

**Background :** Wheat leaf rust and stripe rust cause significant production losses in many wheat producing regions worldwide. GWAS (Genome Wide Association Mapping Study) and QTL analysis are two methods for gene discovery of leaf rust (*Lr*) and stripe rust (*Yr*) resistance. The objective of the study was to identify effective gene(s) for resistance to leaf rust and stripe rust, and identify SNP markers significantly associated with resistance loci for use in marker assisted selection (MAS).

## Materials and Methods

**Plant materials** The panel included 207 bread wheat accessions from different wheat growing regions of China, and 61 accessions from 10 foreign countries.

**Phenotyping** Eight *Pt* pathotypes were used for leaf rust evaluation in the greenhouse. Leaf rust was evaluated in the field at Baoding and Zhoukou in the 2014/2015, 2015/2016, and 2016/2017 cropping seasons and stripe rust at Chengdu in 2015/2016, 2016/2017, and 2017/2018.

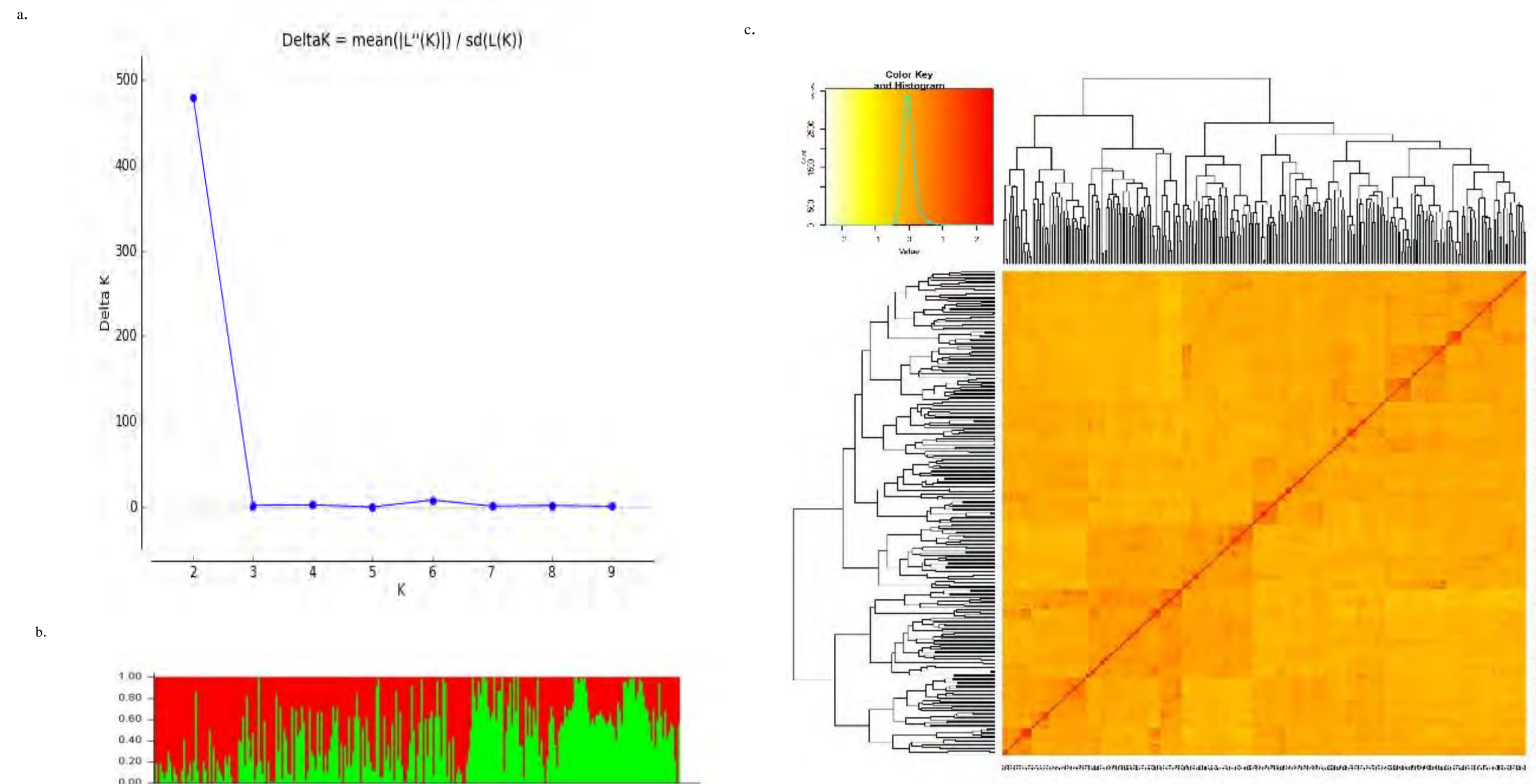
**Genotyping and filtering** Wheat 90K Illumina iSelect SNP array were used for genotyping. A total of 12,931 markers after filtering were used for GWAS.

