BREEDING

Development of Molecular Markers for Common Bacterial Blight and Anthracnose in Dry Beans

Molecular markers for CBB resistance (SU91) were improved based on candidate genes (SU91-CG10 and SU91-CG14) and anthracnose resistance genes and markers ($SAH18_{1100}$ and BM161) were identified in Manitoba-adapted dry bean cultivars.

COMMON BACTERIAL BLIGHT (CBB) and anthracnose are economically important diseases of dry beans across Canada. Antibiotic streptomycin seed treatment or foliar applied copper products can be used to control CBB and DCT (diazinon, captan, thiophanate-methyl) can be used to control anthracnose. A more cost effective and environmentally friendly solution is to breed genetic resistance into new cultivars. Resistance genes for these diseases are available, but conventional selection and pyramiding of resistance genes to multiple diseases have not been effective in developing cultivars with both CBB and anthracnose resistance because of the complex genetic control of resistance genes involved and slow screening process. Most of the major resistance genes and quantitative trait loci (QTL) for anthracnose and CBB resistance have been located on genetic maps and associated with closely linked molecular markers. These markers may be used for selecting individual lines from a cross carrying the genes of interest, speeding up the process of breeding for multi-disease resistance cultivars. This research studied the effectiveness of the available molecular markers for selection of resistant breeding lines and also developed new markers better associated with resistance.

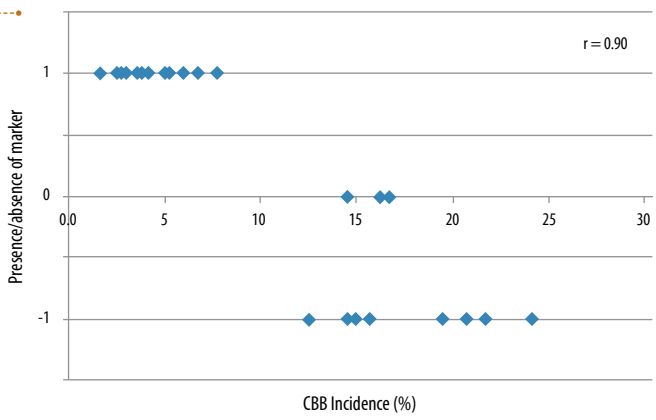
A combination of conventional breeding and marker-assisted selection was used to transfer CBB resistance genes into Manitoba-adapted cultivars with anthracnose and bean common mosaic virus (BCMV) resistance. Previously, crosses were performed between CBB resistant Ontario variety OAC-Rex (navy) and Manitoba varieties: anthracnose resistant Morden003 (navy), CBB and anthracnose susceptible Black Violet (black) and AC Pintoba (pinto).

QTLs conferring CBB resistance in OAC Rex are located on chromosomes Pv08 and Pv04 and linked to the SU91 and PV-ctt001 markers, respectively. Based on candidate gene approach, more reliable markers to SU91 have been developed at Harrow. These markers were used to screen the navy, black and pinto populations for CBB resistance at field trials in Morden, MB and Harrow, ON. A strong correlation between the incidence of CBB leaf infection and the presence of marker SU91 was found (see graph), however, the correlation between CBB and marker PV-ctt001 was low and insignificant.

Three of the 114 navy lines had improved resistance to both CBB and anthracnose, whereas ~50% of the lines exhibited strong resistance to anthracnose. Eleven black and seven pinto had resistance to CBB and four of the seven pinto beans were also presumed resistant to BCMV. There was good correlation between field evaluation and the presence of the marker alleles associated with resistance to anthracnose races 73 and 105 ($SAH18_{1100}$ and BM161).

A second study, using populations from the Morden003/OAC Rex crosses, mapped two race-specific (73, 105) resistance gene loci at the *Co-3* locus on Pv04, flanked by markers BM161 and $SAH18_{1100}$. The map generated in this research also showed strong linkage of the anthracnose resistance loci to markers SW12, PVctt001 and SF10, which were associated with the *Co-3* and *Co-10* loci. A weak, distant linkage of marker SB12 to the *Co-3* locus was also detected.

The new anthracnose molecular markers identified and the CBB, anthracnose, BCMV resistant lines developed possess desirable yield and seed characteristics, and can be used in crossing for future dry bean improvement.



CBB incidence at Morden in 2010–2011 and the presence/absence of the SU91 marker associated with CBB resistance of lines. Lines negative for the resistant allele were rated as -1; those segregating for the marker were given a value of 0; and those homozygous for SU91 as 1.

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