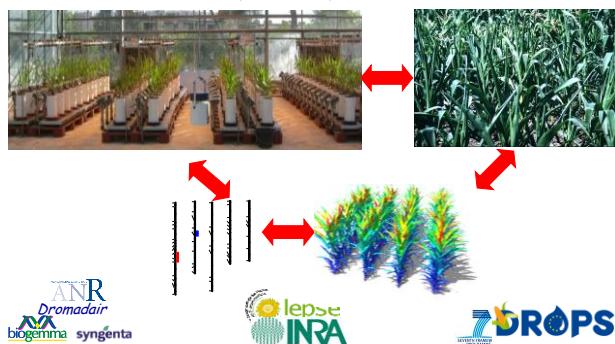
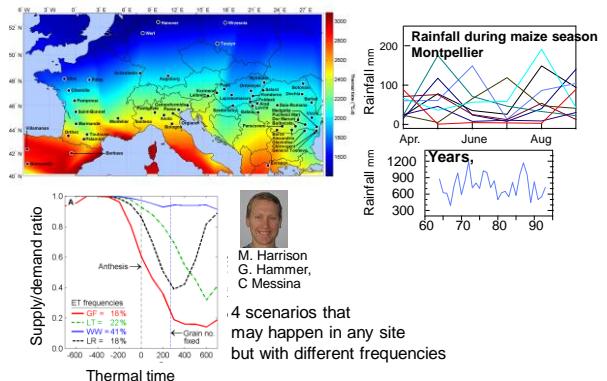


## Model assisted dissection of the genotype x environment interaction

F Tardieu, LI Cabrera, C. Welcker INRA



### I Local adaptation of genotypes and variability of climatic scenarios

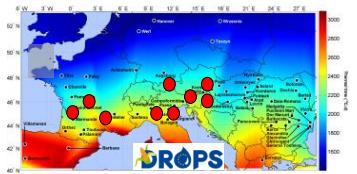


M. Harrison  
G. Hammer,  
C. Messina

4 scenarios that  
may happen in any site  
but with different frequencies

### 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

We shall never represent this variability via a network of experiments :  
10s - 100s experiments needed

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

There is an infinity of "phenotypes" for one plant

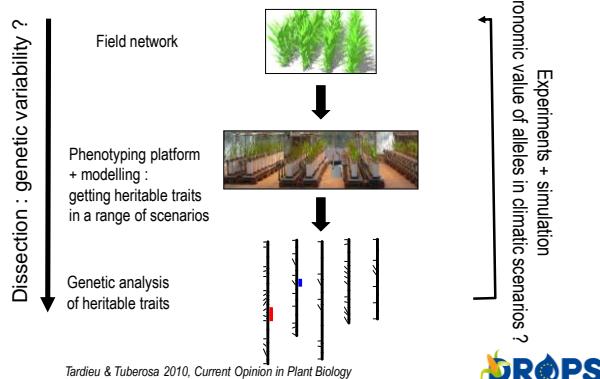
- Variables ? (size, shape, rate...);
- When measured ? (morning evening, plant age or stage...) major effect
- which organ

**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



### II Taking into account the scenarios : general approach

In other terms

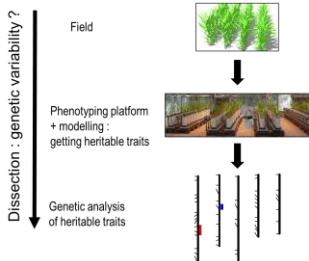
- Phenotyping platforms aim at disentangling the phenotype  
into genotypic characteristics that encapsulate the GxE interaction

*models help to process the information*

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

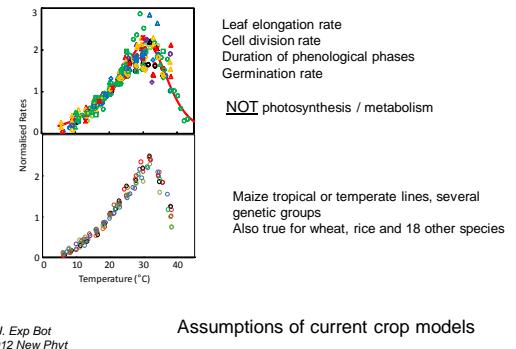
*models help to predict performance in a larger set of scenarios*

