

Marker-assisted breeding for improving resistance to common bacterial blight in common bean

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INTRODUCTION

- Common bacterial blight (CBB), caused by *Xanthomonas axonopodis* pv. *Phaseoli* (*Xap*), is a damaging disease of common bean (*Phaseolus vulgaris* L.) throughout the world.
- Breeding for resistant cultivars is the most effective means of controlling CBB.

OBJECTIVES

- Examine the efficiency of marker-assisted selection (MAS) for breeding resistant cultivars against CBB.

MATERIALS AND METHODS

- Plant Materials.** Four three-way crosses (TC) were performed, in which the F₁ progeny of the crosses between two sources of CBB resistance (Apex, MBE7 or Rexeter) were top-crossed to a susceptible, early-maturity commercial cultivar (Nautica or AC Compass). Their resistant F₁ progeny, based on phenotyping and SU91 genotyping described below, were then backcrossed twice with Nautica or AC Compass to produce four BC₁F₁ and four BC₂F₁ families (Table 1). The progeny from all F₁ were advanced to F₄ by single-seed descent.

Table 1. Cross design of four populations

Entry	TC F ₁	BC ₁ F ₁	BC ₂ F ₁
108	Nautica//Apex/MBE7	Nautica ⁸² //Apex/MBE7	Nautica ⁸³ //Apex/MBE7
113	Nautica//Rexeter/Apex	Nautica ⁸² //Rexeter/Apex	Nautica ⁸³ //Rexeter/Apex
115	Compass//Apex/MBE7	Compass ⁸² //Apex/MBE7	Compass ⁸³ //Apex/MBE7
120	Compass//Rexeter/Apex	Compass ⁸² //Rexeter/Apex	Compass ⁸³ //Rexeter/Apex

- Disease inoculation and phenotyping.** Fully opened unifoliate leaves of all F₁ progeny (TCF₁, BC₁F₁, and BC₂F₁) were inoculated with common isolates of *Xap* using a multiple needle technique (Yu et al. 2000; Plant Breeding 119:411) in a growth room. CBB severity of infected leaves was quantified using image analysis (Assess® 2.0) 18 days after inoculation (Xie et al. submitted). Four TC F₄ populations with 400 lines from each cross were tested for CBB resistance in an artificially inoculated field nursery in Harrow, Ontario in 2010. The disease severity of infected leaves were visually rated using a 0 to 5 scale.

- Genotyping.** Each F₁ plant was also genotyped with the previously known CBB-associated SCAR marker, SU91 (Miklas et al. 2000; Annu. Rep. Bean Improv. Coop. 43:39), which is known to be segregating in the population. From each TC F₄ population, two sub sets of 45 resistant and 45 susceptible lines were also genotyped with SU91.

