Mapping QTL with Molecular Markers

The improvement of quantitative traits has been an important goal for many plant breeding programs. With a pedigree breeding program, the breeder will cross two parents and practice selection until advanced-generation lines with the best phenotype for the quantitative trait under selection are identified. These lines will then be entered into a series of replicated trials to further evaluate the material with the goal of releasing the best lines as a cultivar. It is assumed that those lines which performed best in these trials have a combination of alleles most favorable for the fullest expression of the trait.

This type of program, though, requires a large input of labor, land, and money. Therefore plant breeders are interested in identifying the most promising lines as early as possible in the selection process. Another way to state this point is that the breeder would like to identify as early as possible those lines which contain those QTL alleles that contribute to a high value of the trait under selection. Plant breeders and molecular geneticists have joined efforts to develop the theory and technique for the application of molecular genetics to the identification of QTLs.

Molecular makers associated with QTLs are identified by first scoring members of a random segregating population for a quantitative trait. The molecular genotype (homozygous Parent A, heterozygous, or homozygous parent B) of each member of the population is then determined. The next step is to determine if an association exists between any of the markers and the quantitative trait.

The most common method of determining the association is by analyzing phenotypic and genotypic data by one-way analysis of variance and regression analysis. For each marker, each of the genotypes is considered a class, and all of the members of the population with that genotype are considered an observation for that class. (Data is typically pooled over locations and replications to obtain a single quantitative trait value for the line.) If the variance for the genotype class is significant, then the molecular marker used to define the genotype class is considered to be associated with a QTL. For those loci that are significant, the quantitative trait values are regressed onto the genotype. The R^2 value for the line is considered to be the amount of total genetic variation that is explained by the specific molecular marker. The final step is to take

those molecular marker loci that are associated the quantitative trait and perform a multiple regression analysis. From this analysis, you will obtain an R^2 value which gives the percentage of the total genetic variance explained by all of the markers.

The two types of populations that have been used to identify markers linked to QTLs are F2*3 families (or F3 families from F2 plants) and recombinant inbred lines. Each population type has advantages and disadvantages. The primary advantage of F2*3 families is the ability to measure the effects of additive and dominance gene actions at specific loci. Because RI lines are essentially homozygous, only additive gene action can be measured. The advantage, though, of the RI lines is the ability to perform larger experiments at several locations and even in multiple years. For many crops, it is not possible to generate enough seed to perform a multi-location experiment with population of F2*3 families.