Detection and Mapping of RAPD Markers Associated with QTL Affecting Seed Size and Shape in Common Bean

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Bean seed weight and shape are important traits of different market bean classes. The former is also an important component of yield. Bean seed weight was negatively correlated with yield (White et al., 1992). Quantitative inheritance patterns of seed weight were reported by Sax (1923) and Vallejos and Chase (1991). Quantitative inheritance patterns of bean seed shape such as seed length and seed height were reported by Vallejos and Chase (1991).

An association was found between seed pigmentation determined by the dominant gene \( P \) and seed weight in common bean (Sax, 1923). Isozyme markers (Vallejos and Chase, 1991) and RFLP markers (Koinange et al., 1996) associated with seed weight were detected in common bean grown under one environment condition. A locus for seed protein (phaseolin) was also found to be associated with seed weight (Koinange et al., 1996). Isozyme markers associated with seed length and seed height were also identified (Vallejos and Chase, 1991). The isozyme, seed protein, and RFLP markers associated with bean seed weight offer prospects for marker-assisted selection in bean breeding programs for larger seed size. However, these markers are not convenient for breeders due to several limitations.

RAPD is an alternative molecular marker to overcome the limitations of isozyme and RFLP markers. RAPD markers associated with QTL affecting bean seed weight, seed length, and seed height have not been reported. It is desirable to record phenotypic data on a yield component under field conditions in different environments. The objective was to detect RAPD markers associated with QTL affecting bean seed weight, seed length, and seed height in a molecular marker-based linkage map in an RI population from the common bean cross PC-50 x XAN-159 grown under 2 greenhouse and 2 field tests. Pearson correlations between seed weight and seed length or between seed weight and seed height were also calculated.

Materials and Methods

PLANT MATERIALS. Seventy RI lines derived from a common bean cross PC-50 x XAN-159 were developed using the single-seed-descent breeding method (Arnaud-Santana et al., 1994). PC-50 (ovate seed shape) [Dominican Republic (DR)] has larger seed weight, shorter seed length, and greater seed height than XAN-159 (flat rhomboidal seed shape) [Centro Internacional de Agricultura Tropical (CIAT), Cali, Colombia]. The parents and RI lines were grown in two separate greenhouse (Winter and Summer) and two field (Wisconsin and DR) experiments using a randomized complete block design with 3 to 4 replications.

COLLECTION OF PHENOTYPIC DATA. The weight (g) of 100 seeds per line per replicate was recorded in all experiments. Ten seeds per line per replicate were used to record seed length (cm) and seed height (cm). The percentage of moisture content of the seed was 9.5±0.2% in two greenhouse and one field-Wisconsin experiments and 13.5% in field-DR.

LINKAGE MAP CONSTRUCTION. The linkage map of 180 RAPD markers and 3 morphological markers was developed by Jung et al. (1997). The logarithm of odds (LOD) score of 3.0 was used
as a linkage threshold with 0.3 as the maximum recombination fraction for linkage groups. Recombination fractions and Kosambi's mapping function were used to calculate map distances (cM) for ordered marker loci.

**QTL DETECTION.** Single-factor ANOVA for each pairwise combination of quantitative traits and marker loci was used to analyze the data for detection of QTLs affecting seed weight, seed length, and seed height. Loci with the lowest $P$ value per QTL were chosen and then were added in a stepwise regression to select the best set of markers ($P < 0.05$) for prediction of the total trait phenotypic variation explained by the detected QTL. The interval mapping method was also used to detect the locations of QTLs for the traits. A LOD score of 2.0 was used for the QTL threshold.

**Results and Discussion**

Continuous distributions for seed weight, seed length, and seed height were observed for RI lines indicating quantitative inheritance. Significant intermediate (0.67, 0.63, and 0.66) Pearson correlations were detected between seed weight and seed length. Significant high (0.78) correlations were found between seed weight and seed height.

One to 3 QTLs affecting seed weight explained 14% to 38% of the phenotypic variation based on the stepwise regression analysis and the interval mapping method. Two to 4 QTLs for seed length explained 27% to 40% of the phenotypic variation. One to 3 QTL associated with seed height explained 17% to 37% of the phenotypic variation. A RAPD marker M5.850 on linkage group 3 was consistently associated with seed weight, seed length, and seed height in all experiments, and accounted for 11% to 22% of the phenotypic variation for the traits. A RAPD marker BC420.600 on linkage group 5 was consistently associated with seed weight, seed length, and seed height in all experiments but not in the field-Wisconsin, and explained 7% to 13% of the phenotypic variation for the traits. A seedcoat color pattern marker (the C locus) on linkage group 1 and a RAPD marker N9.850 on linkage group 9 were also associated with seed weight, seed length, and seed height in some experiments. The RAPD marker BC420.600 was associated with both seed weight and common bacterial blight resistance detected by Jung et al. (1997) in this linkage map. RAPD markers and a seedcoat color pattern (the C locus) were detected here for the first time to be significantly associated with seed weight, seed length, and seed height in common bean. The RAPD markers associated with bean seed weight are expected to be useful in bean breeding programs for larger seed size.

**Literature Cited**