RESULTS

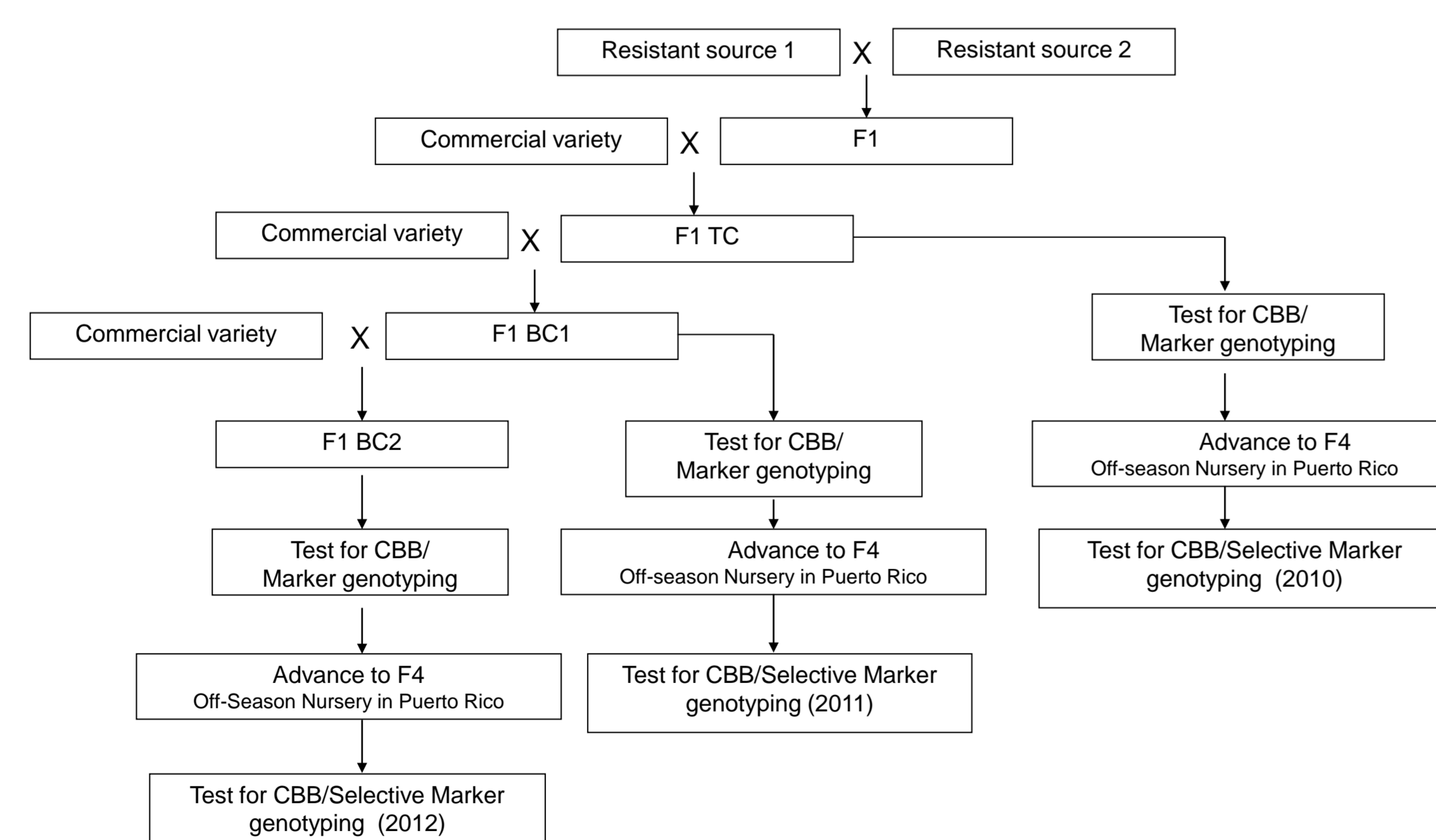


Fig. 1. Crossing scheme and population development for the study of the effectiveness of MAS in CBB resistance breeding.

ACKNOWLEDGMENT

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- All F₁ progeny (TCF₁, BC₁F₁, and BC₂F₁) were phenotyped under artificial inoculation with *Xap* and genotyped with the SCAR marker SU91 (Fig. 2). The estimate of the proportion of the CBB resistance phenotypic variance accounted for by the marker SU91 was 31% to 43% by image analysis (Assess® 2.0).

