

Using modelling and GWAS for the phenotypic and genetic dissection of a complex trait, toward ideotype exploration

Case of rice early vigor response to drought

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Abstract

By formalizing elemental traits, their compensations and their genetic variability, crop modelling can support the phenotypic and genetic dissection of complex agronomic traits. It can accordingly be used to predict optimal trait combinations and theoretical margin for genetic improvement for a given environment (Cooper et al. 2014). The present study aims to develop and provide a proof of concept of such modelling approach applied to the case of rice early vigor and its response to drought. The plant growth model *Ecomeristem* (Luquet et al. 2012) was heuristically parameterized for each of 136 accessions constituting a japonica rice diversity panel, using phenotypic data acquired in a greenhouse at IRRI under two water conditions (well-watered vs. dry-down, Rebolledo et al. 2013).

Model parameters controlling leaf morphogenesis, transpiration rate, light conversion efficiency and their drought regulation, were *in silico* recombined within the range explored by the 136 accessions in order to generate a virtual population of 9000 individuals. Simulations of real and virtual phenotypes under three water treatments pointed out strong and similar tradeoffs between constitutive vigor and drought tolerance, estimated as shoot growth maintenance. A substantial margin for potential genetic improvement of vigor and drought resistance was however pointed out, depending respectively on parameter related to C sink strength and water or light use efficiency (Luquet et al., in press). These results are theoretical as they rely on the prediction of phenotypes from virtual genotypes, based on simple modelling (particularly on gas exchange) and genetic (free, additive trait combinability) assumptions. However they provide further insight into the way genetic and physiological information should be further combined into models toward ideotype exploration. This will be discussed with respect to the results of the Genome Wide Association Study recently performed using 12,221 single-nucleotide polymorphisms and model parameters estimated for the abovementioned 136 rice accessions.

Keywords: Model assisted phenotyping, C source-sink regulation, genetic diversity, heuristics,

ideotype prediction

References

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Additional information: *Please indicate:*

- **The Name of the speaker:** Delphine Luquet
- **Wished session** (tick the box)

Day 1- Session 2: Traits-base strategies for dealing with drought: Roots, genetic variability, consequences, modelling	
Day 1 – Session 2a: Leaf growth and architecture: genetic variability, consequences, modelling	X
Day 1- Session 2b: Grain abortion, modelling and genetic variability	
Day 1 – Session 2c: Transpiration efficiency across species	
Day 1 – Session 2d: Genetic variability of metabolome under drought, consequence on yield	
Day 1 - Poster session 3: Variation for target traits and phenotyping methods	
Day 2 – Session 4a: Dealing with Genotype x Environment interaction - QTLxE in networks of experiments	

<i>Day 2 - Session 4b: Dealing with Genotype x Environment interaction - Modelling G x E x M with explicit genotypic information</i>	
<i>Day 2 Poster session 5: QTL, positional cloning, allelic diversity and breeding application</i>	
<i>Day 2 – Session 6: Breeding for drought, strategies, choices</i>	