Rapid Introgression of Common Bacterial Blight Resistance Genes into Dry Bean Elite Varieties by Marker-Assisted Backcrossing

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Introduction

Common bacterial blight (CBB) caused by *Xanthomonas campestris* pv. *phaseoli* (*Xcp*) is one of the most important bean diseases throughout the world. Yield losses as high as 45 percent have been reported in CBB-affected bean fields in Canada (Wallen and Jackson, 1975). Due to the abundance of sources of blight inoculum and the ability of the bacteria to survive for extended periods, cultural control for this disease is very difficult. Chemical control, including seed treatments, has had limited success and is not considered economical. Therefore, development of resistant cultivars is of major importance to all bean growing regions. An interspecific cross between *P. vulgaris* and either *P. acutifolius* or *P. coccineus* has previously been used to transfer the resistance to *Xcp* into common bean breeding lines. In the past decades a number of CBB resistant lines have been developed (Park and Dhanvantari, 1998; Scott and Michaels, 1992; Singh and Munõz, 1999) and molecular markers linked to the resistance genes have been identified (Ariyarathne et al. 1999; Bai et al. 1997; Jung et al. 1997; Miklas et al. 1996; Nodari et al. 1993; Park et al. 1999; Tar'an et al. 2001; Yu et al. 1998). These genes are distributed among linkage groups B2, B5, B7, B8, B9, B10 and B11 of the bean core map (Gepts 1999; Miklas et al. 2000). These CBB resistant lines, however, are poorly adapted to Western Canadian environments. The current study involves the use of molecular marker assisted backcrossing to rapidly introgress CBB resistance genes into local elite dry bean varieties. Four adapted varieties including CDC Pintium, CDC Whitecap, CDC Jet and 95-83-10 that represent different market classes were chosen as the target parents.

Results and Future works

The marker-assisted backcross breeding scheme involves molecular marker analysis of the target loci as well as full molecular marker analysis using background markers (Figure 1). A number of initial crosses involving adapted varieties and CBB resistant lines were done in 1999-2000. The $F_{2:4}$ lines derived from these crosses were screened for their reaction to *Xcp* under field condition in Saskatoon in 2001. A comparable level of resistance was recovered in the progeny lines (Table 1). Also, in the initial crosses, the two parental lines were analyzed using both the CBB resistant markers (used for tracking the target allele) and a number of additional markers selected from the bean core linkage map at 10 – 15 cM interval that correspond to sequences of DNA throughout the genome. Information from the background markers is used to develop a genetic "fingerprint" of each parent.

Table 1. Range of CBB scores of $F_{2:4}$ lines derived from crosses involving various sources of CBB resistant germplasm

Pedigree/Parents	CBB Score	No. of selected line
747F3//93128/**VAX 2B**	2 - 3.5	1
93708//**ICB-12**/KODIAK	2 - 3.0	5
315-18/**OAC 95-4**	1 - 3.25	7
OAC 95-4/CARIOCA	1.5 - 3.25	6
WEIHING/694-2	2.5 - 3.5	5
OAC 95-4/325-28	2.5 - 3.5	3
VAX1	1.5	
VAX2	1.5	
VAX2B	2	
ICB-10	1	
ICB-12	1.5	
PM-98-CBB-RED	2	
OAC 95-4	1	
WEIHING	2	
Nighthawk	3.5	
CDC Pintium	4	
Crocus	3.5	
OAC Seaforth	3.5	

Bolded = CBB resistant lines; CBB disease rating: 0 = No symptoms; 1 = Necrotic spots only; 2 = Few disease lesions on leaves; 3 = Moderate number of disease lesions on leaves; 4 = Most leaves with large spreading lesions

The resistant progeny from the initial crosses was then selected and selfed to produce $F_{4:5}$ lines. DNA was collected from the $F_{4:5}$ lines and analyzed for the presence of markers (SU91, BC73, BC409, J0455 and BC420) that are linked to the CBB resistance genes. In this manner, individuals that retained the target gene could be rapidly identified. A series of backcrosses is then initiated; in each cycle of backcrossing, the marker for CBB resistance is used to select plants to cross to the recurrent parent (Fig. 1; Table 2). To date, we have developed a series of BC_2F_1 and BC_3F_1 lines from different market classes.

