 0.84 cM – *Mlm2033/Xmag8626/Xmag9060/Xmag2185/Xmag5240* – 0.06 cM – *Xmag8415/Xmag8220* {11190}.		
Mlm80.	**ma:**	*Xwggc4655* – 0.29 cM – *Mlm80* – 0.57 cM – *Xwgrc253/Xwgrc271* {11190}.		

90.4. QTL for resistance to *Blumeria graminis*

QPm-tut-4A {11154}.	4AL {11154}.	
	v:	DT4AL-TM Line 8.1 {11154}.
	tv:	*T. militinae* (AAGG) {11154}.
The 7G segment carrying this resistance likely replaces most of the 7BS segment known to be part of chromosome 4A {11154}.		

96. Reaction to *Fusarium* spp.

96.1. Disease: Fusarium head scab, scab

Fhb1. Add comment at end of section:
Lines combining *Fhb1*and *Sr2* are reported in {11170}; *Fhb1* is located about 2 cM proximal to *Sr2*.

SYN1 / Ocoroni DH population: three QTL from SYN1 were identified, *QFhs.cim-2D* (PVE 25%), *QFhs.cim-7A* (PVE 4.7%) and *Qfhs.cim-7A* (PVE 4.2%) {11165}.

98. 1 Reaction to *Magnaporthe grisea* (Herbert) BarrAdd: Syn. *Pyricularia oryzae*

Current *Mg* list.

98.2 Reaction to *Magnaporthe oryzae*.

Wheat cultivars carrying the 2NS translocation from *Aegilops ventricosa* had 50.4 to 72.3% less head blast than those without 2NS when inoculated with an older isolate (MoT) of *Magnaporthe oryzae* (*Triticum* pathotype) under growth chamber conditions. When inoculated with recently collected isolates from wheat, cultivars with 2NS had 64.0 to 80.5% less head blast {11127}.

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

Add the synonym species name as above.

Stb3. [*Slb3*{1586}]. 6DS, according to {10556} this location is not correct{10105}. 7AS{10556, 11191}. v: Israel 493{1586}.
ma: Please delete present material and replace with:
Xcfa2028-7A – 12.4 cM – *Stb3/Xwmc83-7A* – 2.1 cM – *Xbarc222-7A* {11191}.

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

102.2 Sensitivity to SNB toxins (necrotrphic effectors)

Tsn1. The ma: line listed above this heading should be inserted in the *Tsn1* entry section.

Snn1. *KASP marker Bs00093078_51* was developed at Wang map position 8.361 in the UK MAGIC population {11133}.

QTL: Add:

QSnn.niab-5A.1 {11133}.	**v:**	Identified in the UK MAGIC population {11133}.

105. Reaction to *Puccinia graminis* Pers.

Sr2. Add comment at end of section:
Lines combining *Sr2* and *Fhb1* are reported in {11170}; *Sr2* is located about 2 cM distal to *Fhb1*.

Sr9.

Sr9h. Add note at end of section:
Although {11149} concluded that *Sr28* was present in VL404 and Janz it is more likely that the gene described is the linked gene *Sr9h*. *Sr9h* was frequently present in landraces with field resistance to early isolates of the *Pgt* race Ug99 group {11147}.

Sr11.	**v2:**	Add: Charter *Sr9h* {11177}; Trident *Sr38* {11177}.
	ma:	*KASP_6BL_IWB46893* – 0.3 cM – *Sr11/KASP_6BL_IWB10724* – 0.3 cM – *KASP_6BL_IWB72471* {11177}.

Sr13. Add at end of section:
Markers *Xgwm427-6A* and *AFSr13S* (proximal) and *Xdupw-6A* (distal) showed variable but close (<10 cM) linkage with *Sr13* in six durum crosses – these markers were variously applicable across durum backgrounds, but only *Xgwm427-6A* was variable in a range of hexaploid derivatives with *Sr13* likely originating from a single source {11146}.

Sr26. Add note:

Secondary recombinants with shortened 6AL#1L segments involving chromosomes 6A and 6D are reported in {11141}; five 6A recombinants were accessioned in the Australian Winter Cereals Collection.

Sr28.	**v:**	Add: SD 1691, CI 12499 {11148}.
	ma:	*Xwmc332* – 1.4 cM – *r28* – 6.0 cM – *wPt-7007* {11148}; *Sr28* – 1.6 cM – *wPt-7004* {11148}; *Sr28* – 0.6 cM – *wPt-7004* {11148}.
Although {11149} concluded that *Sr28* was present in VL404 and Janz it is more likely that the gene described is the linked gene *Sr9h*.		

