



QTL mapping for yield components in adapted wheat cultivars TAM 113 and Gallagher

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INTRODUCTION

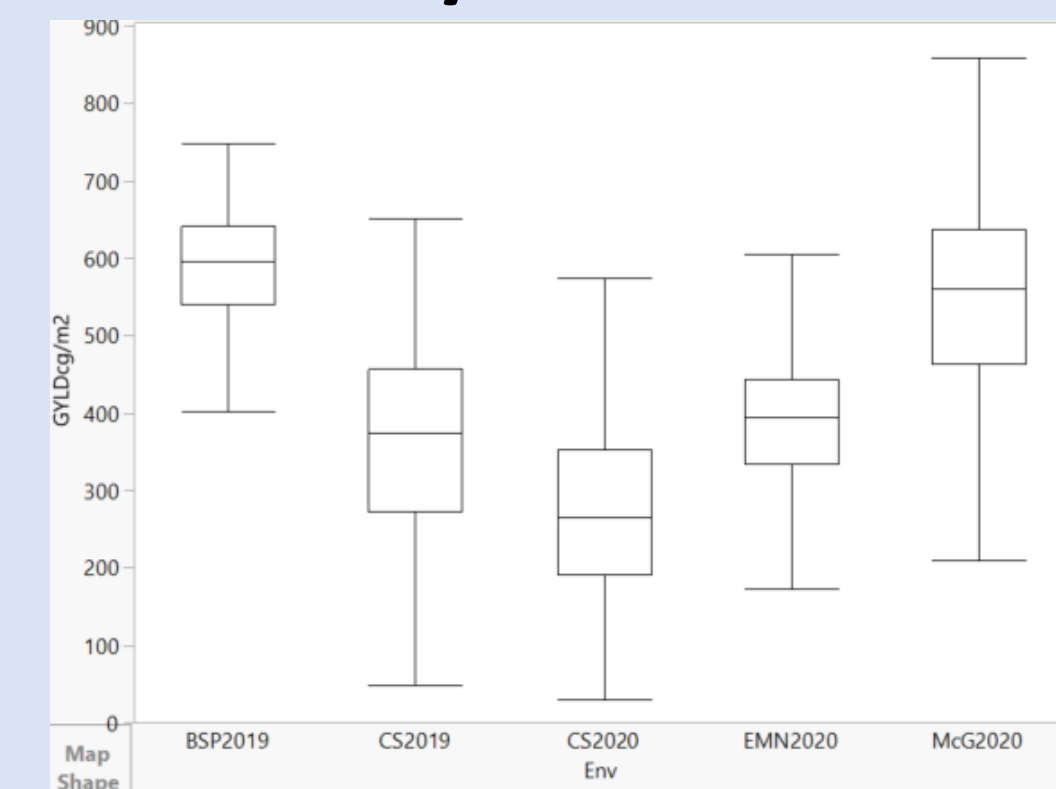
- Wheat (*Triticum aestivum* L.) is known as one of the most stable food crops for human consumption, animal feeding and industrial raw material. With the increasing of the world population, the demand for wheat production increase parallelly (Alexandratos and Bruinsma, 2012).
- Increasing grain yield is closely linked with some traits; plant height (PH), thousand kernel weight (TKW), grain number per spike, total biomass (BM), number of tillers, grain weight per spike.
- Quantitative trait loci (QTL) mapping identifies the genomic regions that linked with quantitative trait and it can also help us to understand genomic structure and how many genes importantly contribute the trait.
- Understanding the genetic structure of yield and yield components in dryland and irrigated conditions could help to develop better germplasm or cultivars.

OBJECTIVES

- Detect the quantitative trait loci (QTL) using Recombinant Inbred Line (RIL) population
- Identify the SNPs linked to yield component QTL and for Marker Assisted Breeding (MAB)

MATERIALS AND METHODS

- A total of 191 RIL from 'TAM 113'/'Gallagher' were grown based on alpha lattice with two replication in College Station, McGregor and Amarillo (EMN and BSP), TX during the 2018/19 and 2019/20.



