Model assisted dissection of the genotype x environment interaction

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I Local adaptation of genotypes and variability of climatic scenarios

18 experiments, 2 years, 32 scenarios, still a small proportion of possible scenarios

I Local adaptation of genotypes and variability of climatic scenarios

Field experiments are one random sampling of the possible scenarios (among many other possible)

There is an infinity of "phenotypes" for one plant
- Variables ? (size, shape, rate...);
- When measured ? (morning evening, plant age or stage...), major effect
- which organ

Many of these trait can have positive, negative or no consequence on yield, depending of the scenario

Each of them brings QTLs of "tolerance", each of them with some relevance (how often ?)

Altogether :
80% of the genome covered by QTLs of drought tolerance

II Taking into account the scenarios : general approach

Dissection : genetic variability ?

Field network
Phenotyping platform + modelling : getting heritable traits in a range of scenarios
Genetic analysis of heritable traits

Experiments + simulation scenarios ?

In other terms
-Phenotyping platforms aim at disentangling the phenotype into genotypic characteristics that encapsulate the GxE interaction

models help to process the information

-Performances in the field are seen as results in a limited amount of scenarios

models help to predict performance in a larger set of scenarios
**III Dissection (getting heritable traits)**

Model-assisted phenotyping

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**III Dissection (obtaining reproducible information) : temperature**

Response to temperature common to several developmental processes

No genetic variability within species

Leaf elongation rate
Cell division rate
Duration of phenological phases
Germination rate

*NOT* photosynthesis / metabolism

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Maize tropical or temperate lines, several genetic groups
Also true for wheat, rice and 18 other species

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**Expression of different experiments with a common time frame**

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PhenoArch
http://bioweb.supagro.inra.fr/phenoArch/

Variation between lines ... and experiments !

Cabrera et al., np

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WE CAN REPRESENT DIFFERENT EXPERIMENTS WITH A COMMON TIME FRAME
III Dissection (obtaining reproducible information) : biomass accumulation

- Raw biomass not reproducible
- The relation intercepted light – biomass is
- Genetic differences in RUE can be estimated

Cumulative intercepted light

Plant biomass (g FW)
III Dissection (obtaining reproducible information) : leaf growth

Growth QTLs colocalise for several organs (shoots, roots, reproductive)

Consensus QTLs:

- Chrom 1
  - Leaf length
  - NIL 1 LER
  - NIL 2 LER
  - NIL 3 LER

- Chrom 4
  - Leaf length
  - NIL 1 LER
  - NIL 2 LER
  - NIL 3 LER

- Sillk DW
- Ear DW
- ASI
- Shoot DW
- Leaf length
- LERmax

Root diameter
Internode length
Shoot DW
Leaf length 4
Leaf length 6
LERmax

Dignat et al. 2013 PCE

III Dissection (obtaining reproducible information) : sensitivity of leaf growth

Sensitivity to evaporative demand reproducible between experiments (greenhouse, growth chamber, field)

Sensitivity to soil water status reproducible between experiments (greenhouse, growth chamber, field)

III Dissection (obtaining reproducible information) : sensitivity of leaf growth

Maize : a large range sensitivities in collections of lines (mapping populations)

\[
d/dt = \left(T - T_0\right) \left(a - b \cdot VPD_{\text{w}} - c \cdot \Psi\right)
\]


MetaQTLs of sensitivity of leaf growth to water deficit,

Commonality of mechanisms/causal polymorphisms between the effects of ev. demand and drought

Incidentally, the a b c model Reymond et al. 2003 is wrong but useful

Introgression lines
1% of the genome appreciably changes the sensitivity

"Dissection":
2. analyse détaillée de QTLs

Env. conditions
Leaf elongation rate

Sensitivity platform

Stable QTLs can be identified in platforms, tested with NILs
QTLs of platforms have a better value than expected
- different organs (which ones ?)
- Different processes (why ?)
- Platform and field

Climatic data

Morphogenetic programme

Chapuis et al. 2012 EJA

Col. Hammer, Chapman U. Queensland
Conclusion

Dissection: is this trait genetically variable? Determinisms?

Allele testing: When and where the trait is favourable?

Adaptation: result of a frequency analysis (not "mean" climate)
Field experiments are one random sample of the possible scenarios
Any climatic scenario can occur in any location

Phenotyping platforms: estimate reproducible characteristics of genotypes, which allow simulation in a wide range of scenarios. “dissection”

Colocations of QTLs, a potent tool for modelling
- Growth of different organs of the plant, common genetic parameters (trivial: different leaves, non trivial: leafs/silks/young ears)
- Response to different cues (soil water content / evaporative demand)
- Platform/field: use for analyze field experiments the parameters estimated in platforms

Simulation of QTL effects: see Hammer and Messina’s presentations