**Genome wide association mapping** using mixed linear model (MLM).

**QTL mapping** for leaf rust using Zhou 8425B/Chinese Spring RIL population and Fundulea 900/ Thatcher F<sub>2:3</sub> population.

## Results

### 1. Population structure and Kinship



**Fig. 1** Population structure and kinship among 268 wheat accessions based on unlinked SNP markers. (a) Plot of delta K against putative K ranging from 1 to 10; (b) stacked bar plots of ancestry relationship of accessions; (c) Heat map of kinship matrix using the IBS method

### 2. Genome wide association mapping

#### Leaf rust response at the seedling stage

Twenty-two resistance loci were identified with the eight *Pt* pathotypes including known leaf rust resistance gene *Lr1*, *Lr26*, *Lr3ka*, and *LrZH22*.

#### Leaf rust response in the field

Seven loci on chromosomes 1BL, 2AL.1, 2BS, 3BS, 4AL, 6BL, and 7BS were detected in at least two environments as well as BLUPs.

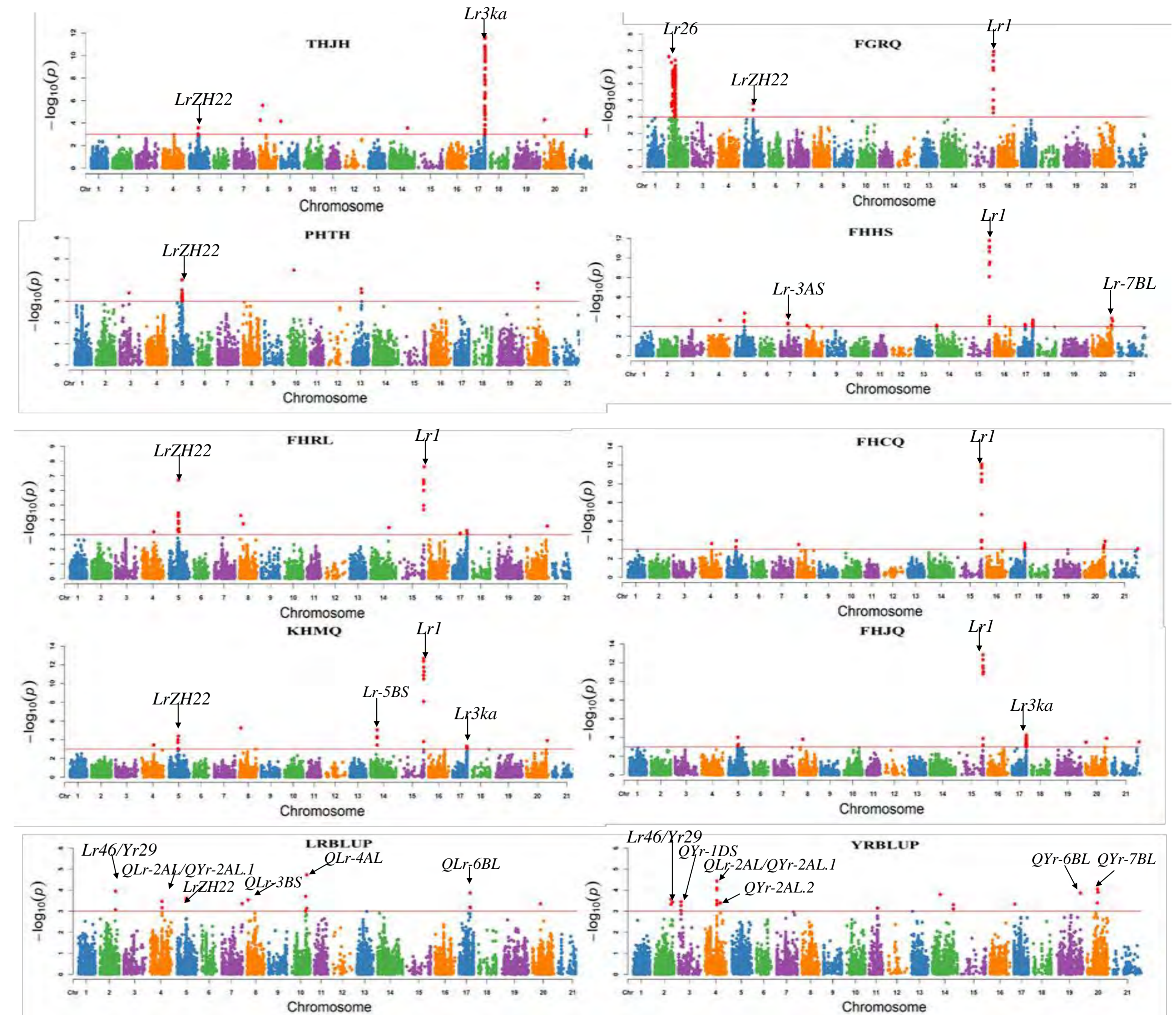
#### Stripe rust in the field

Six loci, *QYr-7BL.1*, *Lr46/Yr29*, *QYr-1DS*, *QYr-2AL.1*, *QYr-2AL.2*, and *QYr-6BS*, were stable identified in at least two environments as well as BLUPs.

