AFLP Markers are Tightly Linked to the Major QTL for CBB Resistance in HR67

Shuyu Liu, Kangfu Yu and Soon J. Park.
Agriculture and Agri-Food Canada, Greenhouse and Processing Crops Research Centre,
2585 County road 20, Harrow, Ontario. N0R 1G0, Canada

Abstract

Common bacterial blight (CBB) of common beans (*Phaseolus vulgaris L.*), caused by *Xanthomonas axonopodis pv. Phaseoli* (*Xap*), is one of the major diseases in bean production areas in North America. The common bean line HR67, which was derived from the crosses Centralia/3/HR13-621//XAN159/OAC Rico, is highly resistant to CBB. The main objective of this study is to find additional molecular markers tightly linked to the major quantitative trait loci (QTL) for CBB resistance in HR67, to map the QTL with flanking markers and to estimate its effects. Five SSR, two SCAR and 58 AFLP markers loci were mapped to a recombinant inbred line (RIL) population of 82 lines. Seven linkage groups were constructed and one major QTL was located on linkage group1 (LG_1). This QTL was mapped to a 9 cM genomic region covered by 5 molecular markers which can explain 30% to 49% of the phenotypic variations individually. Stepwise model selection among these five markers showed that eAAGmCAG183 and eAAGmCAG333 together can explain 51.1% of the phenotypic variations. Conversions of these AFLP markers into sequence tagged site (STS) or SCAR markers are under way.

Materials and Methods

Phenotypic and genotypic data: Disease screening of 82 F_6 recombinant inbred lines (RILs) from the cross HR 67/OAC 95-4 were conducted as described by Yu et al. (2000a). One SSR and two SCAR markers associated with the CBB resistance reported previously were re-screened. Thirty-two more SSR markers (Yu et al., 2000b) were screened for parental polymorphism. The STS marker OD12S linked to V gene was screened as well. Eight *EcoR*I and eight *Mse*I primers with three nucleotide extension forming 64 combinations were screened with the parental and the bulked DNA samples (the resistant vs. the susceptible). Thirteen primer pairs with clear polymorphisms on parents and/or on the two bulks were mapped to the RILs.

Data analysis: The associations between the markers and the CBB rating were analyzed by SAS PROG GLM (version 8, 1999). Genetic maps were constructed by MapMaker 3.0 using Kosmobi function. QTL analyses were conducted by QTL Cartographer. Genetic maps and QTL intervals were drawn with MapChart.

Results and Discussion

Molecular marker and genetic maps: Five SSR, 2 SCAR and one STS marker and 13 AFLP primer pairs with 58 polymorphic loci were mapped to the 82 RILs. Seven genetic linkage groups were constructed covering 411.7 cM of the bean genome (Fig. 1).

Marker and trait association: Seventeen of the 20 markers in linkage group1 (LG_1) are significantly associated with the CBB resistance. Thirteen markers can explain 20% to 49% of the phenotypic variations individually determined by SAS PROG GLM.

QTL location and effect: One major QTL was detected by QTL Cartographer. It is located on LG_1 within a 9 cM genomic region covered by 5 markers. These five markers can explain 30 to 49% of the phenotypic variation individually determined by SAS PROC GLM. Genetic model including markers eAAGmCAG.183 and eAAGmCAG.333 can explain 51.1% of the phenotypic

variations. This major QTL is from HR67 (Fig. 1). Seed coat color gene V and its linked STS marker OD12S.490 were located on B_6 (McClean et al. 2002; Nodari et al. 1992). Jung et al. (1997) found that the V locus was linked to the RAPD marker BC420.900 which was associated a major QTL for CBB resistance from the cross PC50/Xan159. The BC420.900 was converted to SCAR marker UBC420.900 and it is linked to the major QTL for CBB resistance from the cross HR67/OAC95-4 (Yu et al. 2000a; 2004). The LG_1 included both UBC420.900 and OD12S.490. Therefore, LG_1 is probably aligned with B6. Yu et al. (2004) suggested that this QTL may be on B_7. More SSR markers will be screened to confirm the location of this QTL.

Cloning and conversion of the AFLP markers to STS or SCAR markers is under way. These converted markers should be more useful for marker-assisted selection (MAS) in bean breeding programs and they also provide a starting point for physical mapping of the QTL region and map-based cloning of the major CBB resistant QTL in the future.

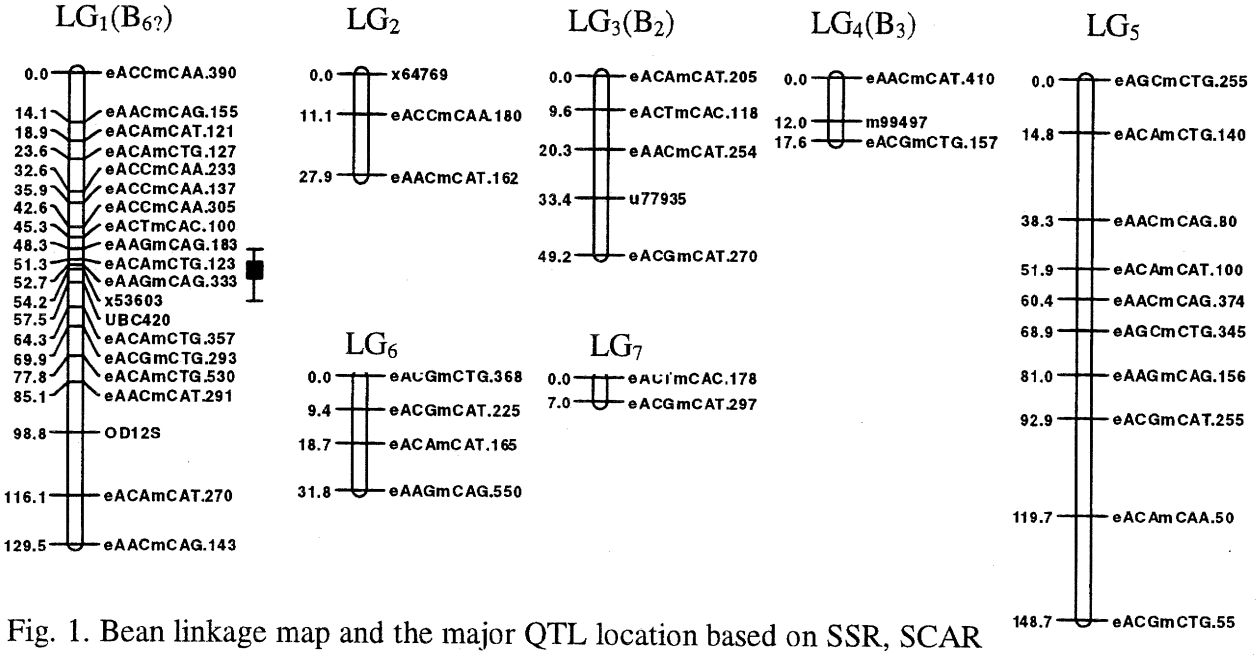

Fig. 1. Bean linkage map and the major QTL location based on SSR, SCAR and AFLP markers.

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