CATALOGUE OF GENE SYMBOLS FOR WHEAT: 2015-2016 SUPPLEMENT

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Laboratory Designators

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Morphological and Physiological Traits

1. Gross Morphology: Spike characteristics

1.2. Club/Compact spike

Insert above QTL:

C$_g$ {11114}.	2BL {11114}.	**bin:**	2BL-0.48-0.89, near breakpoint 0.69.
	v:	Akage Gumbai {11114}; Akage Gumbai 22 {11114 }; Gumbai 22 {11114}; Kiroshita Komugi {11114}; Nakote Gumbai {11114}.	

	ma:	*Xhbg410/Xhbg440-2B* – 18.1 cM – C_g – 15.3 cM – *Xgwm47-2B* {11114}.

9. Brittle Rachis

Following the introductory sentence add:
Wedge (W) type disarticulation is associated with the *Br-1* gene set whereas barrel (B) type disarticulation is caused by a different gene and is limited to species with the D genome {15033}.

Insert after *Br-D1*:

Br-S1 {11080}.	3SS {11080}.	**v:**	Iranian spelts {11080}.
tv:	*Triticum timopheevii* {11080}.	**dv:**	*Aegilops tauschii* {11080}.
ma:	*Xpsr1196-3S* 32.3 cM – *Br-S1* – 1.5 cM – *Xabg471-3D* {11080}.		

Br-D2 {11080}.	3DS {11080}.	**v:** Common wheat {11080}; European spelts {11080}.
	dv:	Al8/78 (shattering 11080}; TA1604 (non-shattering) {11080}.
	ma:	*Xwmg2013-3D* – 1.5 cm – *Br-D2* – 2.9 cM – *Xpsr170-3D* {11080}.

17. Dormancy (Seed)

17.1. Germination index

TaSdr.		2B {11119}.	
	TaSdr-B1a {11119}.	**v:**	Yangxiaomai {11119}.
		c:	GenBank KF021990 {11119}.
This allele is associated with lower germination index.			
	TaSdr-B1b {11119}.	**v:**	Zhongyou 9507 {11119}.
		c:	GenBank KF021991 {11119}.
This allele is associated with higher germination index.			

17.2. Vivipary

17.3. Pre-harvest sprouting

27. Glaucousness (Waxiness/Glossiness)

27.2 Epistatic inhibitors of glaucousness

Iw1.	Add:	**bin:**	2BS3-0.84-1.00.
		v:	WE74 {11094}. Shamrock {11090}.
	ma:	*JIC007* – 1.47 cM – *Iw1* – 0.18 cM – *JIC010/JIC011* {11090}. Co-segregation with BF474014, CJ876545 and CD927782 and flanked by BE498358 and CA499581 within a 0.96 cM interval {11094}.	

Iw2.	Add:	**bin:**	2DS5-0.84-1.00.
		v:	TA4152-60 {11094}.
	ma:	Co-segregation with BF474014 and CJ876545 and flanked by CJ886319 and CJ519831 within a 4.4 cM interval {11094}.	

NEW SECTION

33. Grain Traits

Variation in grain traits based on gene homology with other species

TaGASR7-A1 {11115}.	Snakin/GASA gene family.		7AL {11115}.
		ma:	*Xwmc301*-7A – 17.9 cM – *TaGASR7* – 10.6 cM – *Xwmc9-7A* {11115}.
		c:	GenBank KJ000052{11115 }.
Hap1c in Lumai 14 and Xiaoyan 81 conferred higher grain length and grain weight than *Hap1g* in Hanxuan 10 and Xinmai 10 {11115}.			
TaGS-D1 {11116}.			7DS {11116}.
		ma:	*TaGs-D1* – 8.0 cM – *Xbarc184* {11116}.
	TaGs-D1a {11116}.	**v:**	Doumai {11116}; Jingdong 8 {11116}.
		c	KF687956 {11116}.
	Associated with higher TGW and grain length {11116}.		
	TaGs-D1b {11116}.	**v:**	Shi4185 {11116}; Yumai 21 {11116}.
		c:	KF687957 {11116}.
	Associated with lower TGW and grain length {11116}.		
TaSAP1-A1 {11117}.	Stress association protein gene family.		
	7A {11117}.	**ma:**	*Xwmc530-7A* – 2.1 cM – *TaSAP1-A1* – 13.9 cM – *Xbarc174-7A* {11117}.
		c:	GenBank KC193579 {11117}.
Variation at this locus was associated with 1,000-grain weight, number of grains per spike, spike length, peduncle length and total number of spikelets per spike, but different haplotypes had different effects various traits {11117}.			

41. Height

41.1. Reduced Height: GA-insensitive

41.2. Reduced height: GA-sensitive

Rht18. Add note:
Hexaploid derivatives in the backgrounds of Fengchan 3, Jinmai 47 *Rht8*, and Xifeng 20 are reported in {11096}.

Rht23 {11077}.	5DL {11077}.	**v:**	NAUH164 {11077}.
	ma:		*Xgdm63-5D* – 4.7 cM – *Rht23* – 11.1 cM – *Xbarc110-5D* {11077}.
NAUH164 is an EMS-derived mutant of Sumai 3 {11077}.			

43. Hybrid Weakness

42.1. Hybrid necrosis

Ne2m. Add:

	ma:	*Xbarc55*-2B – 1.1 cM – *Xkwh37* – 4.9 cM – *Lr13*/*Ne2* – 5.8 cM *Xgpw1109* – 3.7 cM – *Xbarc18*-2B {11068}.

47. Leaf Tip Necrosis

Ne3 {11070}.	**i:**	RL6077 {11070}.	**v:**	Chapingo 48 {11070}.
	c:	This multiple disease resistance/necrosis locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.		

67. Response to Vernalization

Vrn-D1b. **v:** Add:
Additional Chinese germplasm {11072}.

Add immediately following the *vrn-D1* listing:
Vrn-D1a, *Vrn-d1b* and *Vrn-D1* were present in 27.3, 20.6 and 52.1% of 689 Chinese wheat accessions {11072}.

82. Proteins
82.3. Endosperm storage proteins

82.3.1. Glutenins

82.3.1.1 Glu-1

Glu-A1. Add:

Glu-A1ba {11106}.	[*Glu-A1g* {11106}].	1.1 {11106}.	**v:**	Barbela 28 {11106}.