### III Dissection (getting heritable traits) model-assisted phenotyping



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

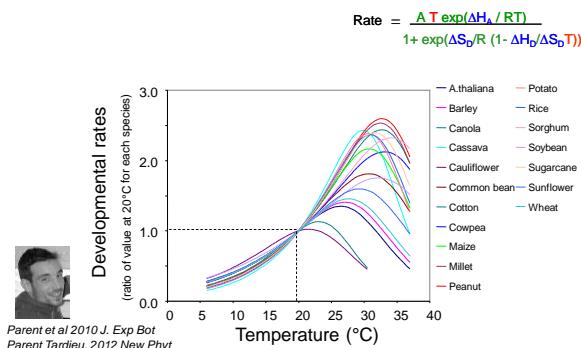
Response to temperature common to several developmental processes  
No genetic variability within species



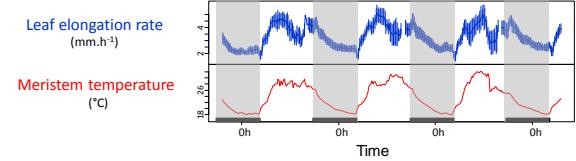
Assumptions of current crop models

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

A unique formalism for 17 species, 2 parameters  
And a new calculation of thermal time (days at 20°C)

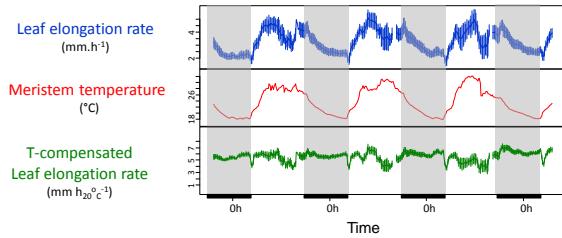


#### III Dissection (obtaining reproducible information) : temperature



**WE CAN REPRESENT DIFFERENT EXPERIMENTS WITH A COMMON TIME FRAME**

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



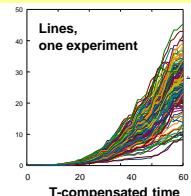
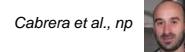
**WE CAN REPRESENT DIFFERENT EXPERIMENTS WITH A COMMON TIME FRAME**

#### III Dissection (obtaining reproducible information) : biomass accumulation

##### PhenoArch

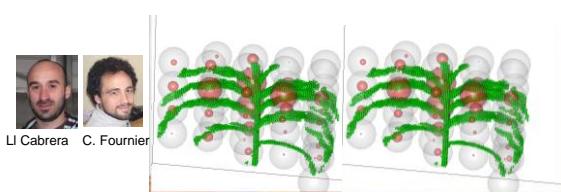
<http://bioweb.supagro.inra.fr/phenoArch/>

Variation between lines  
... and experiments !



### III Dissection (obtaining reproducible information) : biomass accumulation

Calculation of intercepted light

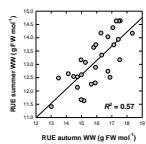
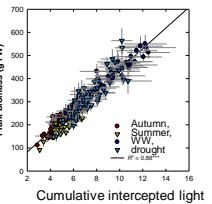


### III Dissection (obtaining reproducible information) : biomass accumulation

- Raw biomass not reproducible

- The relation intercepted light – biomass is

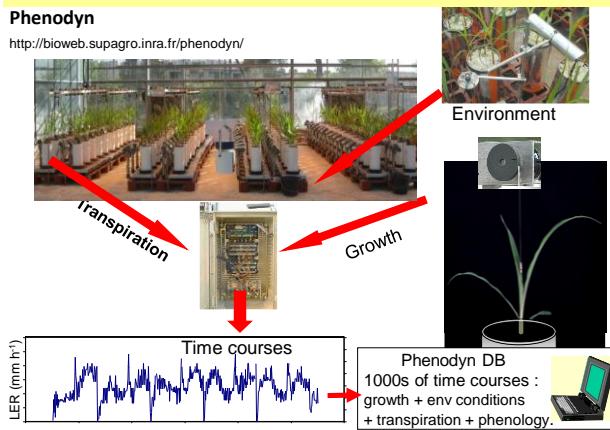
- Genetic differences in RUE can be estimated



