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High Resolution Mapping of QTL

Bapsila Loitongbam[1], P.K. Singh[2], Sameer Upadhayay[2], S.R. Rathi[2] and Priyanka Irungbam[3]
[1]Department of Genetics and Plant Breeding, College of Agriculture, CAU (Imphal), Pasighat, Arunachal Pradesh
[2]Department of Genetics and Plant Breeding, Institute of Agricultural Sciences, BHU Varanasi
[3]Department of NRM, College of Horticulture and Forestry, CAU (Imphal), Pasighat, Arunachal Pradesh

SUMMARY

The preliminary aim of QTL mapping is to identify markers flanking to those QTLs that control the traits of interest. Even the closest markers flanking a QTL may not be tightly linked to a gene of interest due to the recombination between a marker and QTL, thus reducing the reliability and usefulness of the marker. High resolution mapping (or Fine mapping) is used to identify more tightly-linked markers by using large population sizes and a greater number of markers, Hence, high-resolution mapping of QTLs is used to develop reliable markers for marker assisted selection which is ideally <1 cM away from the target gene.

INTRODUCTION

High resolution mapping or Fine QTL mapping consists of identification of markers located very close to the concerned QTL by using larger population sizes and greater number of markers. It involves facilitating the occurrence of crossing over as close to the target QTL as possible. It is also of direct relevance to breeding since it makes QTL more easily integrated into marker-assisted breeding and into genomic selection. Fine mapping of QTL will increase the efficiency of foreground selection in introgression programs through MAS because the genomic region that has to be controlled is smaller. This will reduce the number of individuals that is required and the genotyping cost. Fine mapping enables to go very close to the gene which contributes highest to the total phenotypic expression. In other words, fine mapping reduces the chance of recombination between the marker and gene, hence MAS will be efficient and high chance of getting the gene through map based cloning. When we mapped a certain genomic region and if that region is complex then there would be high chance of recombination and hence, lose marker trait association. So, we need to go for fine mapping to reduce the chance of recombination and hence high marker trait association and efficient MAS. For this, it is always better to have large population size derived from the recombinants of the respective locus as it depends on the size of the target locus. High-resolution maps of specific chromosomal regions may be constructed by using NILs.

Factors Limit the Achievable of High Resolution Mapping

Marker Density

In QTL mapping, markers are evenly or densely distributed in the chromosome to identify the target gene. The more markers one has, the smaller the average interval size and, thus, the higher the map resolution. Therefore, high density markers in a chromosome are reliable for high resolution mapping.

Crossover Density

In high resolution mapping, recombinant chromosomes provide mapping information thereby; chromosome with high crossover density is needed.

QTL Detection Methods

There are different QTL detection method which one can infer the QTL genotype of a given individual or chromosome. Positioning a QTL with respect to a crossover requires knowledge of the QTL allele carried by the corresponding chromosome.

Molecular architecture of the QTL

Many QTL probably reflect the combined effect of not one, but several, linked QTLs. Approaching such a ‘composite’ QTL using a model that assumes a single location may result in distorted positioning.

Types of Molecular Marker Suitable for Fine Mapping

Microsatellite markers can be directly identified from the genomic sequences and suitable primers can be designed and used in fine mapping since they are simple and exchanged among laboratories. However, SSRs are not suitable for fine mapping since the frequency of polymorphism detected using microsatellite locus generally is <10%. Insertions or deletions (INDELs) or single nucleotide polymorphisms (SNPs) in both intergenic and coding regions might be more useful in fine mapping since they are far more efficient than microsatellites in detecting polymorphism.

CONCLUSION

Therefore, to identify more tightly linked markers to the target gene with a distance of < 1 cM high resolution QTL mapping with greater population size with more number of markers is needed.

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