The sequence encoding subunit 1Ax1.1 shows high nucleotide identity with other *Glu-A1* alleles, with the main difference being an insertion of 36 amino acids in the central repetitive region. It is the largest and most acidic subunit currently known at this locus and has been implicated in high dough extensibility in some cv. Barbela wheat lines, although this contrasts with other data showing a similar effect to that of subunit 1Ax1 {11107}.

Pathogenic Disease/Pest Reaction

84. Reaction to Barley Yellow Dwarf Virus

Bdv2.
Add note at end of section:
Small recombinant segments are described in a *pontin* series of lines: recombinants were obtained with *Lr19* but not with *Sr25* {11097}.

86. Reaction to *Blumeria graminis* DC.
86.1. Designated genes for resistance

Pm2		
	Pm2a {11049}.	[*Pm2* {130}], [*Mlu* {1175}, *Mlx* {1088}].
	Remainder as now listed for *Pm2*.	

	Pm2b {11049}.	Putatively derived from *Agropryron cristatum*.	*PmKM2939* {11049}; *PmPB3558* {11075}.		
	bin:	C-5DS1-0-0.63.	**v:**	KM2939 {11049}; PB3558 {11075}	
	ma:	*Xscar112* – 0.5 cM – *Pm2b* – 1.3 cM – *Xscar203/Xmag6176/Xcfd81-5D* {11049}; *Xcfd81-5D* – 5.5 cM – *PmPB3558* – 3.9 cM – *Xbwm25* – 0.9 cM – *Xbwm21* – 0.9 cM – *Xbwm20* {11075}.			
	Pm2c {11061}.	*PmNM* {11061}.	5DS {11061}.	**bin:**	5DS-1-0-0.63
	v:	Niaomai {11061}.			
	ma:	*Xcfd81-5D* – 0.4 /0.1 cM – *Pm2c* – 7.5/4.9 cM – *Xcfd78-5D* {11061}.			

Allelism with *Pm2a* and *Pm2b* was based on more than 7,600 F$_2$ plants.

Pm46. Add:

	v:	Chapingo 48 {11070}.
	c:	This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

Pm51. Correct to:

	ma:	*Xwmc332-2* – 3.2 cM – *Pm51* – 1.5 cm – *BQ246670* {11026}.

Pm54 {11050}.	*PmA2K* {11050}.	6BL {11050}.	**bin:**	6BL-0.450-1.00.
	v:	AGS 2000 PI 612956 {11050}.		
	ma:	*Xgpw2344-6B* – 1.00 cM – *wPt-9256* – *Pm54* – 1.2 cM – *Xbarc134-6B* {11050}.		

Pm55 {11108}.	Derived from *Dasypyrum villosum*.	*Pm5VS* {11108,11109}.		
	5AS (5VS.5AL) {11108}.		**v:**	NAU421 {11108}.
	5DS (5VS.5DL) {11109}.		**v:**	NAU415 (11108,11109}.
	ma:	A 730 bp *5EST-237* band is associated with chromosome 5VS {11109}. 5VS also carries puroindoline genes; therefore all lines with this gene will be soft (5VS.5DL) or supersoft (5VS.5AL).		
The backgrounds of NAU415 and NAU421 are Chinese Spring. The PM resistance conferred by this gene gradually increases from the third leaf stage and reaches an immunity level by the seventh leaf stage.				

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

MlIW172 {11095}.	7AL {11095}.	**bin:**	7Al-16-0.86-0.90.
	tv:	*T. dicoccoides* IW172 {11095}.	
	ma:	*WGGC4664/WGGC4665/WGGC4668* – 0.44 cM – *MlIW172* – 0.7 cM – *WGGC4659* {11095}.	

86.4. QTLs for resistance to *Blumeria graminis*

PmSE5785 {11084}.	Recessive.	2DL {11084}.
	v:	SE5785, Snipe / Yav79 // Dack / Teal /3/ *Ae. squarrosa* 877 11084}; NO7728-1 {11084}; NO7728-2 {11084}.
	ma:	*Xbarc59-2D* – 3.6 cM – *PmSe5785* – 4.6 cM – *Xwmc817-2* {11084}.

Correct spelling:
Reaction to *Colletotrichum cereale*

90. Reaction to *Diuraphis noxia* (Mordvilko)

Dn6.	7D.		
Dn2401 {M14031}.	7DS {11078}.	**v:**	CI2401, PI 97812 {11078}.
	ma:	*Xbarc214-7D* – 1.1 cM – *Dn2401* – 1.8 cM – *Xgwm473-7D* {11078}.	

91. Reaction to *Fusarium* spp.
91.1. Disease: Fusarium head scab, scab

Fhb1. Add:
v: Alsen {11071}; Rollag {11071}.

Fhb5.

Fhb6 {11048}.	Derived from *Elymus tsukushiensis* syn. *Roegneria kamoji*.		
	1AS {11048}.		
	T1AL.1AS-1E^{ts}#1S {11048}.	**v:**	TA5660, KS14WRRC61 {11048}; TA5093 {11048}.
	ma:	Three CAPS and one KASPar SNP (*wg1S-snp1*) markers were developed {11048}.	
TA5660 is in Chinese Spring background; TA5093 is in Everest background.			
	TW.1E^{ts}#1S {11048}.	**v:**	TA5655 {M11048}.

Fhb7 {11060}.	Derived from *Thinopyrum ponticum.*	*FhbLoP* {11118}.	
	T7DS.7Dl-7el$_2$L {11060}.	**v:**	SDAU1881 {11060}; SDAU1886 {11060}.
	ma:	Flanked by 7el$_2$ markers *Xcfa2240* and *XsdauK66* in a 1.7 cM interval {11060}.	
	T7DS.7el$_2$ {657}.	**v:**	KS24-2 {657}.

Tetraploid wheat
Add:
T. dicoccoides Mt. Gerizim#36 /*2 *T. durum* Helidur F$_6$ lines: two QTL for type 2 resistance located on chromosomes 3A (*Xbarc45-3A* – *Xbarc67-3A*) and 6B *Xs13m22_2* – *Xgwm626-6B* {11088}).

92. Modify title to:
Reaction to *Heterodera avenae* Woll., *H. filipjeva* (Madzhidov) Stelter

***Cre* 5.** Add: **v:** Madsen {11102}.

Cre8. **ma** Add: The map in {10343} was reversed: *Cre9* was located closer to the end of chromosome 6BL (11081}. Six markers that can be screened by KASP^{TM} and *wri15* developed from a SNP were reported {11081}.

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

Rmg7. Add: 2AL {11083}. **ma:** *Xcfd50-2A* – 5.6 cM – *Rmg7* – 15.1 cM – *Xhbg327-2A* {11083}.

