

QTL Mapping for Crop Improvement

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Abstract

A quantitative trait locus (QTL) refers to the location of single or multiple loci (defined by markers) that controls the expression of a trait which can be measured on a quantitative (linear) scale. Location of such particular loci/regions on chromosomes is called QTL mapping which is based on the principle of co-segregation of marker locus and QTL. It requires the process of genotyping, phenotyping and finding association between these data using suitable mapping software. The identification and validation of QTLs governing important traits in plants is important for developing suitable varieties through marker-assisted breeding programmes.

Keywords: quantitative trait locus (QTL), marker locus, genotyping, phenotyping, mapping

Introduction

Trait which shows a continuous range of variation in a population and is more or less normally distributed is known as a quantitative trait. A quantitative trait locus (QTL) is the location of individual or multiple loci (defined by markers) that affects a trait that is measured on a quantitative (linear) scale. QTL stands for Quantitative Trait Loci, referring to genes which control the expression quantitative traits (Gelderman, 1975).

What is QTL Mapping?

⇒ This process of constructing linkage maps and conducting QTL analysis to identify genomic regions associated with quantitative traits is known as QTL mapping (Patterson, 1996).

What is done in QTL mapping?

⇒ Identify which regions of the genome affect the trait: where the QTLs are located?

⇒ Explain the QTL's effect on the trait:

- Amount of variation caused by a specific region for a particular trait
- Type of gene action associated with the QTL - whether additive, dominant or epistatic effect?
- Kind of allele is associated with the favorable effect

Principle of QTL of QTL Mapping

- ⇒ Co-segregation of marker locus and QTL.
- ⇒ Co-segregation is due to linkage between marker and QTL.
- ⇒ QTL analysis depends on linkage disequilibrium (non-random association of alleles at different loci in a given population).

Objectives of QTL mapping

- ⇒ Identification of the regions of the genome which affect the trait of interest.
- ⇒ Analyze the effect of the QTL on the respective trait.

Requirements for QTL Mapping

1. A measurable trait
2. mapping population- derived from parents that contrast for the trait(s) of interest
Eg. F₂, F_{2:3}, Recombinant Inbred Lines (RILs), Double Haploid Lines, Near Isogenic Lines (NILs)
3. Molecular markers- Polymorphic, co-dominant markers are desirable
Eg. RAPD, RFLP, SSR, AFLP, SNP etc.
4. A saturated linkage map based on molecular markers using software like MAPMAKER, JOINMAP
5. QTL Mapping Statistics (Software) like QTL CARTOGRAPHER

Steps in QTL mapping

1. Phenotypic evaluation of a relatively large number of plants from a segregating/mapping population.
2. Genotyping of the population.

The mapping population is divided into different genotypic classes using the markers based on the presence or absence of a particular marker locus.

3. Construction of genetic linkage map
4. Statistical analyses to identify the loci that are affecting the trait(s) of interest
 - To detect the tight linkage of a molecular marker to a gene of interest
 - Is there an association between marker genotype and quantitative trait phenotype?
 - Classify progeny by marker genotype
 - Compare phenotypic mean between classes (t-test or ANOVA)
 - Significance = marker linked to QTL
 - Difference between means = estimate of QTL effect

