# WAGENINGEN UNIVERSITY
PLANT SCIENCES

Ecophysiological crop models for QTL analysis: a case study for Capsicum

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Introduction and aim

We conducted a simulation study, applying a crop growth model with 7 independent physiological parameters. The aim was to obtain and analyse genotype by environment (GxE) interaction for yield, while the parameters did not show GxE. In addition we introduced Quantitative Trait Loci (QTL) for these 7 parameters and performed a QTL analysis on simulated yield to assess QTLxE.

Model
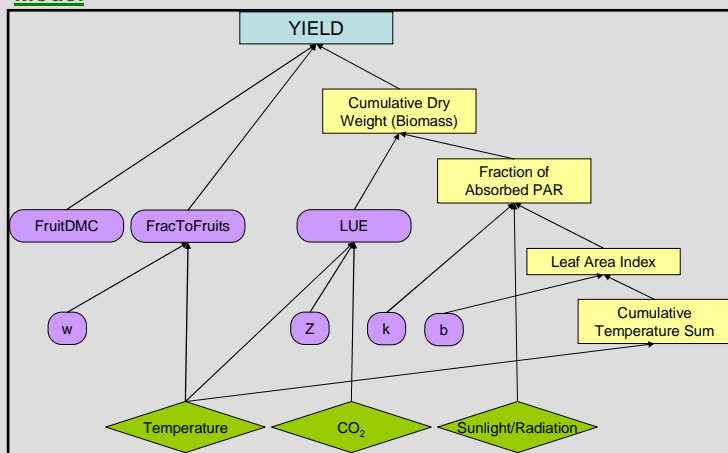
LUE = Light Use Efficiency; Z = temperature dependence of LUE; k= light extinction coefficient; b= slope for the leaf area increase with temperature sum; FracToFruits= fraction of biomass allocated to the fruits (harvest index); w = slope of the linear reduction in harvest index with temperature; FruitDMC = Fruit dry matter content

Simulations

- 36 environmental conditions:
  - 2 locations: Almería (Spain) and De Bilt (The Netherlands)
  - each location 3 years for daily global radiation
  - CO_2: 370 or 1000 µmol mol^{-1}
  - 15, 20 or 25 ºC
- growing season:
  - 10 September till 30 April (Spain): 232 days
  - 10 January till 30 November (Netherlands): 324 days

- 500 genotypes were simulated: random independent drawings from normal distributions for the 7 parameters (Table). For each genotype total yield in each of the 36 environments was simulated.

Parameter	Mean	Standard Deviation	QTL simulated on chromosome
LUE	0.67 (CO_2= 370 µmol mol^{-1})	0.134	
	0.85 (CO_2=1000 µmol mol^{-1})	0.170	2,7,8,10
Z	0.6	0.05	11
k	0.7	0.04	1
b	0.000378	0.0000378	3
FracToFruits	0.65	0.04	4
w	0.04	0.004	9
FruitDMC	0.0774	0.00508	5

Results

Simulated yields for 5 genotypes in 6 environments at ambient CO_2 (SP-15 means Spain, 15ºC). GxE (with cross-overs) is clearly shown.
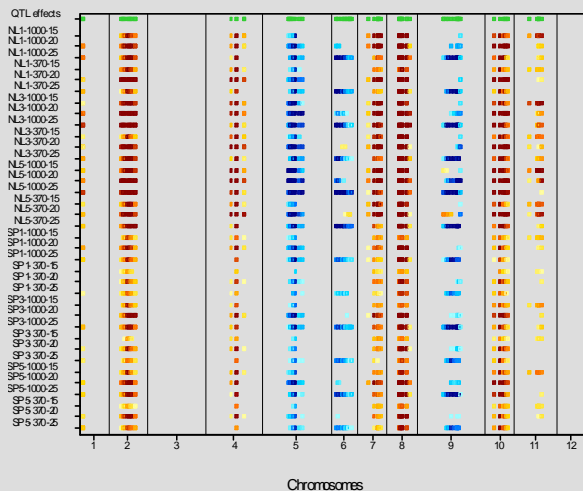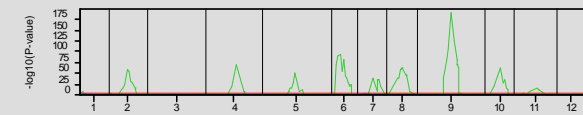
Genome scan for the yield data. The top panel presents the scan with the QTL effects. The red horizontal line is the 5% genome wide significance threshold. The bottom panel depicts the environment specific QTL effects for each environment. Blue (red) indicates that parent A (B) has significantly higher yield values. Darker colors mean stronger QTL effects.

Concluding remarks

➢ A physiological model with 7 parameters creates GxE (with crossovers).
➢ QTLs for yield had effects that depended on the environment, i.e. showed QTLxE, and occurred at loci known to contain QTL for physiological parameters underlying yield, that did not depend on the environment.
➢ QTLxE and GxE for yield is generated from physiological parameters without GxE.

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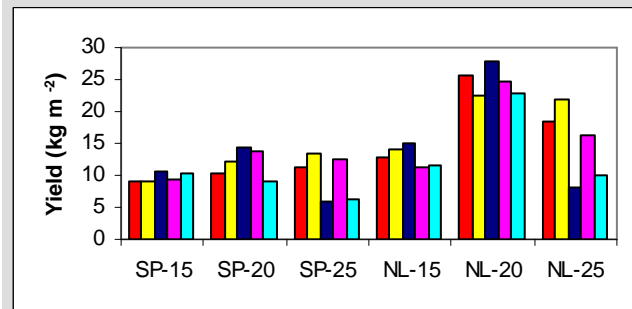2829-516 Caparica, Portugal
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