Agriculture and Agri-Food Canada | Agriculture et Agroalimentaire Canada

Association mapping of common bacterial blight resistance QTL in Ontario bean breeding populations

Chun Shi[1], Alireza Navabi[1,2], and Kangfu Yu[1]

[1]Agriculture and Agri-Food Canada, Greenhouse and Processing Crops Research Centre, Harrow, ON, N0R 1G0, Canada
[2]Department of Plant Agriculture, Crop Science Building, University of Guelph, Guelph, ON, N1G 2W1, Canada

Introduction

➢Common bacterial blight (CBB), incited by *Xanthomonas axonopodis* pv. *Phaseoli* (*Xap*), is a serious seed-borne disease of common bean (*Phaseolus valgaris* L.) in both temperate and tropical production zones.

➢Host genetic resistance is the most effective and environmentally-sound approach to control CBB, as it requires no additional chemical or biological measures to function.

➢To date, at least 24 different CBB resistance QTLs have been reported across all eleven linkage groups of common bean. However, these QTLs were mapped in eight different bi-parental populations and poorly colocalize, thus markers linked to these QTLs are not immediately available for use in bean breeding (Shi et al., 2011).

➢Unlike conventional QTL discovery strategies, in which bi-parental populations (F2, RIL, or DH) need to be developed, association mapping based strategies can use plant breeding populations to synchronize QTL discovery and cultivar development.

Materials and methods

➢A population of 469 bean cultivars and breeding lines were used in this study. It includes: a) 62 navy bean varieties registered in Canada over time, since 1930, b) 29 modern North American cultivars of different gene-pool origins developed and released by public institutions in the US and Canada, and c) 378 advance bean breeding lines of different gene-pool origins, in different stages of variety development in the AAFC/U of Guelph Bean Breeding Program.

➢The breeding population was evaluated in the field in 2009 in the CBB nursery in Harrow, Ontario in Canada.

➢Plant DNA was automatically extracted using an AutoGen 850 alpha DNA automatic system following the manufacturer's manual (AutoGen Inc.).

➢SNP genotyping was performed using the Sequenom iPLEX Gold Assay (Sequenom, Cambridge, MA) in Genome Quebec (Montreal, Quebec).

➢Association mapping was carried out with TASSEL software (www.maizegenetics.net) using unified MLM (Mixed Linear Model) analysis. Both population structure and kinship relationship were taken into account.

➢The mapping information of SNP markers was extracted from McClean (NDSU) 2007 genetic map at Legume Information System (http://www.comparativelegumes.org/index.php/Home)

Results and Discussion

➢All lines were genotyped using 132 SNPs evenly distributed across the genome. Of the 132 SNPs, 26 SNPs had more than 20% missing data, 12 SNPs were monomorphic, and 17 SNPs had a MAF (Minor Allelic Frequency) of less than 0.20, therefore only 75 SNPs were used for association study, based on one SNP per locus.

➢MLM (Mixed Linear Model) analysis, including population structure and kinship, was used to discover marker-trait associations. Eighteen and 22 markers were significantly associated with CBB rating at 14 and 21 DAI, respectively (Table 1). Fourteen markers were significant for both dates and the markers UBC420, SU91, g321, g471, and g796 were highly significant ($p \leq 0.001$) (Table 1).

➢Figure 1 shows 12 significant SNP markers were co-localized with or close to the CBB-QTLs identified previously in bi-parental QTL mapping studies (Shi et al., 2011).