Sr35.	To the chromosome location add: ,$3A^mL$ {11140}.	
	ma:	Add: *AK331487* – 0.02 cM – *Sr35* – 0.98 cM – *AK332451* {11140}.
	c:	*Sr35* is has a coiled-coil-NBS-LRR structure {11140}.

Sr42. Add note at end:
A genetic analysis of six lines, Blouk, Coni, Niini, Pfuneye, Ripper and Tinkio, is reported in {11132}. All had single genes with linkage to *Xcfd49-6D* ranging from 3.9 – 12.5 cM and the genes were not clearly distinguished from *Sr42* or *SrTmp* {11132}.

Sr45. **su:** CS1D5406 {11134}. **ma:** *Xgwm106-1D/BE44426* – 1.82 cM – *Sr45* – 0.39 cM – *csssu45/Af45* {11134}.
To present note add:
One race distinguishing *Sr45* and *Sr21* is reported in {11134}.

Sr56.	**bin:**	Correct to: 5BL16-0.79-1.00.
	ma:	Replace present information with: *Xsun209* (SSR) – 2.6 cm – *Sr56* – 1.2 cM – *Xsun320* (STS from wPt-7665) {10851}.

Sr59.	**ma:**	Three rye-based KASP markers identified lines with *Sr59* {11066}.	
SrPI410966 {11180}.	2BS {11180}.	**v:**	PI 410966 {11180}.
The marker profile for this gene was very similar to that of a line with *Sr36* {11180,10825}. Specificity tests were not reported.			
SrTmp.	**v:**	Add: Digalu {11132}; Ember {11152}; Guard-1 {11152}; Kenya Robin {11152}; Morvarid {11132}; Overland {11152}; Ripper {11132}; Shield {11152}.	
Sr10187.	*SrTA10187* {11181}.		
	ma:	Add: *6DS0027* – 0.2 cM – *Sr10187* – 0.2 cM – *6DS00273* {11181}; *Sr10187* – 0.2 cM – *6DS0039* {11181}.	

At the end of the gene list:
Genotype lists: {Add: 17006}.

106. Reaction to *Puccinia striiformis* Westend.

106.1. Designated genes for resistance to stripe rust

Yr5.	**i:**	Add: Lemhi+Yr5 {11153}.		

	ma:	*Xwmc175-2B* – 4.6 CM – *YR5/ TaAffrx.65234.1.S2-at/Ta.28038* – 0.7 cM – *S23M41-310/STS:S23M41-275* {11153}.
Yr6.	**v2:**	Add: Cadenza *Yr7* {11187}.
	ma:	*Xgwm577-7B* – *Yr6*, <0.4 cM {11187}. Narrowed to an ~60 kb region including *Xgwm577* {11188}. Given the location of *Xgwm577* the gene location should be 7BL.
Yr7.	**v2:**	Cadenza *Yr6* {11187}.
	ma:	*Xwmc175A-2B* – *Yr7*, <0.4 cM {11187}.
Yr10.	**v:**	Add: AC Radiant {11167}; Jacmar {11145}.
	c:	*Yr10* has a CC-NBS-LRR structure {11145}. GenBank AF149112 {11145}.
Yr15.	**ma**:	Add: *Xbarc8-1B* – 3.9 cm – *Yr15* – 2.5 cM – *Xgwm413-1BS* {11173}.
Yr18.	**v:**	Add: Libellula {11139}; Strampelli {11139}.
Libellula had an additional 4 QTL and Strampelli had an additional 3 QTL {11139}.		
Yr32.	**v:**	Toisondor {11144}.
Yr36.	**c:**	Add: *Sr36* was shown to reduce the ability of the thylakoid-associated ascorbate peroxidase to detoxify reactive oxygen species {11128}.
Yr47.	**bin:**	5BS6-0.81-1.00.
	ma:	Change present entry to: *Xgwm234-5B* – 10.2 cM – *Lr52* – 3.3 cM – *Yr47* – 9.6 cM – *Xcfb309-5B* {10679}; *Xcfb309-5B* – *Xsun480/Xmag705/Xfcp552-5B* – 0.4 cM – *Yr47* – 4.3 cM – *icg16c008/Xgwm234-5B* {11200}; *Xsun180* – 0.4 cM – *Lr52* – 0.2 cM – *Yr47* – 1.4 cM – *Xgwm234-5B* {11200}.
Yr51.	*YrAW1* {10850}.	**v2:** Correct to: AUS27859 *Yr57* {10850}.
	ma:	Replace the present entry with: *Xowm45F3R304A* – 1.2 cM – *Yr51* – 2.5 cM – *Xsun104-4A* – 1.8 cM – *Xgwm160-4A* {10850}.
Yr57.	*YrAW2* {10963}.	
Yr60.	Modify the current entry to the following:	
Yr60 {10968}.	4AL {10968}.	**v1:** Almop, Avocet*3//Lalbmono1B*4/Pavon GID 5934039 {10968}.
	v2:	LB (Pavon1B) *Yr29* {10968}.
	ma:	*Xwmc313/Xwmc219-4A* – 0.51 cM – *Yr60/Xwmc776-4A* {10968}.
Yr60 was estimated to be about 10 cM distal to *Yr51*		
Yr69.	Add: Derived from *Thinopyrum ponticum*.	

