

Mapping of QTL for Seed Size and Shape Traits in Common Bean

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Bean seed weight and shape are important traits of different market bean classes. One of the first associations found between a genetic marker and a quantitative trait was reported by Sax (1923) for the relationship between seed pigmentation (*P* gene) and seed weight in common bean. More recently three types of molecular markers have been used to study the genetics of seed weight in common bean including isozyme (Vallejos and Chase, 1991), RFLP (Koinange et al., 1996; Nodari, 1992) and seed protein markers (Koinange et al., 1996; Nodari, 1992). Isozyme markers have also been used to study the genetics of seed length and seed height by Vallejos and Chase (1991). These studies have contributed to our understanding of the genetics of seed size and shape and offer prospects for the use of molecular markers in the modification or maintenance of seed characteristics in bean breeding programs. In a molecular marker based analysis, Jung et al. (1997) detected RAPD markers associated with QTL for resistance to common bacterial blight (CBB). Our objective was to identify QTL for seed weight, length, and height segregating in a recombinant inbred line (RIL) population derived from the common bean cross 'PC-50' (larger seed weight) x XAN-159 (smaller seed weight).

Materials and Methods

PLANT MATERIALS. Seventy RILs derived from a common bean cross 'PC-50' x XAN-159 were developed using the single-seed-descent. 'PC-50' has larger seed weight, shorter seed length, and greater seed height than XAN-159. The parents and RILs were grown in two separate greenhouse experiments in Nebraska, and in field plots in the Dominican Republic and Wisconsin using a RCBD with 3 to 4 replications.

COLLECTION OF PHENOTYPIC DATA. The weight in grams of 100 seeds per line was recorded in all experiments. Ten seeds per line were used to record seed length and seed height in centimeters in two greenhouse experiments. Seed moisture content was 9.5% in two greenhouse experiments and 13.5% in two field experiments.

LINKAGE MAP CONSTRUCTION. The RAPD marker-based linkage map was originally developed by Jung et al. (1997) using 70 RILs of the same cross. Subsequently, to facilitate integration of this map with other RAPD and RFLP maps in bean, the segregation data were reanalyzed by Skroch (1998) with some markers being added and some omitted from the different linkage groups (LGs).

QTL DETECTION. Simple linear regression (SLR), for each pairwise combination of quantitative traits and marker loci, was used to analyze the data for detection of QTL affecting seed weight, length, and height for individual environments and the mean over environments. Significant differences in trait associations were based on *F*-tests ($P < 0.05$). Composite interval mapping (CIM) analysis was applied to the trait means and marker data to more precisely identify the locations of QTL (Zeng, 1994). Cofactors were selected based on the results of a forward stepwise multiple regression analysis (MRA) using the QTL Cartographer program.

Results and Discussion

Seventeen markers were detected to be associated significantly with seed weight in a single environment on the basis of the SLR analysis. Based on the results from the SLR analysis, CIM analysis was then applied to the trait means over environments. Five QTL affecting seed weight were detected on common bean LGs 3, 4, 6, 7, and 8. MRA indicated that these QTL explained 44% of the phenotypic variation for the trait. Three additional candidate QTL were also detected on common bean LGs 4, 5, and 8. All eight markers associated with these QTL were significant in a MRA, where the full model explained 63% of the variation among seed weight means. Two markers, AO15.700 and G08.1150 on LG 4, were consistently associated with seed weight in four individual environments and the mean over environments.

Twelve markers were identified to be associated significantly with seed length based on the SLR analysis. CIM results indicated that three and one QTL affecting seed length on LG 8 and 2 were identified, respectively. Three additional putative QTL were also identified on LGs 3, 4, and 11. The markers associated with the three seed length QTL on LG 8, and the QTL on LGs 2 and 11 were significant in a MRA with the full model explaining 48% of the variation among seed length means. Two markers, BC457.400 on LG 8 and O19.1400 on LG 11, were consistently associated with seed length in two individual environments and the mean over environments.

A total of 19 significant marker locus-seed height associations was found on the basis of the SLR analysis. CIM results indicated that three QTL affecting seed height were found on LGs 4, 6, and 11 and explained 36% of the phenotypic variation for trait means. Three markers, BC406.750, J20.750, and P08.1000 on LG 6, were consistently associated with seed height in two individual environments and the mean over environments.

Taken together the results of Koinange et al. (1996), Nodari (1992), Vallejos and Chase (1991), and the present study indicate as many as 12 QTL for seed weight on common bean LGs 1, 3, 4, 5, 6, 7, 8, and 9. Four of the seven QTL for seed length and two of three QTL for seed height also appeared to correspond to QTL for seed weight in this study. Four QTL for CBB resistance and for smaller seed size were found to be associated on common bean LGs 6, 7, and 8.

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