Rmg8 {11083}.	2BL {11083}.	**v:**	S615 {11083}.	**bin:**	2BL6-0.89-1.00.
	ma:	*Xwmc317-2B* – 12.1 cM – *Rmg8* – 22.4 cM – *Xbarc159-2B* {11083}.			
According to {11083} markers linked to *Rmg8* were independent of those linked to *Rmg7*.					

94. Reaction to *Mayetiola destructor* (Say) (*Phytophaga destructor*) (Say)

H16. Add: , 1AS {15011}. **bin:** 1AS-3-0.86-1.00. **v:** P921682 {11058}. **ma:** Add: *Xpsp2999-1A* – 3.7 cM – *H16* – 5.5 cM – *Xbarc263/Xwem6B-1A* {11058}.

H17. Add: , 1AS {11058}. **bin:** 1AS-3-0.86-1.00. **v:** P921680 {11058}. **ma:** Add: *Xpsp2999-1A* – 6.27 cM – *H17* – 5.1 cM – *Xbarc263/Xwem6B-1A* {11058}.

99. Reaction to *Puccinia graminis* Pers.

Sr9h. Add:
v: Matlabas {10057}. **ma:** *wPt-3132* – 1.9 cM – *Sr9h* – 1.9 cM – *wPt-8460* {11010}. *Sr9h* – 20.7 cM – *Sr28* {11010}.

Sr12. Modify and add: 3BS or centromeric region {1332,682,11103}; 3BL (11104}. **v2:** Condor *Sr8a*{11105}; Celebration *Sr9gSr16* (939}; Condor Thatcher *Sr5Sr9gSr16* {939}; RL6058 (a Thatcher derivative) {11104}.
ma: *IWA6086* – *Sr12* – *IWA4613* {11104}.
Add to note section. Although the association of field resistance and *Sr12* was not definitive allelism or close linkage is clearly involved (11104}.

Sr21. Add:
dv: After einkorn, add: CI 2433, i.e. Einkorn CI 2433 {1460,11110}.
ma: FD52726 – 0.25 cM – *Sr21* – 0.05 cM – EX594406 {11110}.

Sr42. **v:** PI 595667 {11087}. **v2:** PI 410954 *Sr24* {11087}.
ma: Add: *Xcfa49-6D* – *Sr42/IBW31561/IWB30767* – *FSDRSA* {11087}.
Add notes:
Sr42 co-locates with *SrCad*, *SrNini*, SrSh7 and *SrTmp*. Three haplotypes were identified in {11087}: C-C-T, AC Cadillac, Peace, PI 595667; T*-C-T, Norin 40, Eagle 10, Ember, Guard, Ripper, Shield; T-C-T, Triumph 64, CnSSrTMP64, Blouk, Digalu, Pfunye, Robin, PI 410954.

Sr43. 7DL. Add:
, 7DS-7el$_2$S.7el$_2$L {11076}.
Add note: Derivatives RWG33 and RWG34 with shortened alien segments are reported in {11076}.

Sr49. Replace current entry with: **v:** Mahmoudi AUS 28011 {10704}.
and replace current entry with : **ma:** *sun479* – 0.9 cM – *Sr49* – 1.5 cM – *sun209* – 0.5 cM – *Xwmc471-5B* {10704}.

Sr55. Add:
v: Chapingo 48 {11070}. **c:** This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

Sr59 {11066}.	Derived from *Secale cereale*.			2D (T2DS.2RL) {11066}.
	v:	TA5094 {11066}.	**su:**	SLU238 (2R(2D)) {11066}.
	al:	VT828041 (6X triticale) {11066}.		

SrND643 {11092}.	4AL {11092}.	**bin:**	4AL4-0.8-1.00.
	v:	Kenya Sunbird {11092}; Kenya Tai {11092}; ND643/2*Weebill1 GID6302736 {11092}.	
	tv:	ND643 {11092}.	
	ma:	*Xwmc776-4A* – 2.9 cM – *Xgwm350-4A* – 0.5 cM – *SrND643* – 4.1 cM – *Xwmc219-4A* {M14045}.	

SrTm4 {11111}.		Recessive.	2A^{m}L {11111}.
	dv:	*T. monococcum* PI 306540 {11111}.	
	bin/contig:	IWGS_2AL_contig 6401556	
	ma:	BQ461276 – 1.6 cM – *SrTm4* – 0.5 cM – DR732348/*Xgwm526/Xgdm93-2A* {11111}.	

SrTmp. Add: *SrSha7* {11057}. 6DS. **v:** Digalu {11057}; Kenya Robin {11057}.

100. Reaction to *Puccinia striiformis* Westend.

96.1. Designated genes for resistance to stripe rust

Yr18. Add note at end of section:
Forty-three Chinese land varieties predicted to have *Yr18* based on markers had high rust severities. Genetic analyses of four of these landraces (Sichuanyonggang 2, Baikemai, Youmai and Zhangsihuang) indicated the presence of an independent suppressor (11101}.

Yr26. **v:** Guinong 22 {11098}.

Yr46. **v:** Chapingo 48 {11070}. **c:** This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

Yr51. Revisions:
v2: AUS 27858 *Yr57* {10850}. **ma:** sun106 – 0.6 cM – *owm45F3R3* – 1.2 cM – *Yr51* – 2.5 cM – *sun104* – 1.8 cM – *Xgwm160-4A* {10850}.

Yr57. Correction:

ma: Replace present entry with: *sts3B15* – 4.5 cM – *BS00062676* – 2.3 cM – *Yr57* – *Xgwm389-3B* – 2.0 cM – *Xbarc75-3B* {10963}.

***Yr58*.** Correction:
Yr58 was previously located in chromosome 3BL. The location was revised to 3BS. The corrected listing for this gene becomes:

Yr58 {10964}.	3BS {10964}.	**bin:**	3BS3-0.87-1.00.
	v:	Sonora W195 AUS 19292 {10964}.	
	ma:	*1121669/3023704* – 3.9 cM – *Yr58* – 4.6 cM – *100016328/1233292* {10964}.	

Yr68 {11051}.	Adult plant resistance.	4BL {11051}.
	bin:	4BL1-0.86-1.00.
	i:	AGG91587WHEA1 = csAvYr4BL = Avocet S*5 / Undesignated International Nursery ex New Zealand Entry 03.25 {11051}.
	v:	Undesignated International Nursery ex New Zealand 03.25 {11051}.
	ma:	*IWB74301* – 0.5 cM – *Yr68/IWA4640* – 0.5 cM – *IWB28394* {11051}.