- Agronomical data were collected on plant height (PH), heading date, spike per meter (SPM), biomass, thousand kernel weight and grain yield (GYLD) were collected in three environment.
- 25 Linkage groups were created using JoinMap 4.0 (Van Ooijen, 2006) and Inclusive composite interval mapping (ICIM) was performed using IciMapping v4.2.53 (Meng et al. 2015)
- A set of 8261 single nucleotide polymorphisms (SNPs) were used to construct a high-density genetic map and QTL analyses.

RESULTS

Figure 1: Whole genome QTL scan for grain yield across all environment

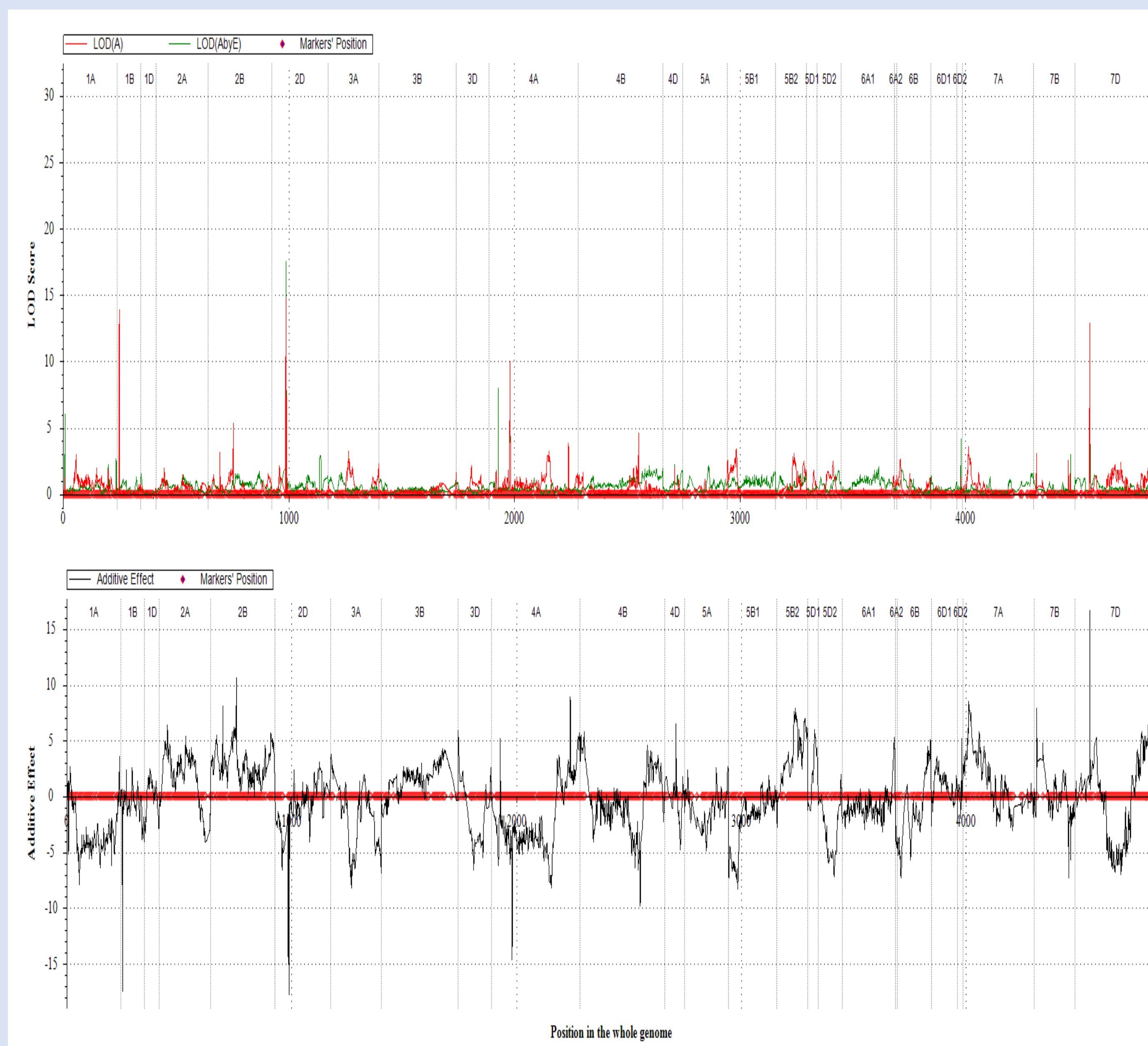


Table 1. Detected QTL for grain yield, HD, PH and SPM

Left Flanking Marker	LOD(A)	LOD(AbyE)	PVE(A)	PVE(AbyE)	Add	trait
chr1A_565388907	5.6	1.7	1.1	0.1	0.5	HD
chr2B_57657606	3.9	3.4	1.1	1.2	-0.5	HD
chr2B_63428577	1.9	8.3	0.5	0.5	-0.4	HD
chr2D_32901354	94	36.3	50.4	6.9	3.5	HD
chr6B_616579	12.3	35.5	3.8	21.9	-1	HD
chr7D_63208599	6.2	4.9	1.8	0.2	-0.7	HD
