

QTL Mapping for Spot Blotch Resistance in Two Bi-parental Mapping Populations of Bread Wheat

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INTRODUCTION

Spot blotch (SB), caused by *Cochliobolus sativus* (anamorph *Bipolaris sorokiniana*), is a major fungal disease of wheat in South Asia and South America, causing significant yield loss in epidemic years. Inheritance of resistance to SB is generally taken as quantitative, although major resistance genes have been identified, including *Sb1* on chromosome 7DS (Lillemo et al. 2013), *Sb2* on 5BL (Kumar et al. 2015), and *Sb3* on 3BS (Lu et al. 2016). In the current study, two bi-parental mapping populations were generated in order to identify SB resistance QTLs and their flanking markers for the potential use in marker assisted selection

MATERIALS AND METHODS

Resistant parent of the first population was a CIMMYT breeding line SOKOLL/W15.92/WBLL1 and that of the second population was WHEAR/KRONSTAD F2004, whereas CIANO T79 was used as the common susceptible parent in the two populations, both having 232 F_{2:7} progenies. The two populations were evaluated for field SB resistance in CIMMYT's Agua Fria station from 2012-13 to 2014-15 cropping seasons. Artificial inoculation was performed by scattering *B. sorokiniana* colonized sorghum grains in the field, and disease evaluation was done three to four times at weekly interval with the double-digit (00-99) scale. Area under disease progress curve (AUDPC) was calculated based on SB evaluation data and was used for subsequent analysis. Two additional traits, plant height (PH) and days to heading (DH), were also scored due to their close relationships with SB. Genotyping was done with the DArTseq genotyping-by-sequencing (GBS) platform and approximately 1,500 high quality and non-redundant GBSs were used for QTL mapping. Several additional SSRs and SNPs that had been reported to be associated with SB resistance and phenological traits were also scored.

Table 1 QTLs for spot blotch resistance in the 'SOKOLL/W15.92/WBLL1' x 'CIANO79' (SC) and 'WHEAR/KRONSTAD F2004' x 'CIANO79' (WKC) populations

Linkage group	Position	Left marker	Right marker	2013	2014	2015	Mean	R source ^a	Traits associated ^b	
SC	1B	210.8-215.6	1042822	1117717	3.5	2.2	3.4	2.5	C	
	2B	121.5-143.1	1228793	1167654		2.8	3	2.9	C	
	4A	25.5-35.3	3023781	992456	4.6	2.8		2.8	S	
	4B	72.6-98.9	Rht-B1	2279882	6.3			2.4	S	DH, PH
	5AL2	44.2-48.6	2341646	Vm-A1	20.8	14.1	22	19.4	S	DH
	5B	73.9-77.7	996745	10592866	8.9	13.9	21.4	17.2	S	
Accumulated percentage of variation explained				35.2	21.9	28.4	47.2			
WKC	1B	149.0-151.8	2263671	100193437		4.6		3.1	W	
	2B	66.2-71.2	1017820	3947227	4.2	6.7	15	8.4	C	
	4B	88.7-91.3	4989130	1114716	8	3.4	4.3	5.7	C	
	4B	94.4-115.4	998971	1095421	5.6		4.5	4.8	W	
	4D	0-17.5	BS00036421	1059032		4.1		2.3	W	PH
	5A	174.6-188.2	987242	IWA4449	25.9	13.5	24.9	25.6	W	DH
Accumulated percentage of variation explained				43.7	32.3	48.7	49.9			