Yr69 {11052}.	*YrCH86* {11052}.		2AS {11052}.
	bin: 2AS5-0.78-1.00.	**v:**	CH7086 {11052}.
	ma:	*Xwmc25-2A* – 2.7 cM – *X2AS33* – 1.9 cM – *Yr69* – 3.1 cM – *Xmag3807-2A* {11052}.	
Linkage with *Yr17*: (F_2 seedling test) 30.0 cM {11052}.			

Yr70 {11055}.	Derived from *Ae. umbellulata*.		*YrUmb* {11055}.
	5DS {11055}.	**v:**	IL 393-4 {11055}, *T. durum* cv. WH890 / *Ae. umbellulata* Pau 3732 // CS Ph^{I} /3/ 2*WL711 {11055}.
		al:	*Ae. umbellulata* Pau 3732 {11055}.
	ma:	*Yr70* – 7.6 cM – *Xgwm190-5D* {11055}; A co-segregating 450 bp *Lr57-Yr40*-CAPS16 marker was present in IL 393-4, but not in many Australian wheat cultivars {11055}.	
Yr70 behaves as an allele of *Yr40* derived from *Ae. geniculata*. The low infection types are also different.			

Yr71 {11056}.	Adult plant resistance.		*YrSA3* {11056}.
	3DL {11056}.	**v:**	AGG91588WHEA, Sunco / Avocet S RIL4667.153.11.1 {11056}.
	v2:	Sunco *Yr18* {11056}.	
	ma:	*Yr71* – 1.6 cM – *IWB17207/IWB10438/IWB23615/IWB63653* – 0.5 cM – *IWB57983* – 0.9 cM – *IWB23518* – 2.4 cM – *Xgwm114b-3D* – 5.6 cM – *Sr24/Lr24* {11056}.	

Yr72 {11059}.	*YrAW4* {11059}.	2BL {11059}.	**bin:**	2BL-5-0.59-0.89.
	v:	AUS27507 11059}; AUS27894 {11059}.		
	ma:	*Xsun481-2BL* – 1.8 cM – *Yr72* – 1.2 cM – *IWB12294* – 1.5 cM – *Xsun482-2BL* – 1.5 cM – *IWB69000* {11059}.		

Yr73 {11062	Complementary gene involved in the *YrA* specificity.			
	3DL {11064,11062}.			
	v2:	Avocet R {11063}; Anza = WW15 {11062}. Banks R {11063}; Condor R {11063}; Egret R {11063}; Funo {11062}; Jupateco 73 {11062}; Lerma Rojo-64 {11062}.		
	ma:	Located and mapped by DArT-Seq markers {11062}.		

Yr74 {11062}.	Complementary gene involved in the *YrA* specificity.	
	5BL {11062}.	
	v2:	Avocet R {11063}; Anza = WW15 {11062}; Banks R {11063}; Condor R {11063}; Egret R {11063}; Funo {11062}; Jupateco 73 {11062}; Lerma Rojo-64 {11062}.
	ma:	Located and mapped by DArT-Seq markers {11062}.

The cross Avocet R/Teal used to map *Yr73 and Yr74* included a 5BL-7BL reciprocal translocation. Susceptible lines carrying the individual genes will be permanently accessioned after screening candidate lines for the Avocet R = Chinese Spring chromosome configuration. The translocated chromosomes are present in Teal and do not involve *Yr74.*

Yr75 {11065}.	Adult plant resistance.	*YrAxe* {11065}.		
	7AL {11065}.	**bin:**	7AL16-0.86-0.90.	
	v:	Axe / Nyabing-3 RIL#5 {11065}.	**v2:**	Nyabing-3 *Yr29* {11065}.
	ma:	*Xcfa2016-7A* – 1.0 cM – *Yr75* – 0.3 cM – *IWB36240* {11065}.		

Yr76 {11067}.	*YrTye* {186}.	3AS {11067}, 6D {186}.		
	bin:	3AS4-0.45–1.00 {11067}.	**i:**	AvS*4 / Tyee {11067}.
	v:	Tyee CItr 17773 {11067}; ARS-Amber {11067}; Cara {11067}; Chukar {11067}.		
	v2:	Hyak *Yr17* {11067}.		
	ma:	*Xbarc321-6D* – 6.2 cM – *Xbarc57-6D* – 4.3 cM – *Xwmc11-6D* – 2.6 cM – *Yr76* – 3.4 cM – *Xwmc532-6D* – 6.9 cM – *Xgwm369-6D* – 2.6 cM – *Xbarc12-6D* {11067}.		

100.2. Temporarily designated genes for resistance to stripe rust

YrC591. Add:
bin: 7BL-3-0.85-1.00. **ma:** *Xmag1714-7B* – 1.2 – *YrC591* – 0.4 cM – *Xbarc182-7B* {11099}.

YrHA {11100}.	1AL {11100}.	**v:**	H901414-121-5-5-9 {11100}.
	ma:	*Xwmc469-1A* 3.4 cM – *YrHA* – 4.6 cM – *Xgwm497-1A* {11100}.	

YrSD {11085}.	5BL {11085}.	
	i:	Taichung 29*6 / Strubes Dickkopf 11085}.
	v:	Strubes Dickkopf {11085}.
	ma:	*Xwmc640-5B* – 3.6 cM – *YrSD* – 2.4 cM – *Xbarc59-5B* – 3.0 cM – *Xwmc783-5B* {11085}.

The authors concluded that this gene was different from *Yr25*, which was located in chromosome 1D {158}.

YrSP. Add:
bin: 2BL-C-0.5. **ma:** *IWA638* – 0.6 cM – *YrSP* – 1.5 cM – *dp269-2* – 1.9 cM – *Xwmc332-2B* {11091}.

100.3. Stripe rust QTLs

At the end of section add:
A summary of published QTL locations is provided in {11089}; 49 chromosome regions on 20 of the 21 wheat chromosomes were proposed.

101. Reaction to *Puccinia triticina*

101.1. Genes for resistance

Lr3. Add:

	Lr3d {11054}.	**i:**	RL6062, Thatcher*6 / PI 268316 {11054}.	
		v:	PI 268316 {11054}.	

Lr11. Add:
LrBP2 {11074}. Add: ‘,2DS {11074}’. **v2:** Buck Poncho *Lr10* {11074}. **ma:** *Lr11* – 0.3 cM – *SCAR32/35* – 1.6 cM – *Xgwm614-2D* {11074}.