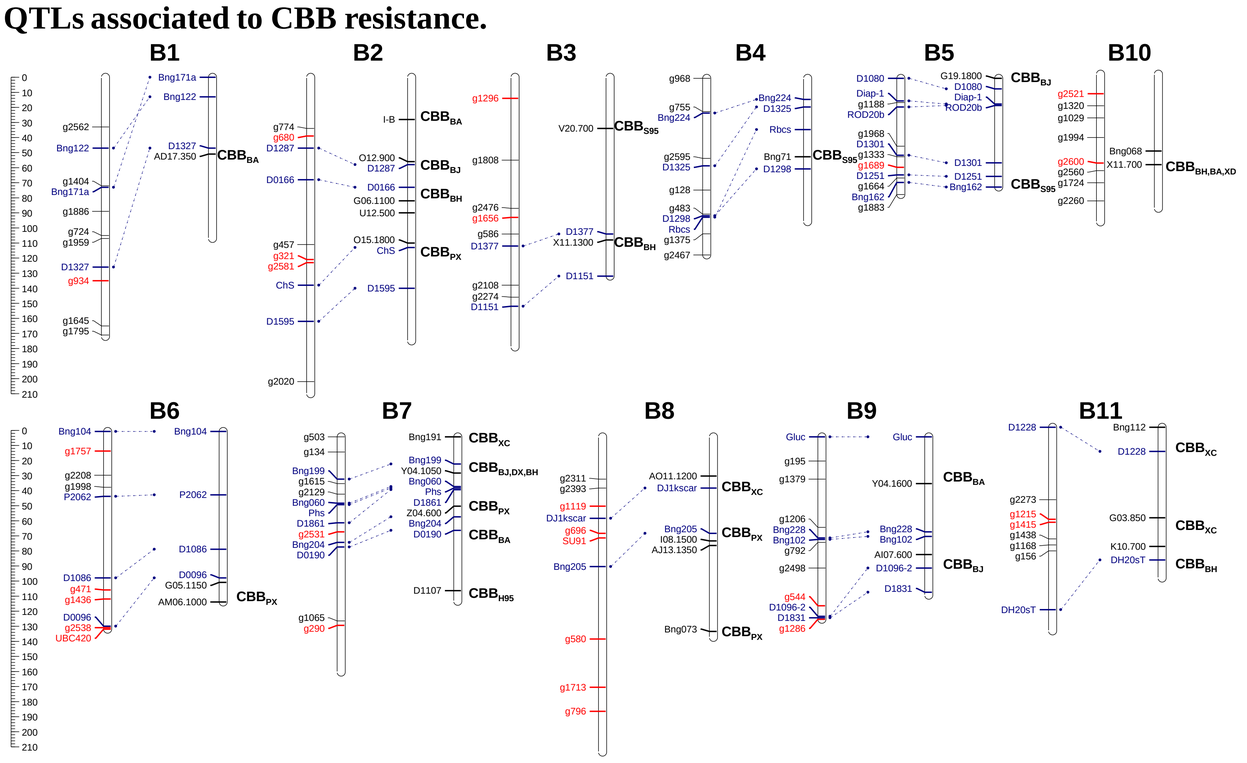
Table 1. Testing of association between marker loci and common bacterial blight severity using unified MLM (Mixed Linear Model) method

[a] n.s., not statistically significant; *, $P \leq 0.05$; **, $P \leq 0.01$; ***, $P \leq 0.001$.

[b] R^2_marker was calculated as the proportion of sum square due to marker after accounting for all other effects in model.

Chr.	CM	Marker[a]	14 DAI		21 DAI	
			p	R^2_marker[b]	*p*	R^2_marker
1	135	g934	n.s.		*	0.0061
2	39	g680	***	0.0098	*	0.0094
2	121	g321	***	0.0151	***	0.0141
2	123	g2581	*	0.0065	n.s.	
3	14	g1296	**	0.0104	*	0.0072
3	93	g1656	*	0.0076	***	0.0208
5	59	g1689	*	0.0090	**	0.0142
6	13	g1757	n.s.		**	0.0079
6		UBC420	***	0.0136	***	0.0215
6	105	g471	***	0.0227	***	0.0471
6	111	g1436	n.s.		*	0.0049
6	130	g2538	*	0.0075	*	0.0088
7	63	g2531	n.s.		***	0.0126
7	125	g290	***	0.0129	**	0.0085
8		SU91	***	0.0495	***	0.0320
8	46	g1119	**	0.0102	**	0.0136
8	64	g696	n.s.		*	0.0071
8	134	g580	n.s.		*	0.0048
8	166	g1713	**	0.0125	n.s.	
8	182	g796	***	0.0128	***	0.0148
9	112	g544	**	0.0101	*	0.0068
9	121	g1286	n.s.		*	0.0045
10	13	g2521	n.s.		*	0.0109
10	59	g2600	**	0.0068	n.s.	
11	61	g1215	*	0.0049	n.s.	
11	63	g1415	**	0.0073	***	0.0171

Figure 1. The distribution of molecular markers co-localized with previously identified QTLs associated to CBB resistance.



Conclusions

➢This study demonstrated that association mapping using a reasonable number of markers, distributed across the genome and with application of plant materials that are routinely developed in a plant breeding program can detect significant QTLs for traits of interest. Unlike conventional QTL discovery strategies, in which bi-parental populations (F2, RIL, or DH) need to be developed, association mapping-based strategies can use existing plant breeding populations with wide coverage of the existing genetic diversity. This may address some of the concerns with conventional QTL mapping that the biparental mapping populations rarely give rise to new cultivars, the identified QTLs may not be effective in multiple genetic backgrounds and that the QTL-linked markers are not immediately available for MAS.

References

➢Shi, C., Navabi, A., & Yu, K. (2011). Association mapping of common bacterial blight resistance QTL in Ontario bean breeding populations. BMC Plant Biology, 11:52.

Acknowledgements

The authors would like to thank Ontario Colored Bean Growers' Association, Ontario White Bean Growers' Association, Ontario Research Fund and Agriculture and Agri-Food Canada for their financial support.

© 2011

Canada