chr1A_11207721	1.3	5.8	0.7	3.9	-5.2	GYLD
chr1B_566956619	13.9	4.8	8.4	6.3	-17.5	GYLD
chr2B_76076511	5.3	0.5	3.1	1.1	10.6	GYLD
chr2D_32901354	10.3	8.9	6.2	11.9	-15	GYLD
chr2D_36584261	13.9	17.5	8.6	18.9	-17.6	GYLD
chr4A_69708392	1.3	8	0.7	5.4	5.2	GYLD
chr4A_486382996	10	8.3	5.9	7.6	-14.7	GYLD
chr4B_623071554	4.1	1.8	2.4	1.2	-9.3	GYLD
chr7D_51735477	12.9	8.4	7.6	6.4	16.6	GYLD
chr1A_45627022	3.5	5.8	2.6	2.9	-0.5	PH
chr1A_265556603	3.5	2.8	2.5	2.5	-0.5	PH
chr2D_31103643	11.6	6.4	8.6	7.5	0.9	PH
chr2D_68797075	2.7	3.5	2	3.2	0.4	PH
chr4B_56298857	2.2	4	1.6	3.4	-0.4	PH
chr4B_430792975	6.1	10.4	4.5	11.1	0.7	PH
chr4B_475417745	8.5	15.7	6.2	18.8	-0.8	PH
chr4B_612610190	1.2	4.6	0.9	2.4	-0.3	PH
chr5B_488397473	6.3	2.8	4.6	2.4	0.7	PH
chr6A_100368136	2.8	6.9	2	6.3	-0.5	PH
chr6A_86557461	5.3	12.6	3.9	12.9	-0.6	PH
chr6A_383955363	2	6.6	1.4	3.5	-0.4	PH
chr6A_184344892	4.1	5.4	3	6.1	-0.5	PH
chr5A_636992509	4.1	0.2	7.6	2.7	-1.9	SPM