Lr13. Add:
ma: *Xbarc55-2B* – 1.1 cM *Xkwh37* – 4.9 cM – *Lr13/Ne2* – 5.8 cM – *Xgpw1109* – 3.7 cM – *Xbarc18-2B* {11068}.

Lr21. **v:** Add: Barlow {11093}; Faller {11093}; Prosper {11093}.

Lr28. **v:** Sunland {11069}. **ma:** *Xbarc343-4A* – 7.7 cM – *Lr28/Psr119/SCS421/mag3092* – 1.1 cM – *Xwmc219-4A* – 2.2 cM – *Xwmc219-4A* {11069}.

Lr39. **v:** Add: Armour {11086}; Bullet {11086}; PostRock {11093}; TAM 112 {11086}; Winterhawk {11086}.

Lr48. Add:
ma: *Xgwm429b-2b* – 4.2 cM – *Sun563/Sun497* – 0.6 cM – *IWB31002/IWB39834/IWB34324/WB72894/Lr48* – 0.3 cM – *IWB70147* – 2.0 cM – *Xbarc67-2B* {11112}.
Based on haplotype analysis *Lr48* was postulated in 13 Australian Condor relatives {11112}.

Lr67. Add:
v: Chapingo 48 {11070}. **c:** This multiple disease resistance locus was identified as a hexose transporter most similar to the STP13 family and containing 12 predicted transmembrane helices {11070}.

The following is a revised entry for *Lr74*.

Lr74 {11031}.	Adult plant resistance.	3BS {11031}.	**bin:**	3BS8-0.78-0.87.
	v1:	AGG91583WHEA = BT-Schomburgk Selection {11031}; Spark {11031}.		
	ma:	*Xcfb5006-3B* – 1.9 cM – *Lr74* – 2.2 cM – *BS00009992* – 2.7 cM – *Xgwm533-3B* {11031}.		

Lr75 {11053}.	Adult plant resistance.	*QlrP.sfr-1BS* {10066}.	
	1BS {10066,11053}.	**v1:**	ArinaLr75, Arina*2 // Forno / Arina#F7NIL85 {11053}, IPKXXXXX, C14.20 {11053}.
		v2:	Forno *Lr34* {10066; 11053}.
		ma:	*Lr75* – 2.74 cM – *Xgwm18-1B* {11053}.

Lr76 {11055}.	Derived from *Ae. umbellulata*.	*LrUmb* {11055}.	
	5DS {11055}.	**v:**	IL 393-4 {11055}, *T. durum* cv. WH890 / *Ae. umbellulata* Pau 3732 // CS Ph^I /3/ 2*WL711, C14.21 {11055}.
	al:	*Ae. umbellulata* Pau 3732 {11055}.	
	ma:	*Lr76* – 7.6 cM – *Xgwm190-5D* {11055}.	
Lr76 behaves as an allele of *Lr57* derived from *Ae. geniculata*. The low infection types are also different. A co-segregating 450 bp *Lr57-Yr40*-CAPS16 marker was present in IL 393-4, but not in many Australian wheat cultivars {11055}.			

***LrBi16*.** Add:

bin: 7BL-10. **ma:** *Xcfa2257-7B* – 2.8 cM – *LrBi16* – 2.5 cM – *Xgwm344-7B* {11082}. A closer AFLP marker could not be converted to a STS/SCAR marker {11082}.

Allelic with *Lr14c*, but showed different reaction patterns compared to lines with *Lr14c* and *LrFun* {11082}.

Add after *LrZH84*:

Lr6Ai#2 {11079}.	6Ai#2 {11079}.	
	v:	Tulaikoskaya 5 {11079}; Tulaikoskaya 10 {11079}; Tulaikoskaya 100 {11079}

116. Reaction to Wheat Yellow Mosaic Virus

QTL:

RIL population: Xifeng (R) / Zhen 9523 (S): Three QTLs, *Qym.njuy5A.1* (R^2 = 0.26-0.54), *Ym.njau-3B.1* (R^2 = 0.03- 0.01) and *QYm.njau-7B.1* (R^2 = 0.03-0.05 in some trials). The chromosome 5A gene was closely associated with *Xwmc415.1*, *CINAU152* and *CINAU153* and was phenotyped as a single Mendelian gene {11073}.

References

Updates	
10704.	Bansal UK, Muhammad S, Forrest KL, Hayden MJ and Bariana HS 2015 Mapping of a new stem rust resistance gene *Sr49* in chromosome5B of wheat. Theoretical and Applied Genetics 128: 2113-2119.
10850.	Randhawa M, Bansal U, Valarik M, Klocova B, Dolezel J and Bariana HS 2014 Molecular mapping of stripe rust resistance gene *Sr51* in chromosome 4AL of

	wheat. Theoretical and Applied Genetics 127317-324.
10936.	Olsen EL, Rouse MN, Pumphrey MO, Bowden RL, Gill BG and Poland J 2013 Introgression of stem rust resistance genes *SrTa10187* and *SrTA10171* from *Aegilops tauschii* to wheat. Theoretical and Applied Genetics 126: 2477-2484.
10963.	Randhawa MS, Bariana HS, Mago R and Bansal UK 2015 Mapping of a new stripe rust resistance locus*Yr57* on chromosome 3BS of wheat. Molecular breeding 35:65, 8pp.
11010.	Rouse MN, Nirmala J, Jin Y, Chao S, Fetch TG, Pretorius ZA and Hiebert CW 2014 Characterization of *Sr9h*, a wheat stem rust resistance allele effective to Ug99. Theoretical and Applied Genetics 127: 1681-1688.
11023.	Lu Y, Wang MN, See D, Chen XM, Chao SM and Jing JX 2014 Mapping of *Yr62* and small-effect QTL for high-temperature adult-plant resistance to stripe rust in spring wheat PI 192252. Theoretical and Applied Genetics 127: 1449-1459.
11026.	Zhan HX, Li GR, Zhang XJ, Li X, Guo HJ, Gong WP, Jia JQ, Qiao LY, Ren YK, Yang ZJ and Chang ZJ 2014 Chromosomal location and comparative genomics analysis of powdery mildew resistance gene *Pm51* in a putative wheat-*Thinopyrum ponticum* introgression line. PLoS One 9(11): e113455.
11031.	Revised reference: Temesgen B, Chhetri M et al. 2015 Personal communication.
11046.	Update: 2015. Phytopathology 105: 495-499.