Yr77 {11174}.	Adult plant resistance.	*QYr.ucw-6D* {11174}	
	6DS {11174}.		
	v:	PI 322118 {11174}; PI 164377 {11174}; PI 388095 {11174}; PI 520350 {11174}; PI 623378 {11174}.	
	ma:	*Yr77* was strongly associated with *IWA167* in the region *Xbarc54-6D* (6DS) – 15.2 cM – *IWA167* (6DS) – 3.9 cM – *Xcfd188-6D* (6DL) {11174}.	
Among the listed accessions two were from India, one from Pakistan, one from Iran, and one from the USA.			
Yr78 {11174}.	Adult plant resistance.	*QYr.ucw-6B* {11174}.	
	6BS {11174}.	**v:**	PI 519805 {11174}; Nine others {11174}.
	ma:	The *Yr78* peak fell within a 4.3 cM interval, *IWA7257* – *Xwmc737-6B* {11174}.	

106.2. Temporarily designated genes for resistance to stripe rust

YrF {11156}.	2BS {11156}.	**v:**	Francolin#1 *Yr46* {11156}.	
Francolin#1 is also released under the names Ufam and BARI Gom 27 {11156}.				
YrJ22 {11195}.	2AL { 11195.}.	**v:**	Jimai 22 {11195}.	
	ma:	*Xgwm382-2AL* – 1.0 cM – *YrJ22* – 7.3 cM – *IWA1348* {11195}.		
Yrwh2 {11150}.	Recessive.	3BS {11150}.	**v:**	Wuhan 2 {11150}.
	ma:	*Xwmc540-3B* – 5.9 cM – *Yrwh2* – 10 cM – *Xgwm566-3B* {11150}.		

106.3. Stripe rust QTL

Camp Remy/Recital: Add: Differential reactions of RILs possessing different QTL occurred between old and new *P. striiformis* races {11144}.

Coker 9835 (S) / VA96W-270 RIL population: Adult plant resistance was conferred by *QYr.ar-3BS* (nearest markers *Xbarc147, ger9-3p, IWA6092*) and *QYr.ar-4BL* (nearest markers *Xbarc163*, *Xcfd39* and several *IWA* markers {11175}. Cultivar Pat had the same haplotype {11175}.

USG 3555 / Neuse: Add: Three QTL on chromosomes 1AS, 4BL and 7D (not *Yr18*) were derived from USG 3555 and one QTL on chromosome 3A was from Neuse {11142}.

107. Reaction to *Puccinia triticina*

107.1. Genes for resistance

Lr19.	**v:**	Pallada {11161}.
Lr48.	**ma:**	Add: *Xsun563/Xsun497* – 0.6 cM – 5 SNP markers/*Lr48* – 0.3 cM – *IWB70147* – 2.0 cM – *XBARC0-7-2B* – 9.4 cM – *Lr13* {11172}.
Add comment: The suggestion that this gene is present in 13 Australian varieties		

carrying *Lr48* markers and hence *Lr48* {11172} needs verification.			
Lr52.		**bin:**	5BS6-0.81-1.00.
	ma:	Change present entry to: *Xgwm234-5B* – 10.2 cM – *Lr52* – 3.3 cM – *Yr47* – 9.6 cM – *Xcfb309-5B* {10679}; *Xcfb309-5B* – *Xsun480/Xmag705/Xfcp552-5B* – 0.4 cM – *Yr47* – 4.3 cM – *icg16c008/Xgwm234-5B* {11200}; *Xsun180* – 0.4 cM – *Lr52* – 0.2 cM – *Yr47* – 1.4 cM – *Xgwm234-5B* {11200}.	
Lr70 {10904}.	5DS {10904}.	**v2:**	KU3198 *Lrk1* {10904}.
	ma:	*Lr70* – 5.6 cM – *Xbarc130-5D* – 1.7 cM – *Xwmc233-5D* {10904}.	
Lr75.	Remove the '*P*' from the synonym.	**bin**	1BS10-0.5-1.00.
	v2	Update to: Forno *Lr14a Lr34* {11053}.	
	Bin:	Update to: *Xgwm604-1B* 1.6 – cM – *Lr75* – 2.70 cM – *swm271* – 0.14 cM – *Xgwm11-1B/Xgwm18-1B/swm294/swm278/swm275* {11053}.	
Lr77 {11164}.	Adult plant resistance	3BL {11164}.	
	v:	Tc*3 / Santa Fe 8-1C.9 {11164}.	
	v2:	Duster *Lr3a Lr11 Lr34* PI 639233{11164}; Santa Fe *Lr3a Lr17a Lr37* PI 641772{11164}.	
	ma:	*IWB32653* – 1.15 cM – *KASP23680* – 1.15 cM – *Lr77/KASP10344/Kasp73555* – 0.62 cM – *KASP12260* – 2.46 cM – *IWB79797* {11164}.	
LrK1 {10904}.	5BS {10904}.	**v2:**	Ku3198 *Lr70* {10904}.
	ma:	*LrK1* – 0.6 cM – *Xcfd20/Xgwm234-5B* {10904}.	
LrK1 could be *Lr52* or an allele {10904}.			

