

Module 5: Genetic Maps and QTL Mapping

Introduction

Now that genetic markers have been introduced, and measures of genetic polymorphism explored, we begin the process of applying genetic markers to dissect quantitative traits, that is to identify QTL. In this module, we introduce the process of creating a linkage map and show how it is used for QTL mapping. Association mapping of QTL is introduced in Module 6. Both strategies are used for marker breeding (Modules 7&8). Just as different types of geographic maps are used for different purposes, so do different types of genome maps have different purposes. Genetic maps are built around the inheritance of linked genes. This module describes how segregating populations are used in creating genetic maps. When phenotypic data are combined with segregation data, correlations of marker genotypes and phenotypes are combined to infer the location of unseen QTL.

Key Messages

- Genome maps include cytological maps, physical maps, genetic maps, and in some cases, a whole genome sequence
- Genetic maps are built on the observation that alleles of linked genes tend to be inherited together.
- Genes affecting quantitative traits are called QTL, and their location can be inferred from segregation data, even if QTL are not observed directly
- QTL mapping requires that both markers and phenotypes be polymorphic, and measured in related individuals
- QTL mapping can be done without a genetic map, but using a genetic map is advantageous because the data are used more efficiently

Outcomes

Course attendees will:

- learn about different types of genome maps and how they are useful in different ways
- learn how to test for genetic linkage, and how genetic maps are constructed
- understand how different types of mapping populations are constructed, and how these populations can be useful
- see how mapping efficiency can be affected by availability of maps and markers, or by controlling phenotypic variation (experimentally or through clonal replicates)
- gain hands-on familiarity with mapping QTL given segregating marker and phenotypic data

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Outline

- I) Background and introduction to mapping and QTLs
- II) Types of maps
 - A) Cytological maps
 - B) Physical map: research applications and genome sequencing
 - C) Genetic (linkage) maps
- III) Creating linkage maps
 - A) Essential resources
 - 1) Genetic markers
 - 2) Mapping population: e.g. full-sib, half-sib, grand-daughter
 - B) Data acquisition and analysis
 - 1) Collecting and assaying marker genotypes
 - 2) Mapping steps
 - 3) Mapping software
- IV) Dissecting complex traits
 - A) By definition: complex traits are affected by many genes. How is this done?
 - 1) Terminology (with examples): QTL, ETL, ATL, etc; & QTN
 - 2) These are broad categories related to the type of trait being mapped
 - B) Key challenge: none of these phenotypes are observed directly as Mendelian traits. Presence/absence of alternative QTL alleles is inferred from measurements of quantitative phenotypes.
 - C) Experimental designs
 - 1) Field designs
 - 2) Trait measurement and reduction
- V) Approaches for QTL Mapping
 - A) Single marker analysis (without a map)
 - B) Interval mapping (with a map)
 - C) Interpretation and application
 - 1) Interpreting marker segregation and unseen QTL
 - 2) Verifying QTL and comparative maps of QTL
 - 3) How can QTL info be used in breeding
- VI) Lab: Genetic and QTL Mapping
 - A) Mapping Software (e.g. Joinmap, Mapmaker, Cri-map)
 - B) QTL Analysis (QTL Express)