Sudha M
Assistant Professor (Biotechnology)
Dept. of Plant Biotechnology
Centre for Plant Molecular Biology and
Biotechnology
Tamil Nadu Agricultural University
Coimbatore
Tamil Nadu
India - 641 003

Veera Ranjani R
Research Associate (Biotechnology)
Dept. of Plant Biotechnology
Centre for Plant Molecular Biology and
Biotechnology
Tamil Nadu Agricultural University
Coimbatore
Tamil Nadu
India - 641 003

Hemaprabha K
Assistant Professor (Biotechnology)
Dept. of Fruit Science
Horticultural College and Research
Institute
Tamil Nadu Agricultural University
Coimbatore
Tamil Nadu
India - 641 003

Corresponding Author
Sudha M
sudhatamil@gmail.com

Dissecting the Complex Agronomic Traits using the QTL Mapping Approach

Quantitative trait locus (QTL) mapping is an analysis of the number, genomic locations, effects, and interactions of quantitative trait loci (QTL). When examining a set of quantitative traits, QTL mapping looks at the link between genotype at various genomic regions and phenotype. Finding the chromosomal regions that significantly affect how quantitative traits differ among populations is the primary objective of QTL mapping. This localization is crucial for both the eventual identification of the implicated genes and our comprehension of the genetic mechanisms behind the variance.

INTRODUCTION

Finding the QTLs responsible for phenotypic variation that occurs naturally is the goal of genetic mapping. Linkage mapping and association or linkage disequilibrium (LD) mapping are two techniques that have been widely utilized in plant genetic mapping. In order to create mapping populations, linkage mapping, a traditional mapping technique, relies on genetic recombination. Many QTL have been cloned or marked during the past 20 years in numerous plant species using linkage mapping. Linkage mapping's drawbacks include its slow pace, poor allele richness, and relatively low mapping resolution.

Multiple factors such as genetic characteristics of QTL, size of the population, environmental effects and experimental error, frequently limit the ability to detect QTL. A QTL mapping study should therefore be independently confirmed. These confirmation studies may make use of similar parental genotypes or genotypes that are very similar to those used in the primary QTL mapping study in independent

populations. Occasionally, larger population sizes may also be used. In a few recent studies, it has also been suggested that QTL placements and effects should be evaluated in distinct populations because QTL mapping based on average population sizes results in low QTL detection power and high QTL effect bias. Unfortunately, QTL mapping studies are seldom confirmed because of limitations such a lack of research funds and time as well as lack of understanding of the necessity to confirm results.

META-ANALYSIS OF QTL

Even while QTLs for a number of similar attributes were identified, no shared markers could be found between these investigations, preventing direct comparisons from being made. There are limitations on the size of the detectable QTL effects, found QTLs are held up among families are limited to a specific population. Therefore, combining data from numerous researches using meta-analysis is one direction for QTL analysis. Even though comparative marker densities, variation in recombination rates across crosses, variation in gene densities throughout the genome, and other factors limit the level of resolution, combining QTL from various populations into a single map makes it easier to investigate their allelic relationships.

CONCLUSION

In order to pinpoint the genetic areas causing significant phenotypic variation, QTL mapping plays crucial role. New developments and improvements in marker technology, the incorporation of functional genomics with QTL mapping, and the availability of more high-density maps will have a substantial impact on future MAS research on QTL mapping and the application of QTL data for crop improvement.