

Resistance to Spot Blotch in Two CIMMYT Wheat Breeding Lines is Conditioned by Multiple QTLs of Minor Effects

Xinyao He, Susanne Dreisigacker, Carolina Sansaloni, Etienne Duveillier, Ravi P. Singh, Pawan K. Singh

International Maize and Wheat Improvement Center (CIMMYT), Apdo. Postal 6-641, 06600 Mexico DF, Mexico



INTRODUCTION

Spot blotch (SB), also known as *Helminthosporium* leaf blight or foliar blight, is a major fungal disease of wheat in South Asia and South America, with yield losses of up to 85% (Singh et al. 2016). Host resistance is regarded as an effective, economical and environmentally friendly approach of controlling SB, and the inheritance of resistance is mostly quantitative. CIMMYT develops and distributes regularly *Helminthosporium* Leaf Blight Screening Nurseries (HLBSN, previously known as CSISA-SB, Figure 1) to help breeders/pathologists in South Asia and South America to cope with this disease (Singh et al. 2015). HLBSN entries are elite breeding lines with promising resistance to SB, good agronomy and high yield potential. Two bi-parental mapping populations were generated and analyzed in this study in order to gain a better understanding on the SB resistance mechanism in CIMMYT germplasm.

MATERIALS AND METHODS

Elite CIMMYT breeding lines, BABAX/LR42//BABAX/3/ER2000 and WAXWING*2/CIRCUS, were used as resistant parents, whereas CIANO T79 was used as the common susceptible parent in the two mapping populations, both comprising 232 F_{2:7} progenies. The two populations were evaluated in field for SB reaction in CIMMYT's Agua Fria station for three years, i.e. from 2012-13 to 2014-15 cropping seasons. Artificial inoculation was done by scattering *Bipolaris sorokiniana* colonized sorghum seeds in the field, and SB scoring was made three to four times at weekly interval with the double-digit scale. Phenological traits like plant height (PH) and days to heading (DH) were also scored. Genotyping was done with the DArTseq genotyping-by-sequencing (GBS) platform and approximately 1,500 high quality and non-redundant markers were used for QTL mapping. Selected SSRs and SNPs for previously reported SB resistance QTLs and phenological traits were also used in genotyping the populations.

RESULTS AND DISCUSSION

- ▶ The most prominent QTL in both populations was found on chromosome 5AL at *Vrn-A1* (Table 1). However, when DH and PH were used as covariates in the analysis, the effects of this QTL decreased significantly, implying a disease escape mechanism.
- ▶ Minor QTLs were found on 1A, 1B, 3A, 3B, 4B, 4D, 5B and 6D in BABAX/LR42//BABAX/3/ER2000 and on 1B, 2A, 2D and 4B in WAXWING*2/CIRCUS, all showing phenotypic effects less than 10%.
- ▶ Additionally, minor QTLs contributed by CIANO T79 were identified on 1B, 1D, 3A, 4B and 7A.
- ▶ Resistance to SB in the two mapping populations was conditioned by multiple minor QTLs, with strong influence of *Vrn-A1*.

Table 1. QTLs for spot blotch resistance in the 'BABAX/LR42//BABAX/3/ER2000' x 'CIANO79' (BC) and 'WAXWING*2/CIRCUS' x 'CIANO79' (WC) populations and their association with phenological traits

Linkage group	Position	Left marker	Right marker	2013	2014	2015	Mean	R source ^a	Traits associated ^b	
BC	1B	0.4-2.8	995296		7.1	5.4	6.5	C		
	1B	209.4-218.6	5324988	1110815	5.5	8.5	7.0	B		
	1D	48.4-53.3	100142243	1037975		3.5	2.9	C		
	3A	103.2-146.0	1109808	990692	5.1		3.2	C		
	4B	111.3-117.1	1247021	1702494	5.2	2.2	3.0	3.3	B	
	4D	0-9.8	BS00036421	1119387		3.6		B	PH	
	5A	175.9-179.4	Vrn-A1	3064415	21.9	8.9	6.9	12.5	B	DH
	6D	21.9-33.2	1239681	1095962	2.4	2.6	2.7		B	
	Accumulated percentage of variation explained				40.1	32.9	28.5	37.3		
	WC	1B	232.3-252.9	1283166	2263671	2.9	4.4	4.5	8.3	W
2D		2.0-3.2	1085831	1098973	7.3	4.9	4.7	9	W	DH
4B		47.9-54.1	Rht-B1	1241652		2.6	2.7	2.3	C	PH
4B		99.2-107.4	1217659	997944		4.7	6	4.5	W	
5A		147.5-148.4	1135154	2260918	27.1	21.9	24.3	25.1	W	DH
Accumulated percentage of variation explained				37.3	38.5	42.2	49.2			

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 B 'BABAX/LR42//BABAX/3/ER2000', W 'WAXWING*2/CIRCUS', C 'CIANO'; ^b PH plant height, DH days to heading

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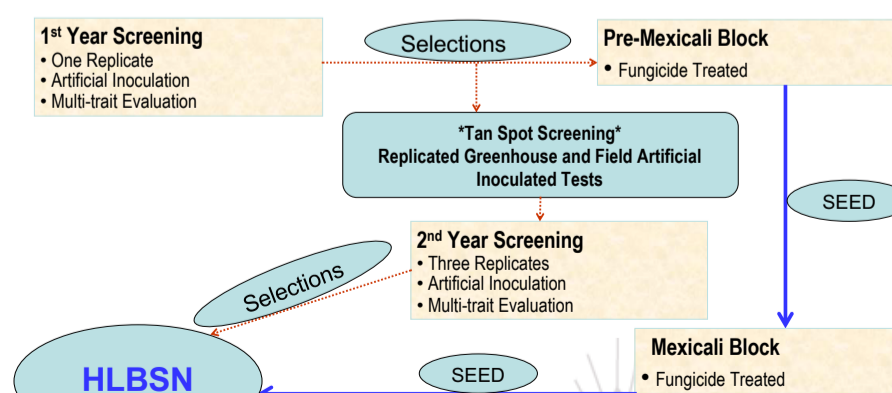


Figure 1 Workflow for the development of CIMMYT's Helminthosporium Leaf Blight Screening Nurseries (HLBSN)