#### Potentially pleiotropic loci

*Lr46/Yr29*, *QYr-2AL.1/QYr-2AL.1*, *QYr-2AL.2/QYr-2AL.2*, and *QYr-5BL/QYr-5BL.1*, indicated potentially pleiotropic situations.

*Lr46/Yr29* and *QYr-2AL.1/QYr-2AL.1* (new) showed stable effects on response to both rusts.



**Fig. 2** Manhattan plots for rust resistance

### 3. QTL mapping

**Table 1** QTL for MDS to leaf rust by ICIM in the RIL population from Zhou 8425B/Chinese Spring

QTL	Environment	Pos	Marker interval	LOD	PVE	Add
<i>QYr.hebau-2AL</i>	2013BD	193	Excalibur_c96_670 - BS00057060_51	3	4.8	6.1
	2015BD	191	wmc181 - Excalibur_c96_670	2.5	4.5	5.5
<i>QYr.hebau-2BS (LrZH22)</i>	2012BD	89	JD_c767_567 - BS00102480_51	5.2	7.5	-4.9
	2013BD	90	w SNP_Ex_c45094_50985067 - Ra_c5609_231	5.6	8	-8.1
	2013ZK	89	JD_c767_567 - BS00102480_51	7.8	10.6	-5.8
	2014BD	89	JD_c767_567 - BS00102480_51	8.3	10	-7.7
2014ZK	89	JD_c767_567 - BS00102480_51	5.9	9.4	-7.2	
<i>QYr.hebau-3A</i>	2014BD	64	w SNP_Ex_c1660_3159173 - Tdurum_contig5096_193	3	2.9	-4.1
<i>QYr.hebau-3BS</i>	2012BD	43	BobWhite_c9711_71 - Excalibur_c6330_1158	2.8	3.5	-3.3
	2014BD	73	BobWhite_c15697_675 - Ra_c1082_1100	3.4	3.4	4.4
<i>QYr.hebau-4AL</i>	2014ZK	78	BS00022839_51 - Excalibur_c2827_580	2.9	7.5	6.6
	2013BD	69	gwm149 - BS00109813_51	3.9	5.5	6.7
<i>QYr.hebau-4BS</i>	2013ZK	71	Ra_c106922_296 - Excalibur_c37565_709	6	7.9	5
	2014BD	69	gwm149 - BS00109813_51	8.4	8.8	7.1
	2014ZK	68	w SNP_Ex_c40815_47789152 - wms375	5.9	9	6.9
	2015BD	67	BS00022181_51 - BS00041093_51	17.1	24.4	12.4
	2013ZK	193	w SNP_Ex_c3175_5864335 - BobWhite_c16916_658	4.4	5.4	-4.1
<i>QYr.hebau-7DS</i>	2012BD	6	Kukri_c92151_216 - CSLV34	9.9	17.8	7.5
	2013BD	7	Kukri_c92151_216 - CSLV34	10.8	17	11.6
	2013ZK	9	Kukri_c92151_216 - CSLV34	8.9	12.4	6.3
	2014BD	8	Kukri_c92151_216 - CSLV34	11	12.7	8.7
	2014ZK	8	Kukri_c92151_216 - CSLV34	6.6	11.2	7.9
2015BD	9	Kukri_c92151_216 - CSLV34	12.4	20.9	11.6	

**Table 2** QTL for MDS to leaf rust in 188 F<sub>2:3</sub> lines from Fundulea 900/Thatcher

Environment	QTL	Marker interval	LOD	AE	DE	R <sup>2</sup>
2011	<i>QYr.hebau-7DS</i>	Xgwm295-csLV34	48.5	-36.5	-36.5	75.2
2012	<i>QYr.hebau-1BL(Lr46)</i>	csLv46G22-Xwmc728	5.6	-9.0	-5.1	5.5
	<i>QYr.hebau-7DS</i>	Xgwm295-csLV34	41.5	-27.9	-6.7	61.4
	<i>QYr.hebau-2DS</i>	Xgwm261-Xgwm484	3.4	5.8	-4.9	3.5
2013	<i>QYr.hebau-1BL(Lr46)</i>	csLv46G22-Xwmc728	6.4	-10.6	-11.0	11.5
	<i>QYr.hebau-7DS</i>	Xgwm295-csLV34	17.7	-18.9	-5.1	33.5

QTL in red font is same as the QTL identified by GWAS

## Conclusion

Both GWAS and QTL mapping identified *LrZH22*, *Lr46* and *QYr-3BS* at APR stage. GWAS had identified some known and potentially new genes/QTLs for rust resistance. *QYr-2AL.1/QYr-2AL.1* was a potentially pleiotropic new QTL with stable resistance. *LrZH22* showed resistance at both seedling and APR stage, and *LrZH22* has been cloned in our lab (unpublished data).

## Reference

- Zhang et al. *Frontiers in Plant Science*, 2017, 8: 793.  
Zhang et al. *Plant Breeding*, 2017, 136:1-7.