New	
11048.	Cainong JC, Bockus WW, Feng YG, Chen PD, Qi LL, Sehgal SK, Danilova TV, Koo D-H, Friebe B and Gill BS 2015 Chromosome engineering, mapping, and transferring of resistance to Fusarium head blight disease from *Elymus tsukushiensis* into wheat. Theoretical and Applied Genetics 128: 1019-1027.
11049.	Ma PT, Xu HX, Xu YF, Li LH, Qie YM, Luo QL, Zhang XT, Li XQ, Zhou YL and An DG 2015 Molecular mapping of a new powdery mildew resistance gene *Pm2b* in Chinese breeding line KM2939. Theoretical and Applied Genetics 128: 613-622.
11050.	Hao YF, Parks R, Cowger C, Chen ZB, Wang YY, Bland D, Murphy, Guedira M, Brown-Guedira and Johnson J 2015 Molecular characterization of a new powdery mildew resistance gene *Pm54* in soft red winter wheat. Theoretical and Applied Genetics 128: 465-476.
11051.	Spielmeyer W 2014 Personal communication.
11052.	Hou et al. 2014. Molecular mapping of stripe rust resistance gene *YrCH86* in wheat chromosome 2AS. Draft manuscript.
11053.	Singla J 2014 Personal communication.
11054.	Kolmer J 2014 Personal communication
11055.	Bansal M, Kaur S, Dhaliwal HS, Baines NS, Bariana HS, Chhuneja P and Bansal UK 2016 Mapping of *Aegilops umbellulata* – derived leaf rust and stripe rust loci in wheat. Plant Pathology DOI: 10.1111/ppa.12549.
11056.	Bariana HS and Bansal U 2014 Unpublished manuscript.
11057.	Singh RP, Hodson DP, Jin Y, Lagudah ES, Ayliffe MA, Bhavani S, Rouse MN, Pretorius ZA, Szabo L, Huerta-Espino J, Basnet BJ, Lan CX and Hovmoller MS 2015 Emergence and spread of new races of wheat stem rust fungus: Continued threat to food security and prospects for genetic control. Phytopathology 105: 872-884.
11058.	Kong LR, Cambron SE and Ohm HW 2008 Hessian fly resistance genes *H16* and *H17* are mapped to a resistance gene cluster in the distal region of chromosome 1AS

	in wheat. Molecular Breeding 21: 183-194.
11059.	Chhetri M, et al. 2015 Draft manuscript.
11060.	Guo J, Zhang ZL, Hou YL, Cai JN, Shen XR, Zhou TT, Xu HH, Ohm HW, Wang HW, Li AF, Han FP, Wang HG and Kong LR 2015 Development and characterization of wheat lines carrying Fusarium head blight resistance gene *FhbLoP* derived from *Thinopyrum ponticum* and its pyramiding with *Fhb1*. Manuscript.
11061.	Xu HX, Yi YJ, Ma PT, Qie YM, Fu XY, Xu YG, Zhang XT and An DG 2015 Molecular tagging of a new broad-spectrum powdery mildew resistance allele *Pm2* in Chinese wheat landrace Niaomai. Theoretical and Applied Genetics 128: 2077-2084.
11062.	Dracatos PM, Zhang P, Park RF, McIntosh RA and Wellings CW 2016 Complementary resistance genes in wheat selection ‘Avocet R’ confer resistance to stripe rust. Theoretical and Applied Genetics 129: 65-76
11063.	Wellings CR, McIntosh RA, Hussain M 1988 A new source of resistance to *Puccinia striiformis* f. sp. *tritici* in spring wheats (*Triticum aestivum*). Plant Breeding 100: 88-96.
11064.	Bariana HS 1991 Genetic studies on stripe rust resistance in wheat. PhD Thesis, University of Sydney.
11065.	Bansal U 2015 Personal communication.
11066.	Rahmatov M et al. 2015. A new Robertsonian translocation transfers stem rust resistance gene *Sr59* to wheat. Personal communication.
11067.	Xiang C, Feng JY, Wang MN, Chen XM, See D, Wan AM and Wang T 2016 Molecular mapping of *Yr76* for resistance to stripe rust in winter club wheat cultivar Tyee. Manuscript in preparation.
11068.	Zhang P, Hiebert CW, McIntosh RA, McCallum BD, Thomas JB, Hoxha S, Singh D and Bansal U 2016 The relationship of leaf rust resistance gene *Lr13* and hybrid necrosis gene *Ne2m* on wheat chromosome 2BS. Theoretical and Applied Genetics 129: 485-493.
11069.	Sohail Y, Bansal U, Bariana H, Chhuneja P, Mumtaz A, Atiq R and Trethowan R 2014 Identification of a co-dominant eSTS marker linked with leaf rust resistance gene *Lr28* in wheat (*Triticum aestivum* L.). Australian Journal of Crop Science 8: 1210-1215.
11070.	Moore JW, Herrera-Foessel S, Lan CX, Schnippenkoetter W, Ayliffe M, Guerta-Espino J, Lillemo M, Viccars L, Milne R, Periyannan S, Kong XY, Spielmeyer W, Talbot M, Bariana H, Patrick JW, Dodds P, Singh R and Lagudah E 2015 A recently evolved hexose transporter variant confers resistance to multiple pathogens in wheat. Nature Genetics 47: 1494-1498.
11071.	Li X, Shin SH, Heinen S, Dill-Macky R, Berthiller F, Nersesian N, Clemente T, McCormack S and Muehlbauer G 2015 Transgenic wheat expressing a barley UDP-glucosyltransferase detoxifies deoxynivalenol and provides high levels of resistance to *Fusarium graminareaum*. Molecular Plant-Microbe Interactions 28: 1237-1246.
11072.	Guo XR, Wang YY, Meng LZ, Liu HW, Yang L, Zhou Y and Zhang HJ 2015 Distribution of the *Vrn-D1b* allele associated with facultative growth habit in Chinese wheat accessions. Euphytica 206: 1-10.
11073.	Zhu XB, Wang HY, Guo J, Wu ZZ, Cao AH, Bie TD, Nie MJ, You FM, Cheng ZB, Xiao J, Liu YY, Cheng SH, Chen PD and Wang XE 2012 Mapping and validation of quantitative trait loci associated with wheat yellow mosaic bymovirus resistance