$$a = \frac{Q_+Q_+ - Q_-Q_-}{2}$$

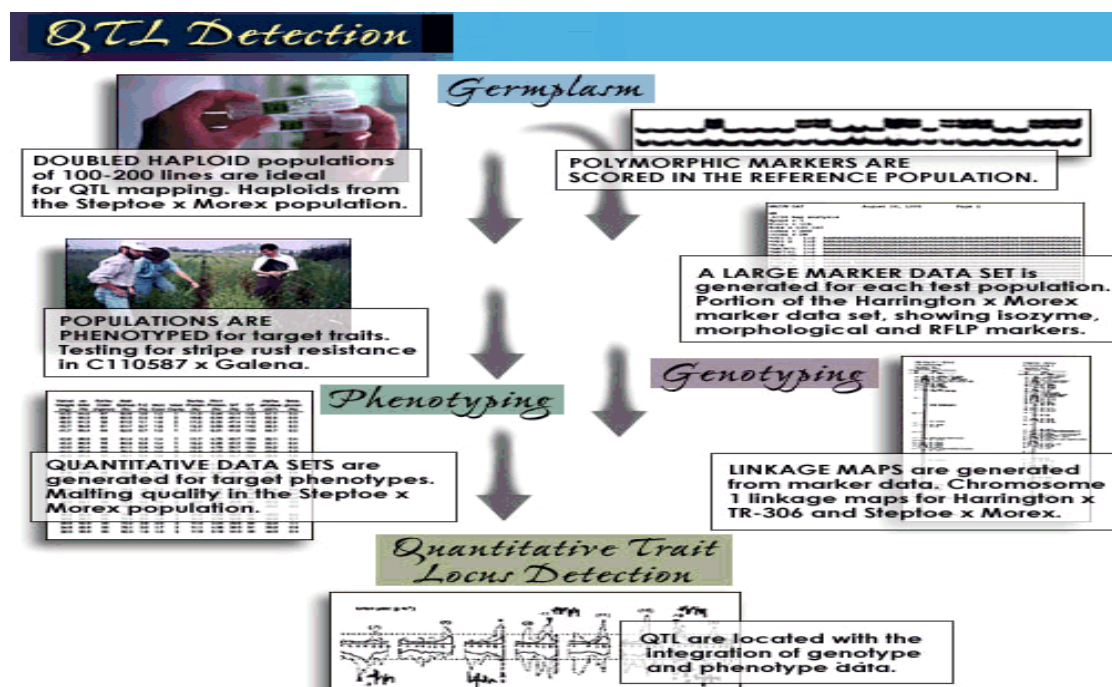


Fig 1. The steps involved in QTL mapping

Table 1. Statistical methods for QTL Analysis

Method	Programme	Significance
Single Marker Analysis (Single Point Analysis)	T-test, analyses of variance (ANOVA) and linear regression	Done for each marker locus independent of information for other loci
Interval mapping (Lander and Botstein, 1989)	MAPMAKER	Localizes QTL into marker intervals
Composite interval mapping (Zeng 1994; Basten <i>et al.</i> , 2001)	CIM in QTL CARTOGRAPHER	Uses adjacent markers and/or other QTL as cofactors
Multiple interval mapping (Zeng <i>et al.</i> , 1999)	MIM in QTL CARTOGRAPHER	Searches for multiple QTL simultaneously, using a single test of a chromosome
Bayesian Interval Mapping (Satagopan <i>et al.</i> , 1996)	BMAPQTL, also BIM in QTL CARTOGRAPHER	Can estimate QTL effect and position separately, use of a prior information may improve power
Bayesian Interval Mapping (Satagopan <i>et al.</i> , 1996)	QTL EXPRESS	Least squares regression in some outbred crossing designs including sibs and pedigrees

QTL databases for different crops

- ⇒ Gramene; www.gramene.org – different species like rice, wheat, maize, beets, *Brassica*, carrot etc.
- ⇒ Q- TARO Database; <http://qtaro.abr.affrc.go.jp/>- rice
- ⇒ PlantQTL- GE; <http://www.scbt.org/ctl2gene/new/>- rice and *Arabidopsis*
- ⇒ LIS- Legume Information System; <https://legumeinfo.org/>- adzuki bean, bean, lotus, Medicago, peanut, chickpea, cowpea, lupin, mungbean, lima bean, lupin, pea, soybean
- ⇒ Pulse Crop Database; <https://www.pulsedb.org/>- lentil, pea, chickpea, bean, cowpea, pigeonpea

Applications of QTL Mapping

After mapping and validation of QTLs, the knowledge of QTL mapping can be employed for:

- ⇒ Genetic analysis

To find the number of genes responsible for the expression of particular trait, location of genes/ QTLs on specific linkage groups, nature of gene action, linkage or pleiotropy, epistasis, transgressants and their genetic basis, genetic basis of heterosis and genotype x environment interaction.

- ⇒ Marker assisted selection (MAS)

markers found to be linked with QTLs can be used for development of new varieties through various marker aided breeding methods like Early Generation MAS, Marker Assisted Backcrossing, Marker Assisted Recurrent Selection, Combined MAS, Marker Assisted Gene Pyramiding etc.

- ⇒ Introgression breeding

With the availability of recent molecular marker based QTL analysis, breeders can make their attempt to transfer the favourable QTLs from wild species to cultivated varieties. For eg. Advanced Back Cross-QTL analysis (AB-QTL analysis) as suggested by Tanksley and Nelson (1996).

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