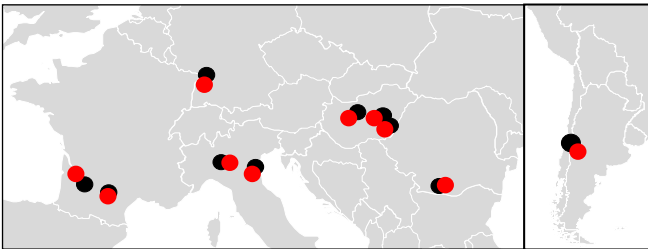


Multisite prediction of yield based on phenomics, genomic prediction and environmental information

F. Tardieu

Rationale of EMPHASIS and EPPN²⁰²⁰



A tension between genetic variability of

- “mechanisms” (organ, minutes)
- yield (canopy, months)

‘Understand’

‘Dissect’

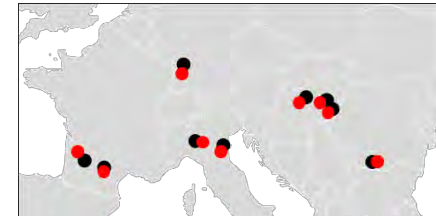
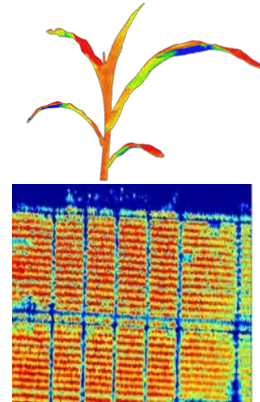
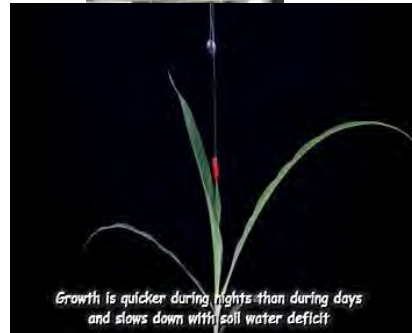
‘Predict’

Why so many installations ? different categories of installations are required

A tension between genetic variability of

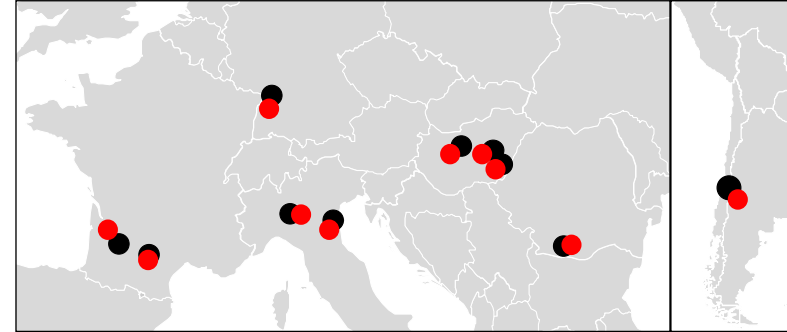
- “mechanisms” (organ, minutes)
- yield (canopy, months)

	<i>High precision platforms</i>	<i>High throughput platforms (controlled or field)</i>	Field multi-environment network
	‘Understand’	‘Dissect’	‘Predict’
Level of organization	Cell- Organ Minute/days	Plant or Canopy Minute to weeks	Canopies in a range of environments Weeks to months



PHENOME
Réseau Français
Phénomique végétale
F P P N

EMPHASIS



Sensor networks, remote sensing and European grids:
*One can measure or estimate environmental conditions in any field
 + combine with simple experiments + databases + modelling*
Is this affordable phenotyping ?

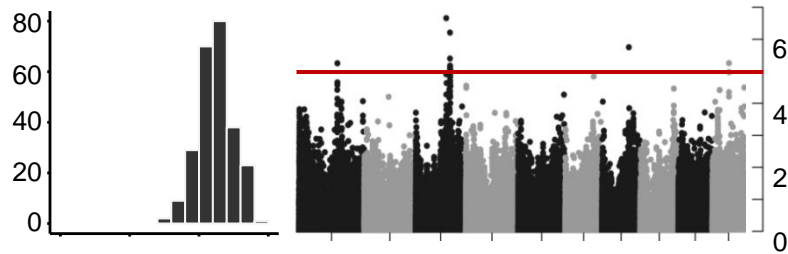
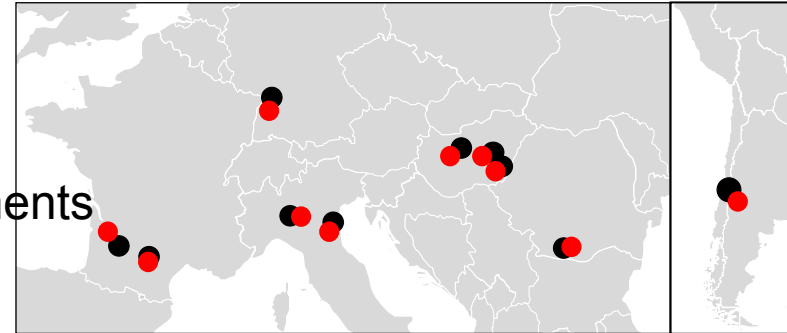
Example:

