Modelling crop physiology and genetics to simulate Genotype x Management x Environment (GxMxE) interactions

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Background

- Productivity advance has occurred through improvement of G x M

*Duvick et al., 2004*
• Productivity advance has occurred through improvement of $G \times M$

• Complexity of the problem: Progress in crop improvement is limited by the ability to identify favourable combinations of genotypes ($G$) and management practices ($M$) in the target population of environments ($E$) given the resources available to search among possible combinations.
Background

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- Complexity of the problem: Progress in crop improvement is limited by the ability to identify favourable combinations of genotypes (G) and management practices (M) in the target population of environments (E) given the resources available to search among possible combinations.

- Here we seek an integrated approach to model G x E x M in order to aid crop improvement
Connecting understanding of traits

- Evaluating trait value -
Connecting understanding of traits – Example of wheat root system architecture

1. Drought adaptation in dryland wheat (G*E) for contrasting wheat varieties

   ![Image showing wheat varieties under drought conditions]

   Yield advantage = 19%

   ![Bar chart showing grain yield in 2004 and 2005 for Hartog and SeriMS2 varieties]

2. Field experiments => difference in water capture

   ![Image of field experiments showing water capture]

Connecting understanding of traits – Example of wheat root system architecture

Controlled experiments => Seri has a root system more compact

Connecting understanding of traits – Example of wheat root system architecture

Controlled experiments => Seri has - a root system more compact - a better “occupancy” at depth

Simulated effect of root traits modification on wheat yield

Modified root archi.
⇒ Gain in water-use efficiency for yield

⇒ Currently seeking genomic regions associated to these root traits
Point II - Modelling Emergent Properties
- Functional Modelling -
Modelling Emergent Properties – Example: Sorghum – Effect of dwarfing gene on staygreen

Simulation of tall & short sorghum hybrids

Analysis of C and N dynamics:
- higher RUE for taller hybrid
- similar N uptake

Modelling Emergent Properties –
Example: Sorghum – Effect of dwarfing gene on staygreen

Dwarfing gene results in staygreen

Staygreen: Emergent response

=> Importance of functional modelling, at the organ-level

Point III - Modelling the effects of the genetic variability
Modelling the effects of the genetic variability –
Example: Leaf expansion rate in maize

LER = dl/dt = (T-T₀)(a + b VPD_{air-feuille} + c \Psi)

a = \bar{a} + \Sigma \alpha \text{QTL}

b = \bar{b} + \Sigma \beta \text{QTL}

c = \bar{c} + \Sigma \gamma \text{QTL}

1 genotype \rightarrow 1 set of parameters of response curves (parameter ‘indep.’ of env.)

Estimation of the yield impact of organ-level QTL

The effect of single QTLs with similar effect on leaf growth may have substantially different effects on yield in different environments.

Point IV - Modelling breeding strategies
Modelling breeding strategies - Research framework

Genetic & Breeding info

Env. & Management info

Breeding model

Crop model

Crop Improvement Strategies
Point V - Modelling the plant environment
Integration of the plant interactions with their environment
Frequency of occurrence of the main env. types

**Main drought patterns**

- Identification of main drought patterns experienced by wheat
- Characterize region by frequency drought occurrence
  
  e.g. severe stresses (ET3-4) from 16 to 82%

Chenu et al 2011 (Wheat Breeders Assembly)
Env. Characterisation - Applications to breeding

- Weight breeding trials in respect to their representativeness
- Improve understanding of GxE interaction in genetic analysis
- Look for traits adapted to the main environment types

Summary

Whole-plant / Crop modelling for:

- Identification of traits of interest (e.g. wheat root architecture) with if possible reduced/removed context dependency (i.e. stable across environments, genetic background)
- Scaling up the impact of traits & gene/QTL on more integrated traits (e.g. yield) in various environmental situations (e.g. organ-level QTL in maize)
- Characterisation of the plant environment to unravel the GxE interactions (find some “hidden” physiological response; select for genotype better adapted to the target population of environments).
- Linkage with breeding models to fix more efficiently interesting genes and traits
- Test of the impact of genotype, management, future climatic scenarios and aid creation of future varieties, and identification of ‘best’ associated management
Implications

• Functional whole-plant modelling (if done well) can add significant value to crop improvement
• Major avenues are -
  – using predicted phenotypic value of genomic regions in target environments/managements for weighted selection in molecular breeding
  – informing phenotyping and identifying target genomic regions
• Key aspects are -
  – understanding and quantifying plant/crop functional dynamics
  – linking G-to-P (P-to-G) so as to reduce G and E context dependencies
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