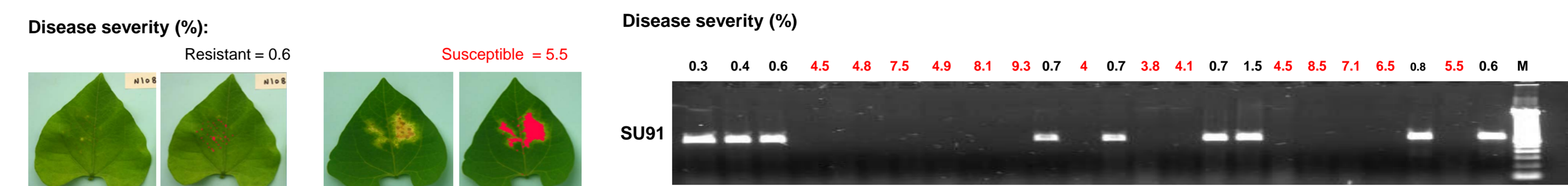
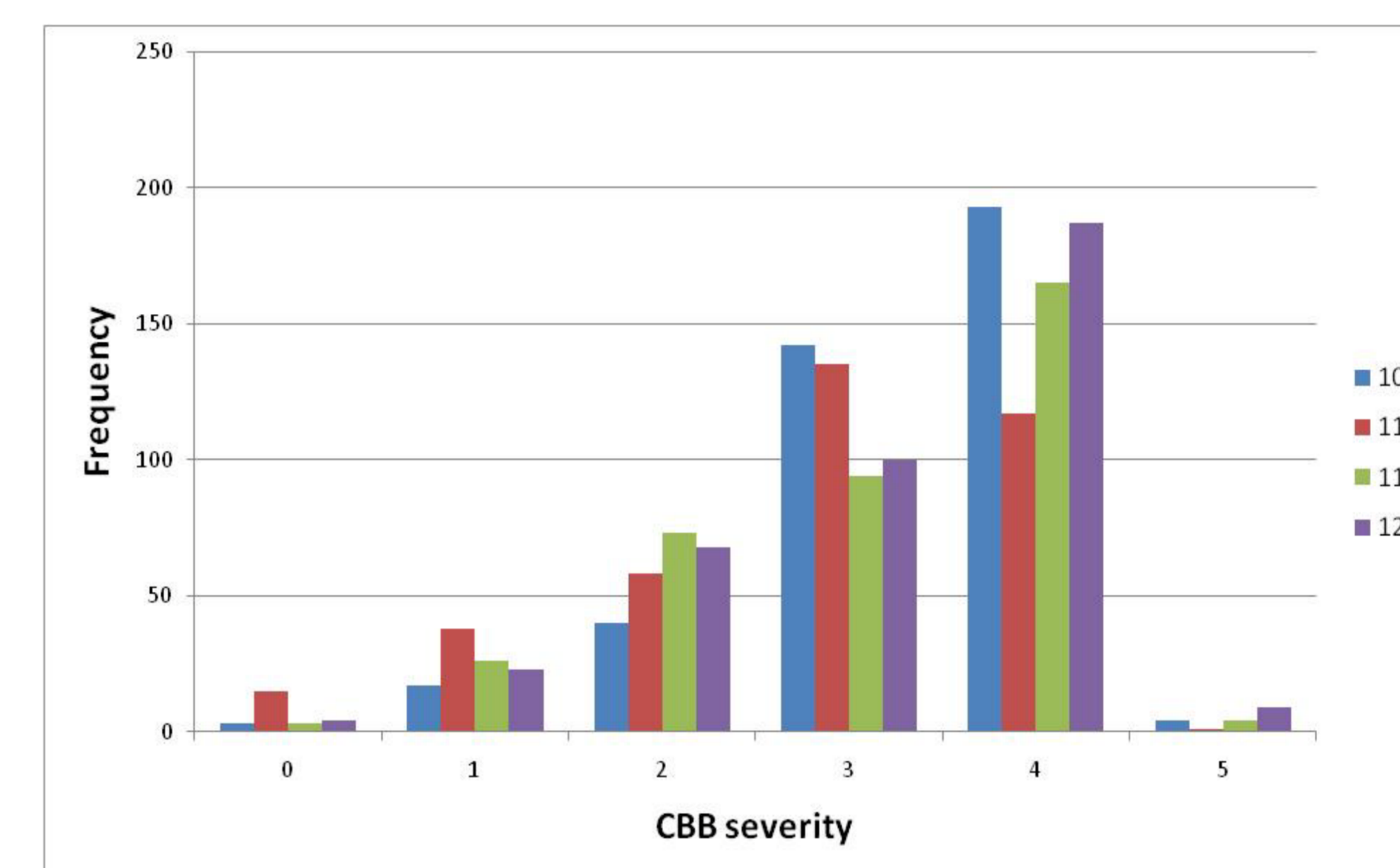


Fig. 2. Association between disease severity and marker SU91 in BC₁F₁ generation.