### III Dissection (obtaining reproducible information) : leaf growth

#### Phenodyn

<http://bioweb.supagro.inra.fr/phenodyn/>

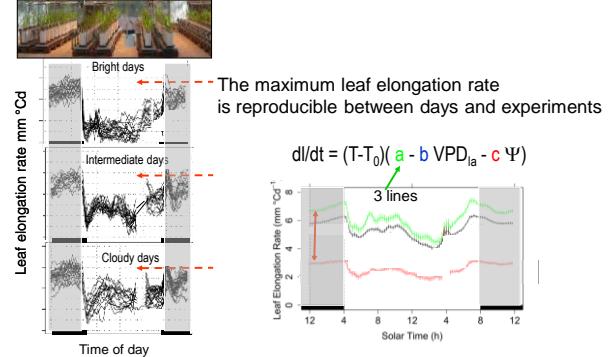


### III Dissection (obtaining reproducible information) : leaf growth



Bright days  
Intermediate days  
Cloudy days

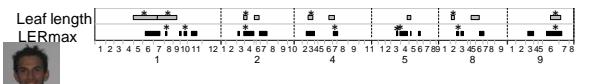
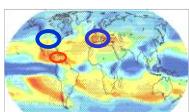
The maximum leaf elongation rate is reproducible between days and experiments



Highly variable in a diversity panel : 3.8 to 7 mm  $^{\circ}\text{Cd}^{-1}$   
Heritability : 0.8

### III Dissection (obtaining reproducible information) : leaf growth

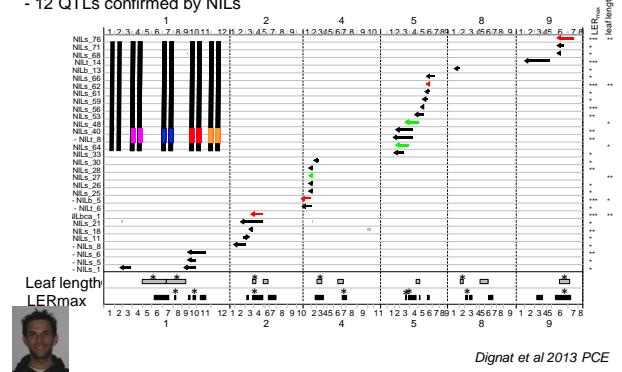
- 9 consensus QTLs in three mapping populations



### III Dissection (obtaining reproducible information) : leaf growth

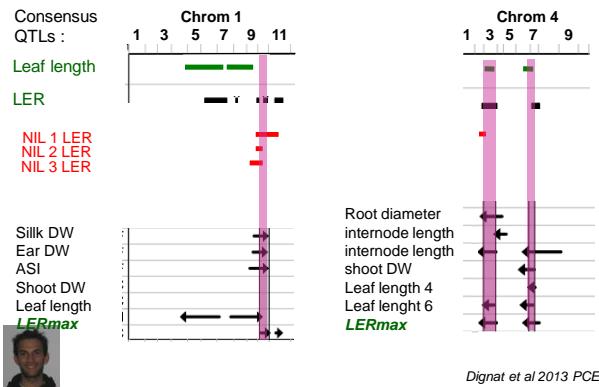
- 9 consensus QTLs in three mapping populations

- 12 QTLs confirmed by NILs



### III Dissection (obtaining reproducible information) : leaf growth

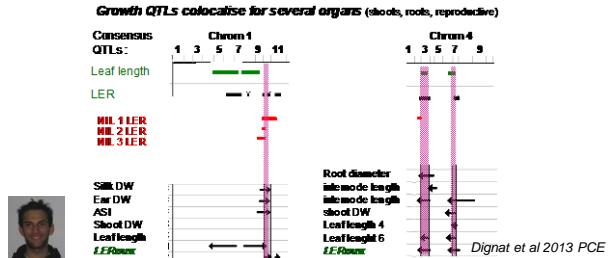
**Growth QTLs colocalise for several organs** (shoots, roots, reproductive)



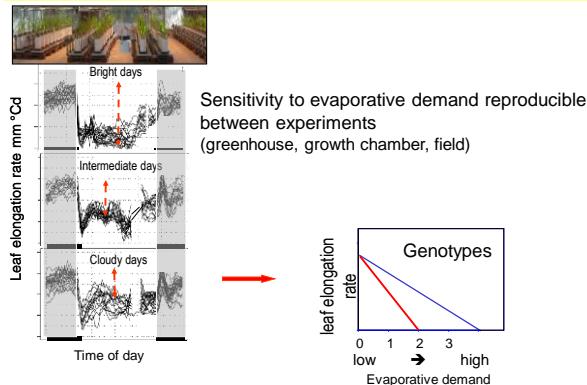
### III Dissection (obtaining reproducible information) : leaf growth

- Common mechanisms / polymorphisms control the expansions of different organs (pleiotropy ? common processes ? causal links ?)

