

New genotype to phenotype models: The EU-SPICY project

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Introduction

The prediction of phenotypic responses from genetic and environmental information is an area of active research in genetics, physiology and statistics where a wealth of data is currently accumulating:

- Automated high throughput phenotyping tools
- New genotyping platforms
- Continuous monitoring of environmental conditions
- Wide array of -omics data become accessible

The SPICY Project

The SPICY project proposes a drastic rethinking of the quantitative genetic approach to modeling phenotypic variation in terms of genetic and environmental differences. Project aims:

- High-throughput phenotyping
 - Mobile imaging system, automatic image analysis
 - Chlorophyll fluorescence measurements
- Crop growth modeling
- Functional Quantitative Trait Locus Modeling
- Genetical genomics to identify potential candidate genes

Model crop: Pepper

- greenhouse crop with a continuous fruit production
- growth and yield models available
- genotyped RIL population available

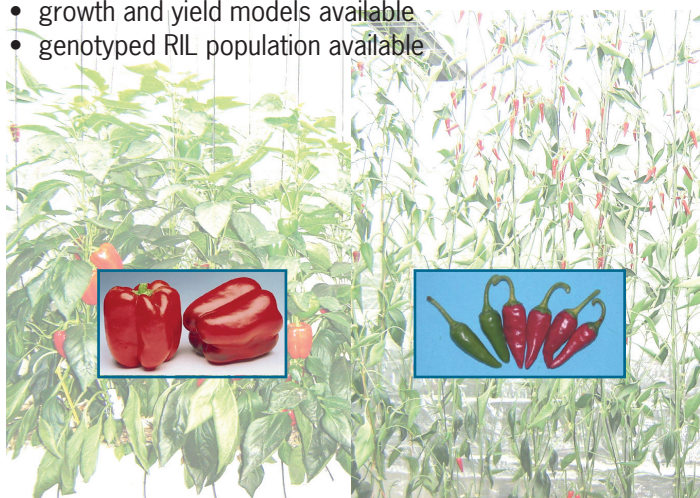


Figure 1. The parents Yolo Wonder and CM334 of the RIL mapping population (149 individuals).

Crop Growth Modeling

- Do we obtain more robust QTLs for model parameters (e.g. yield components), compared to QTL analysis on primary measurements of e.g. yield?
- Distribution of parameters is determined in several experiments with full RIL population
- Probabilistic sensitivity analysis is conducted
- Which model does best serve our goal: simple or complex?
 - Complex model is more flexible and physiologically sound
 - For simple model all parameters can be determined for all genotypes

Functional Quantitative Trait Locus Modeling

- Can we achieve accurate phenotypic predictions across a variety of genetic and environmental configurations?
- Develop genotype-to-phenotype models that integrate genetic, genomic, physiological and environmental data, for example:
 - Fit suitable growth curve \Rightarrow estimate parameters
 - Apply QTL models to growth curve parameter estimates as if these parameters were traditional response variables in QTL analyses
 - Adapt a Bayesian approach to account for uncertainties in these parameters while performing QTL analyses

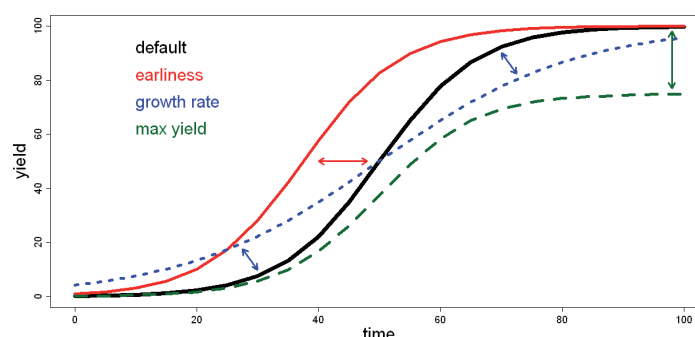


Figure 2. Example of crop growth model (logistic function, black line) where QTL may be mapped for model parameters "earliness" (red line), "growth rate" (blue line), and "maximum yield" (green line).

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