Figure 2: epistatic interactions of QTL for grain yield

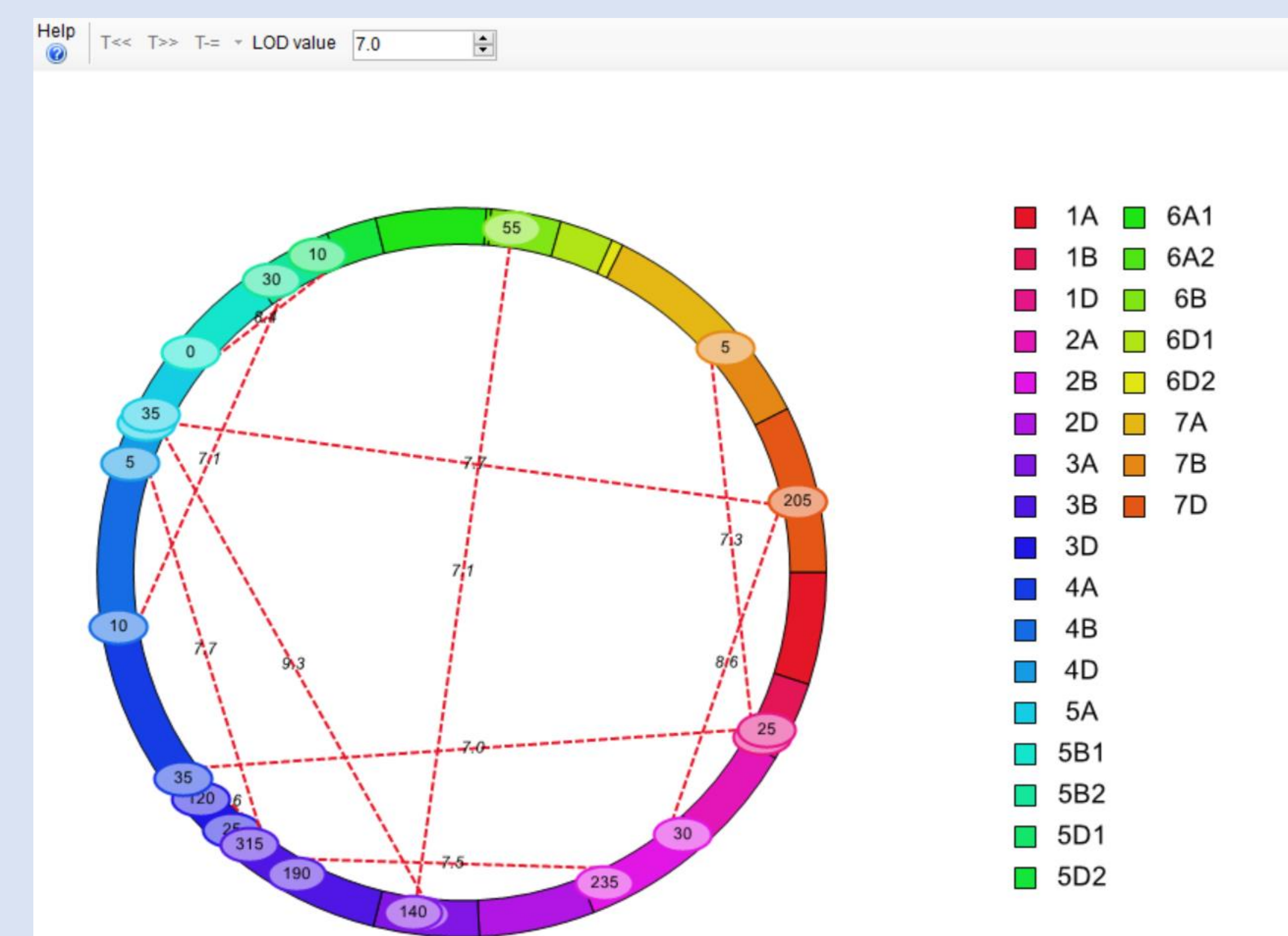


Table 2: Phenotypic correlation between traits

Traits	GYLD	HD	PH	BM	SPM
HD	-0.35***				
PH	-0.15ns	0.33***			
BM	0.08	0.11ns	0.31***		
SPM	-0.04ns	0.07ns	0.06ns	0.65***	
BM\YLD	0.26**	-0.20*	0.08ns	0.86***	0.64***

CONCLUSION

- Twenty-nine QTL associated with traits of GYLD, HD, PH, BM and SPM. More traits are under analyses.
- Additionally, one QTL has a pleiotropic effect on heading date and grain yield were identified on 2D at 32 Mb. It is close to Ppd-D1.

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