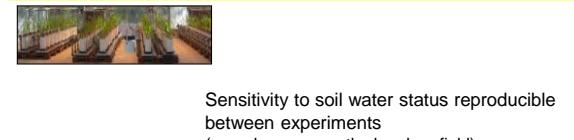
- What we learn from a QTL analysis in a platform on one organ is relevant for other organs



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

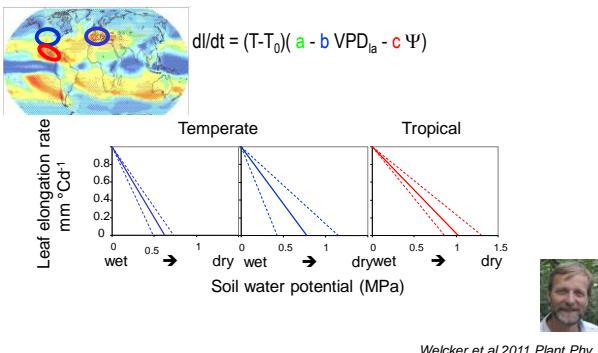


### III Dissection (obtaining reproducible information) : sensitivity of leaf growth



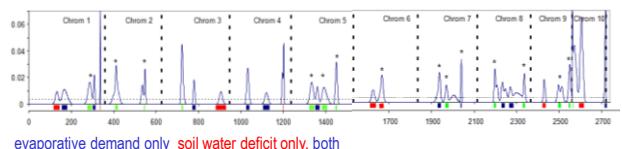
### III Dissection (obtaining reproducible information) : sensitivity of leaf growth

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



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

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

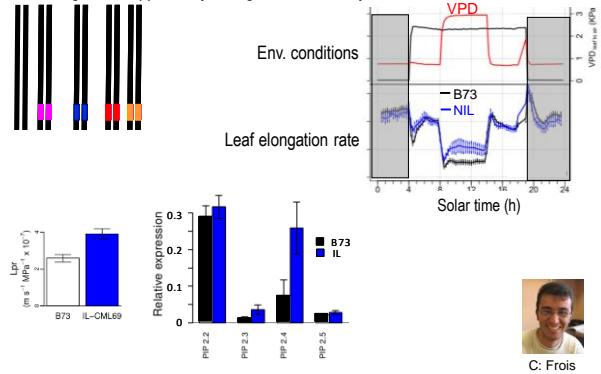
Welcker et al.2011 Plant Phy.



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

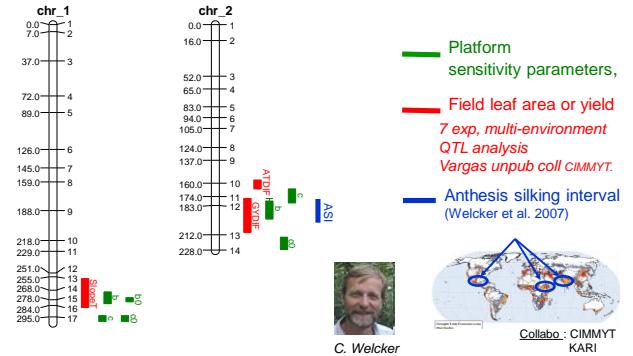
Introgression lines

1% of the genome appreciably changes the sensitivity



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

QLTs of sensitivity in platforms colocalise with QTLs of yield or leaf area in dry fields



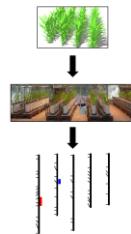
### III Dissection (getting heritable traits) model-assisted phenotyping