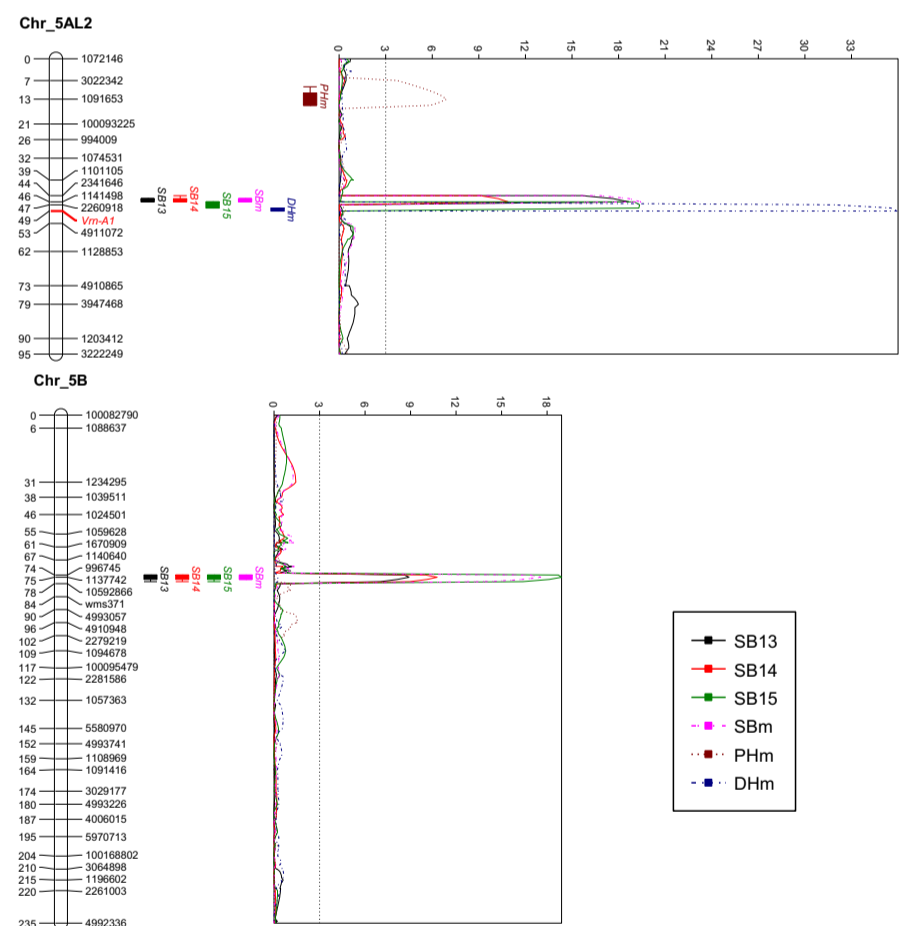
The percentage of explained phenotypic variation is shown in the table, QTLs are listed if they were over the LOD threshold of 3 in at least one environment or over the threshold of 2 in multiple environments.

^a S 'SOKOLL/W15.92/WBLL1', W 'WHEAR/KRONSTAD F2004', C 'CIANO'; ^b PH plant height, DH days to heading

RESULTS AND DISCUSSION

- ▶ A major QTL on chromosome 5AL at *Vrn-A1* was found at both populations (Table 1, Figure 1), which turned up to be less- or non-significant when DH and PH were used as covariates in the analysis, implying a disease escape mechanism.
- ▶ Another major QTL was located on 5BL in the SOKOLL/W15.92/WBLL1 population, most likely being *Sb2* (Table 1, Figure 1).
- ▶ Minor QTLs were found on 4A and 4B in SOKOLL/W15.92/WBLL1 and on 1B, 4B, 4D and 7A in WHEAR/KRONSTAD F2004.
- ▶ Additionally, minor QTLs contributed by CIANO T79 were identified on 1B, 2B, 4B and 6D.

Figure 1. QTL profiles for spot blotch resistance in the 'SOKOLL/W15.92/WBLL1' x 'CIANO79' (SC). Genetic distances are shown in centimorgans to the left of the chromosomes. A threshold of 3.0 is indicated by a dashed vertical line in the LOD graphs. Only framework markers are presented except for the QTL regions.



REFERENCE

- Lillemo M, Joshi AK, Prasad R, Chand R, Singh RP (2013) QTL for spot blotch resistance in bread wheat line Saar co-locate to the biotrophic disease resistance loci *Lr34* and *Lr46*. *Theor Appl Genet* 126:711-719
- Kumar S, Röder MS, Tripathi SB, Kumar S, Chand R, Joshi AK, Kumar U (2015) Mendelization and fine mapping of a bread wheat spot blotch disease resistance QTL. *Mol Breed* 35
- Lu P, Liang Y, Li D, Wang Z, Li W, Wang G, Wang Y, Zhou S, Wu Q, Xie J, Zhang D, Chen Y, Li M, Zhang Y, Sun Q, Han C, Liu Z (2016) Fine genetic mapping of spot blotch resistance gene *Sb3* in wheat (*Triticum aestivum*). *Theor Appl Genet* 129:577-589