	in bread wheat. Theoretical and Applied Genetics 124: 177-188.
11074.	Darino MA, Dieguez MJ, Singh D, Ingala LR, Pergolesi MF, Park RF, McIntosh RA and Sacco F 2015 Detection and location of *Lr11* and other leaf rust resistance genes in the durably resistant wheat cultivar Buck Poncho. Euphytica 206: 135-147.
11075.	Lu YQ, Wu XY, Yao MM, Zhang JP, Liu WH, Yang XM, Li XQ, Du JA, Gao An and Li LH 2015 Genetic mapping of a putative *Agropyron cristatum*-derived powdery mildew resistance gene by a combination of bulked segregant analysis and single nucleotide polymorphism array. Molecular Breeding 35: 96, 13pp.
11076.	Niu Z, Klindworth DL, Yu G, Friessen TL, Chao S, Jin Y, Cai X, Ohm J-B, Rasmussen JB and Xu SS 2014 Development and characterization of wheat lines carrying stem rust resistance gene *Sr43* derived from *Thinopryrum ponticum*. Theoretical and Applied Genetics 127: 969-980.
11077.	Chen SL, Gao RH, Wang HY, Wen MX, Xiao J, Bian NF, Zhang RQ, Hu WH, Cheng SH, Die TD and Wang XE 2015 Characterization of a novel reduced height gene (*Rht23*) regulating panicle morphology and plant architecture in bread wheat. Euphytica 203: 583-594.
11078.	Fazel-Najafabadi M, Peng JH, Peairs FB, Simkova H, Kilian A and Lapitan NLV 2015 Genetic mapping of resistance to *Diuaphis noxia* (Kurdjomov) biotype 2 in wheat (*Triticum aestivum* L.) accession CI2401. Euphytica 303: 607-614.
11079.	Salina EA, Adonina IG, Badaeva ED, Kroupin PU, Stasyuk AI, Leonova IN, Shishkina AA, Divashuk MG, Starikova EV, Khuat TM, Syukov VV and Karlov GI 2015 A *Thinopyrun intermedium* chromosome in bread wheat cultivars as a source of genes conferring resistance to fungal diseases. Euphytica 204: 91-101.
11080.	Li WL and Gill BS 2006 Multiple genetic pathways for seed shattering in the grasses. Functional and Integrative Genomics 6: 300-309.
11081.	Jayatilake DV, Tucker EJ, Brueggemann J, Lewis J, Garcia M, Dreisigacker S, Hayden MJ, Chalmers K and Mather DE 2015 Genetic mapping of the *Cre8* locus for resistance against cereal cyst nematode (*Heterodera avenae* Woll.) in wheat. Molecular Breeding 35: 66, 12pp.
11082	Zhang PP, Zhou HX, Lan CX, Li ZF and Liu DQ 2015 An AFLP marker linked to the leaf rust resistance gene *LrBi16* and test of allelism with *Lr14ai* on chromosome arm 7BL. The Crop Journal 3: 152-156.
11083.	Ahn VL, Anh NT, Tagle AG, Vy TTP, Inoue Y, Takumi S, Chuma I and Tosa Y 2015 *Rmg8*, a new gene for resistance to *Triticum* isolates of *Pyricularia oryzae* in hexaploid wheat. Phytopathology 105: 1568-1572.
11084.	Wang YJ, Wang CY, Qual W, Jia XJ, Fu Y, Zhang H, Liu XL and Chen CH 2016 Identification and mapping of *PmSE5785*, a new recessive powdery mildew resistance locus in synthetic hexaploid wheat. Euphytica 207: 619-626.
11085.	Feng J, Xu JJ, Lin RM, He YQ and Xu SC 2013 Genetic analysis and location of a gene for resistance to stripe rust in wheat international differential host Strubes Dickkopf. Journal of Genetics 92: 267-192.
11086.	Kolmer JA 2015 First report of a wheat leaf rust (*Puccinia triticina*) phenotype with high virulence to durum wheat in the Great Plains region of the United States. Plant Disease 99: 156-157.
11087.	Gao LL, Kielsmeier-Cook J, Bagjain P, Zhang XF, Chao SM, Rouse MN and Anderson JA 2015 Development of genotyping by sequencing (GBS)- and array-derived SNP markers for stem rust resistance gene *Sr42*. Molecular Breeding 35: 207, 14pp.
11088.	Buerstmeyer M, Alimari A, Steiner B and Buerstmeyer H 2013 Genetic mapping

	of QTL for resistance to Fusarium head blight (type 2 resistance) in a *Triticum dicoccoides* × *Triticum durum* backcross derivative. Theoretical and Applied Genetics 126: 2825-2834.
11089.	Roswarne GM, Herrera-Foessel SA, Singh RP, Huerta-Espino J, Lan CX and He ZH 2013 Quantitative trait loci of stripe rust resistance in wheat. Theoretical and Applied Genetics 126: 2427-2449.
11090.	Adamski NM, Bush MS, Simmonds J, Turner AS, Mugford SG, Jones A, Findlay K, Pedentchouk N, von Wettstein-Knowles and Uauy C 2013 The inhibitor of wax 1 locus (*Iw1*) prevents formation of b- and OH-b-diketones in wheat cuticular waxes and maps to a sub-cm interval on chromosome arm 2BS. The Plant Journal 74: 989-1002.
11091.	Feng JY, Wang MN, Chen XM, Dee DR, Zheng YL, Chao SM and Wan AM 2015 Molecular mapping of *YrSp* and its relationship with other genes for stripe rust resistance in wheat chromosome 2BL. Phytopathology 105: 1206-1213.
11092.	Basnet BR, Singh S, Lopez-Vera E, Huerta-Espino J, Bhavani S, Jin Y, Rouse MN and Singh RP 2015 Molecular mapping and validation of *SrND643* A new wheat gene for resistance to the stem rust pathogen Ug99 race group. Phytopathology 105: 470-476.
11093.	Kolmer JA and Hughes ME 2015 Physiologic specialization of *Puccinia triticina* on wheat in the United States in 2013. Plant Disease 99: 1261-1267.
11094.	Wu HB, Qin JX, Han J, Zhao XJ, Ouyang SH, Liang Y, Zhang D, Wang ZZ, Wu QH, Xie JZ, Cui Y, Peng SH, Sun QX and Liu ZY 2013 Comparative high resolution mapping if the wax inhibitors *Iw1* and *Iw2* in hexaploid wheat. PLoS One 8(12): e84691.
11095.	Ouyang SH, Zhang D, Han J, Zhao XJ, Cui Y, Song W, Huo NX, Liang Y, Xie JZ, Wang ZZ, Wu QH, Chen YX, Lu P, Zhang DY, Wang LL, Yang TM, Keeble-Gagnere G, Appels R, Dolezel R, Ling HQ, Luo MC, Gu YQ, Sun QX and Liu ZY 2014 Fine physical and genetic mapping of powdery mildew resistance gene *MlIW172* originating from wild emmer (*Triticum dicoccoides*). PLOS One 9(6): e100160.
11096.	Yang ZY, Zheng JC, Liu CY, Wang YS, Condon AG, Chen YF and Hu YG 2015 Effects of the GA-responsive dwarfing gene *Rht18* from tetraploid wheat on agronomic traits of common wheat. Field Crops Research 18: 92-101.
11097.	Ayala-Navarrete LI, Mechanicos AA, Gibson JM, Singh D, Bariana HS, Fletcher J, Shorter S and Larkin PJ 2013 The *Pontin* series of recombinant alien translocations in bread wheat: single translocations integrating combinations of *Bdv2*, *Lr19* and *Sr25* disease-resistance genes from *Thinopyrum intermedium* and *Th. ponticum*. Theoretical and Applied Genetics 126: 2467-2475.
11098.	Li QA, Ma DF, Fan Y, Shen XX, Jing JX, Wang BT and Kang ZS 2016 Genetic analysis and molecular mapping of a stripe rust resistance gene in Chinese wheat differential Guinong 22. Journal of Phytopathology, doi: 10.111/jph.12473
11099.	Xu HX, Zhang J, Zhang P, Qie YM, Niu YC, Li HJ, Ma PT, Xu YF and An DG. 2014 Development and validation of molecular markers closely linked to the wheat stripe rust resistance gene *YrC591* for marker-assisted selection. Euphytica 198: 317-323.
11100.	Ma DF, Zhou XL, Hou L, Bai YB, Li Qiang, Wang HG, Yang MS and Jing JX 2013 Genetic analysis and molecular mapping of a stripe rust resistance gene derived from *Psathynrostachys huashanica* Keng in wheat line H9014-121-5-5-9. Molecular Breeding 32: 365-372.
11101.	Wu L, Xia XC, Rosewarne GM, Zhu HH, Li SZ and Zhang ZY 2015 Stripe rust