- All four TC F₄ populations showed continuous variation for CBB severity in the field nursery in Harrow, with population means shifted towards susceptibility (Fig. 3).

Fig. 3. Frequency distribution of CBB severity of four three-way cross F₄ populations inoculated with *Xap* in a field nursery in Harrow, Ontario.

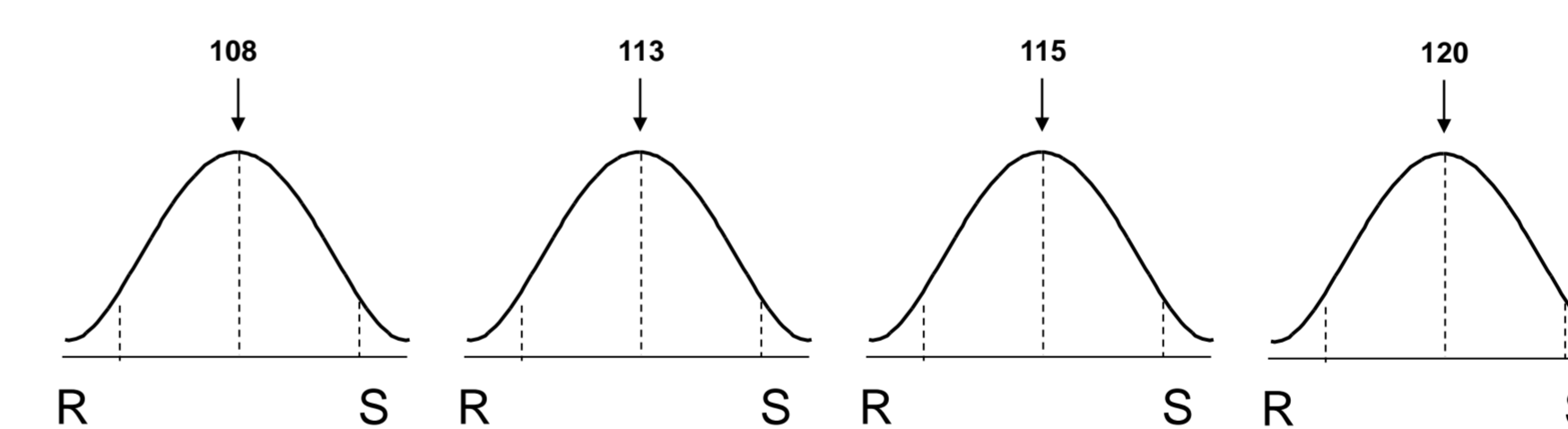


Fig. 4. Two sub sets of 45 resistant and 45 susceptible lines of each of four TC F₄ populations.

Table 2. Frequency of SU91 genotype in the resistant and susceptible selected subsets of four three-way cross F₄ populations

Population	SU91	
	R	S
108	98%	2%
113	93%	2%
115	80%	2%
120	93%	4%

SUMMARY

- The frequency of SU91 ranged between 80 to 98% in the resistant sub sets and between 2 to 4% in the susceptible subsets in four TC F₄ populations (Fig. 4; Table. 2).
- The lines with SU91 marker, however, had a range of CBB responses, indicating the existence of other QTL for CBB resistance.
- SU91 should be a useful tool in early generation selection.
- The combination of SU91 MAS and phenotypic selection will be the most efficient way to achieve high levels of CBB resistance.

FUTURE WORK

- Identification of markers linked to additional QTL and the effectiveness of markers in multiple generations of breeding program will be further investigated.