At the end of the gene lists:
Genotype lists: Insert 'Croatian cultivars {11135}'. 'Kazakhstan cultivars {11161}'.
At the end of section add:
See {11178} for review and analysis of leaf rust resistance genes in six durum wheats.

111. Reaction to *Sitodiplosis mosellana* (Gehin)

Sm1.	**v:**	Add: Augusta {11137}; Robigus {11137}; Skalmeje {11137}.
	ma:	Add: A combination of 2BS-5344126_kwm707 and 2BS-6229175_kwm693 appeared to be predictive of *Sm1* but there was variation between sources {11137}.

113. Reaction to Soil-Borne Cereal Mosaic Virus (SBCMC)

Sbm1.	**v:**	Add: Claire {11138}; Moulin {11138}; Tremie {11138}.
	ma:	Add: *E37M49* – 9.0 cM – *Sbm1* – 1.0 cM – *Xgwm469-5D* – 2.0 cM – *Xwmc765-5D* {11138}. Resistant varieties carried 152 or 154 bp alleles at *Xgwm469-5D*; all susceptible genotypes had a null allele {11138}.

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

Ut4 Add reference {,11168}.	*QUt.spa-7B* {11168}.	7B {11168}.
	v:	TD1{11168}; Glenlea {11168}; 9340-CP {11168}.
The current information listed for *Ut-X* can be transferred to *Ut5* using *Ut-X* as a synonym.		
Ut5 {11168}.	*Ut-X* {1164}.	
Ut6 {11169}.	*QUt.spa-5B* {11168}.	5BL {11169}.
	v:	AC Foremost {11169}; AC Karma {10040}; AC Vista {11168}; Chinese Spring {11169}; Glenlea {11169}; HY320 {11169}; Oasis {11169}.
	ma:	*Xgpw5029-5B* **–** 2.8 cM – *Ut6* – 2.8 cM – *Xbarc232-5B* {11169}.
Ut7 {11168}.	*QUt.spa.7A* {11168}.	7A {11168}.
	v:	SC8021V2 {11168}.
Ut8 {11168}.	*QUt.spa-3A* {11168}.	3A {11168}.
	v:	9340-SP{11168}; Glenlea {11168}.
Ut9 {11168}.	*QUt.spa-6B* {11168}.	6B {11168}.
	v:	SC8021V2 {11168}.
Ut10 {11168}.	*QUt.sps-6D* {11168}.	6D {11168}.
	v:	SC80-21V2 {11168}.

QTL

Existing entry: Correct spelling of: Blizard.

Idaho 444 (R) / Rio Blanco S: RIL population: Three QTL for dwarf bunt resistance: *QDB.ui-7DS* (R^2 = 0.3 – 0.6), *QDB.ui-1A* (r^2 = 0.11 – 0.15) and *QDB.ui-2B* (R^2 = 0.06). Two PCR-based markers were developed for the wPt-2565 sequence on chromosome 7DS {11182}

119. Reaction to Wheat Streak Mosaic Virus

Wsm1.	4D = T4DL.$4J^{S}$S.	**v:**	Mace PI 651043 {11179}.
Add note: *Wsm1* confers resistance at temperatures below 19C {11179}.			

122. Reaction to Wheat Yellow Mosaic Virus

Following the entry *YmYF* and above the QTL: add:

QYr.nau-2D {11186}.	2DL {11186}.	**bin:**	2DL9-0.76-1.00.
	v:	Yining Xiaomai {11186}.	
	ma:	*Xwmc41-2D* – 3.7 cM – *2SNP86.2* – 0.4 cM – *QYm.nau-2D* – 1.0 cM – *2EST784* {11186}.	

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Update	

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