	resistance gene *Yr18* and its suppressor gene in Chinese wheat landraces. Plant Breeding 134: 634-640.
11102.	Wu Lf, Cui L, Li HL, Sun L, Gao X, Qiu D, Sun YL, Wang XM, Murray TD and Li HJ 2015 Characterization of resistance to cereal cyst nematode in the soft white winter wheat ‘Madsen’. Plant Disease 100: 679-685.
11103	Rouse MN, Talbert LE, Singh D, Sherman JD 2014 Complementary epistasis involving *Sr12* explains adult plant resistance to stem rust in Thatcher wheat *Triticum aestivum* L.). Theoretical and Applied Genetics 127: 1549-1559.
11104.	Hiebert CW, Kolmer JA, McCartney CA, Briggs J, Fetch T, Bariana H, Choulet F, Rouse MN, Spielmeyer W 2016 Major gene for field stem rust resistance co-locates with resistance gene *Sr12* in ‘Thatcher’ wheat. PLoS One 11(6): e0157029.
11105.	McIntosh RA, Park RF and Wellings CR 19905 Wheat Rusts: An Atlas of Resistance Genes. CSIRO Publications, East Melbourne, Australia.
11106	Igrejas G, Branlard G, Carnide V, Gateau I and Guedes-Pinto H 1997 Storage protein diversity within the old Portuguese bread wheat Barbela population. Journal of Genetics and Breeding 51: 167-173.
11107	Ribeiro M, Bancel E, Faye A, Dardevet M, Ravel C, Branlard G and Igrejas G 2013 Proteogenomic characterization of novel x-type high molecular weight glutenin subunit 1Ax1.1. International Journal of Molecular Sciences 14: 5650-5667.
11108.	Zhang RQ et al. 2015 Draft manuscript.
11109.	Zhang RQ, Cao YP, Wang XE, Feng YG and Chen PD (2010) Development and characterization of a *Triticum aestivum–D. villosum* T5VS.5DL translocation line with soft grain texture. Journal of Cereal Science 51: 220-225.
11110.	Chen SS, Rouse MN, Zhang WJ, Jin Y, Akhenov E, Wei YM and Dubcovsky J 2015 Fine mapping and characterization of *Sr21*, a temperature sensitive diploid wheat resistance gene effective against the *Puccinia graminis* f. sp. *tritici* race group. Theoretical and Applied Genetics 128: 645-656.
11111.	Briggs J, Chen SS, Zheng WJ, Nelson S, Dubcovsky J and Rouse MN 2015 Mapping of *SrTm4*, a recessive stem rust resistance gene from diploid wheat effective to UG99. Phytopathology 105: 1347-1354.
11112.	Nsabiyera V, Qureshi N, Bariana HS, Wong D, Forrest KL, Hayden MJ and Bansal UK 2016 Molecular markers for adult plant leaf rust resistance gene *Lr48* in wheat. Molecular Breeding 36: 65, 9pp.
11114.	Amigai Y, Kubayama T and Watanabe N 2016 Microsatellite mapping of the gene conferring compact spike in Japanese “Gumbai” landraces of common wheat *Triticum* aestivum L.). Euphytica 2019: 547-554.
11115.	LL, Wang FM, Liu T, Dong ZY, Li AL, Jing RL, Mao L, Li YW, Liu X, Zhang KP and Wang DW 2014 Natural variation of *TaGASR7-A1* affects grain length in common wheat under multiple cultivation conditions. Molecular Breeding 34: 937-947. DOI 10.1007/s11032-014-0087-2.
11116.	Zhang YJ, Liu JD, Xia XC and Zhonghu He 2014 *TaGS-D1*, an ortholog of rice *OsGS3*, is associated with grain weight and grain length in common wheat. Molecular Breeding 34 1097. DOI 10.1007/s11032-014-0102-7.
11117.	Chang JZ, Zhang JN, Mao XG, Li A, Jia JZ and Jing RL 2013 Polymorphism of *TaSAP1-A1* and its association with agronomic traits in wheat. Planta 237: 1495-1508.
11118.	Zhang XL, Shen XR, Hao YF, Cai JJ, Ohm HW and Kong LR 2011 A genetic map of *Lophopyrum ponticum* chromosome 7E, harbouring resistance genes to Fusarium head blight and leaf rust. Theoretical and Applied Genetics 122: 263-270.

11119.	Zhang YJ, Miao XL, Xia XC and He ZH 2014 Cloning of seed dormancy genes (*TaSdr*) associated with tolerance to pre-harvest sprouting in common wheat and development of a functional marker. Theoretical and Applied Genetics 127: 855–866.