Raw phenotypes are messy, need work to identify relevant variables

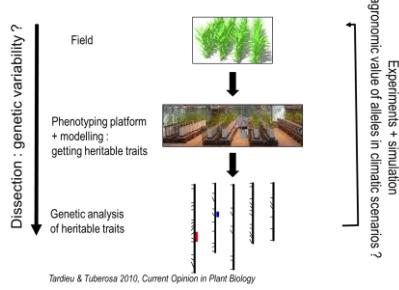
Stable QTLs can be identified in platforms, tested with NILs

QTLs of platforms have a better value than expected

- different organs (which ones ?)
- Different processes (why ?)
- Platform and field

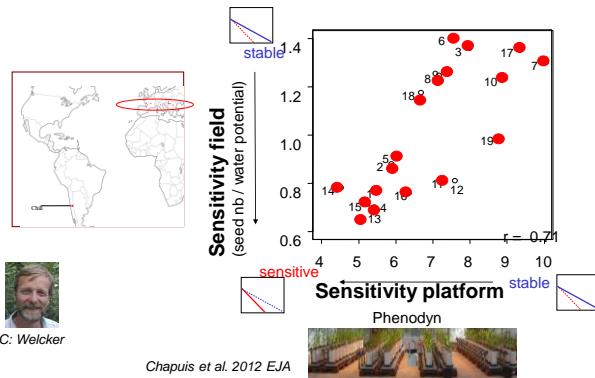


### IV From platforms to fields experiments and simulation models



### IV From platforms to field : experiments and simulation models

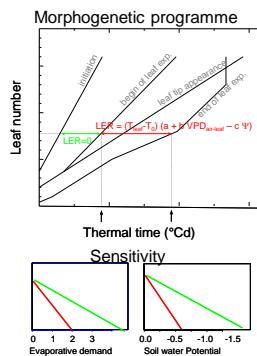
#### Sensitivity to water deficit in field and platforms



Chapuis et al. 2012 EJA

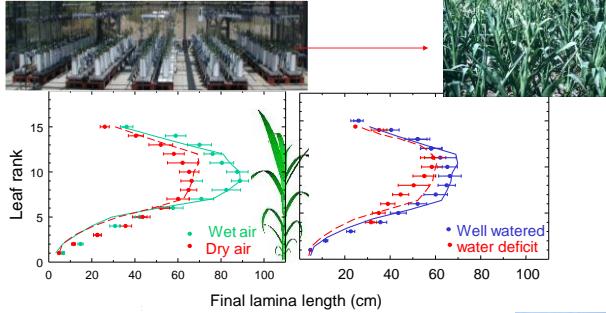
### IV From platforms to field : simulation models

#### Climatic data



Chenu et al. 2008 Plant Cell Environment 31, 378–Col. Hammer, Chapman U. Queensland

#### IV From platforms to field : experiments and simulation models

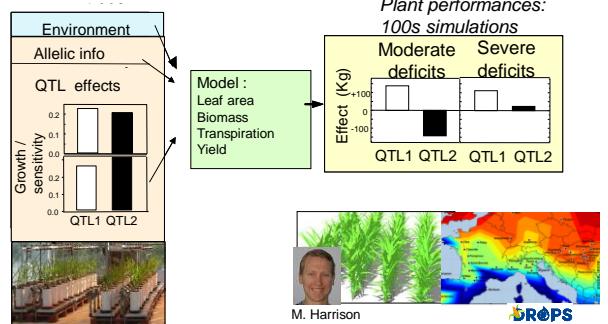


Chenu et al. 2008 *Plant Cell Environment* 31, 378–



#### IV From platforms to field : experiments and simulation models

##### Yield simulation from QTLs identified in platforms :

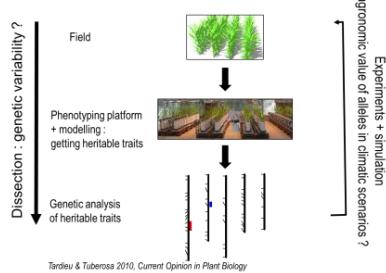


Chenu et al. 2009 *Genetics*, Tardieu and Tuberosa 2010 *Current Opinion Plant Biol*

#### Conclusion

Dissection : is this trait genetically variable ? Determinisms ?

Allele testing : When and where the trait is favourable ?



#### Conclusion

**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 : leaves/silks/young ears)
- Response to different cues (soil water content / evaporative demand)
- Platform / field : use for analyse field experiments the parameters estimated in platforms

**Simulation of QTL effects** : see Hammer and Messina's presentations