Table 2. Sources of CBB resistance and molecular markers used to introgress the resistant genes into adapted bean varieties by marker-assisted backcrossing

Source of Resistance	Donor parent	Marker for CBB resistant genes	Linkage Group	Recurrent (target) Parent	Market class of the target parent
P. coccineus	ICB 10	BC409;SAP6	B10	CDC Jet (315-18)	Black
P. coccineus	ICB 12	BC409:SAP6	B10	CDC Pintium	Pinto
P. acutifolius	OAC95-4	SU91; BC73;J0455	B8	CDC Jet	Black
P. acutifolius	OAC95-4	SU91; BC73:J0455	B8	CDC Whitecap	Navy
P. acutifolius	VAX 2B	BC409:SAP6	B10	95-83-10	Pinto

The selfed progeny of BC_3F_1 lines will be analysed again using markers to identify resistant plants. In addition, the background markers are used to fingerprint the plants that have the adapted (recurrent) parent genotype. Based on these fingerprints, it is possible to select individual plants at the DNA level that most closely resemble the recurrent parent after only three cycles of backcrossing.

BC_3S_1 lines that retain the CBB resistance genes and contain the highest proportion of the recurrent recipient parent genome will be selected and increased. Disease phenotyping as well as field evaluation for agronomic characters will be conducted to confirm the CBB resistance and similar performance to the target parents.

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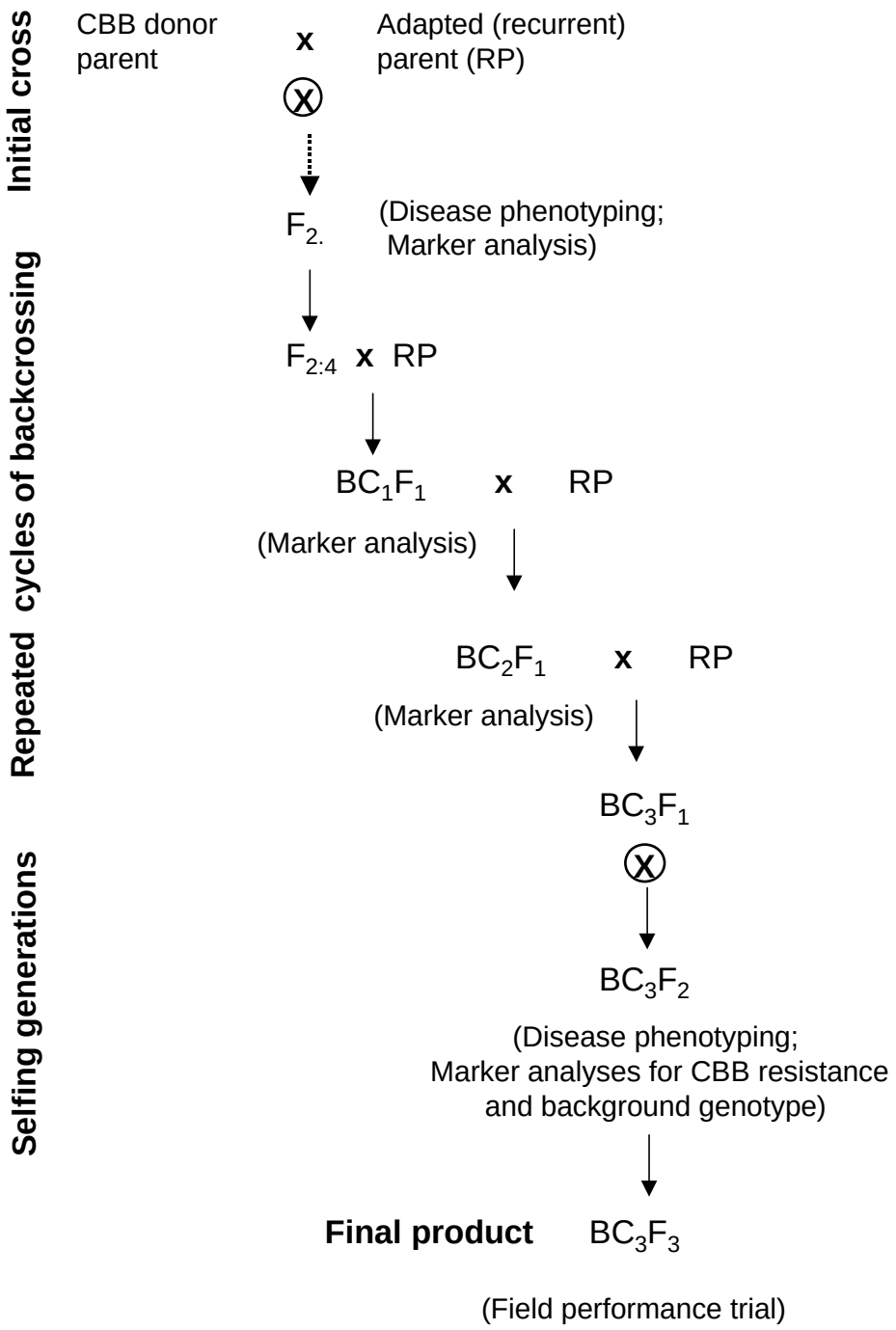

Figure 1. Marker-assisted backcross breeding scheme for the rapid introgression of genes for resistance to CBB in common bean