GWAS in 40 European fields. Environment + yield components

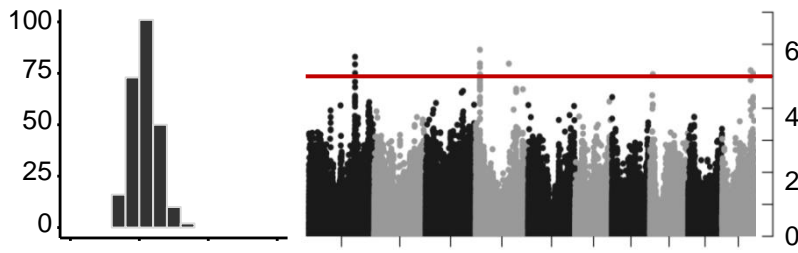
Affordable phenotyping : yield + sensor networks + modelling

252 genotypes
 950k polymorphic markers
 Yield variations from 5 to 12 T ha⁻¹

16 fields
 X
 2 years
 X
 2 W treatments

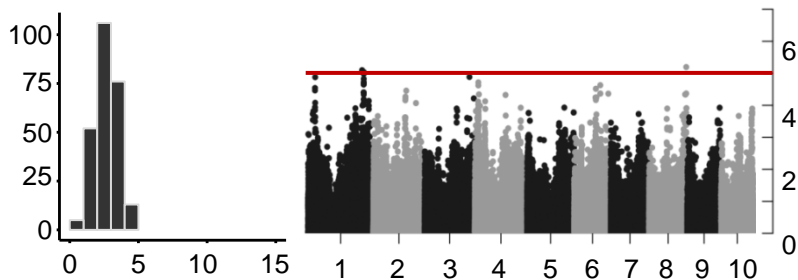


WW, cool



WW, hot

*490 significant SNPs,
 few in common*

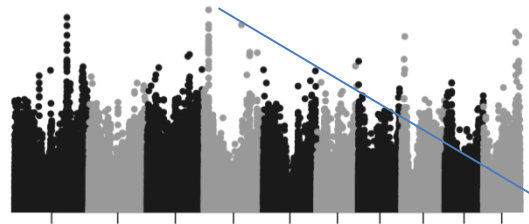
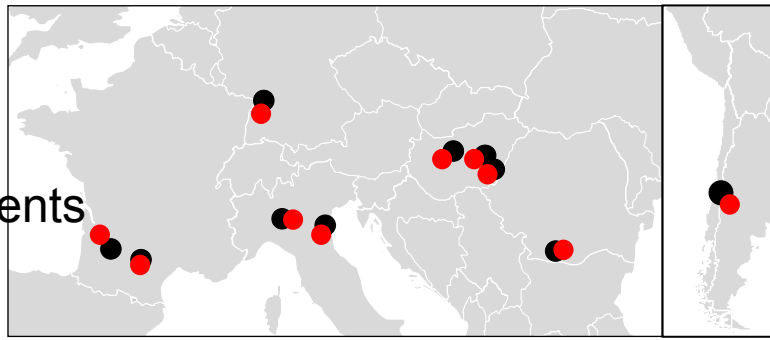


WD, hot

Grain Yield (t ha⁻¹)

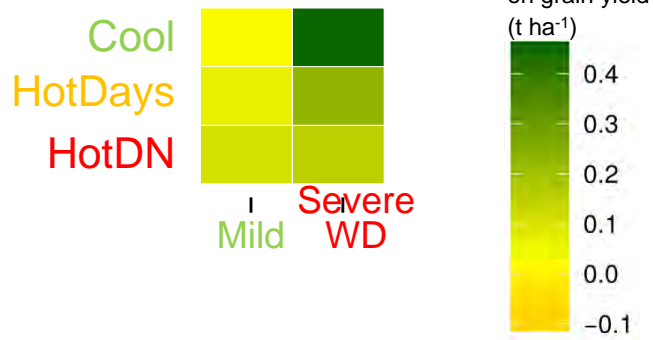
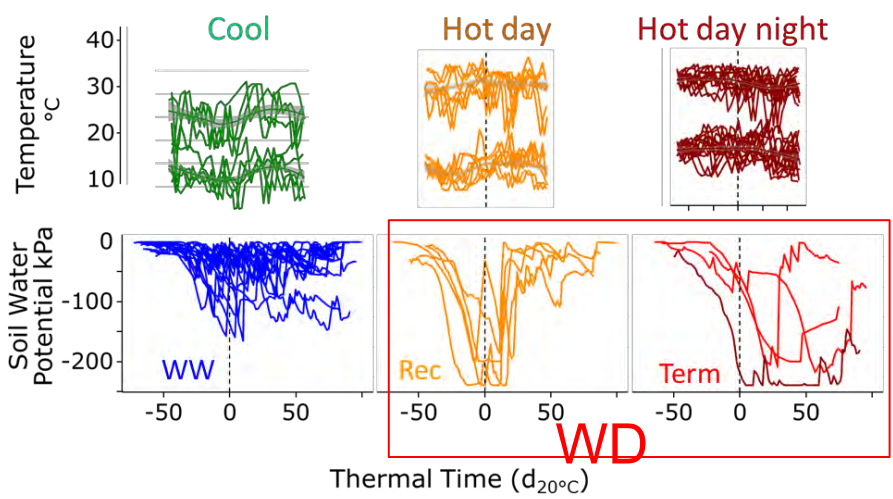
Affordable phenotyping : yield + sensor networks + modelling

16 fields
 X
 2 years
 X
 2 W treatments



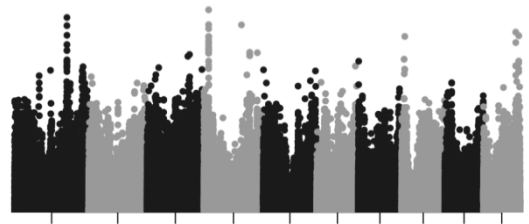
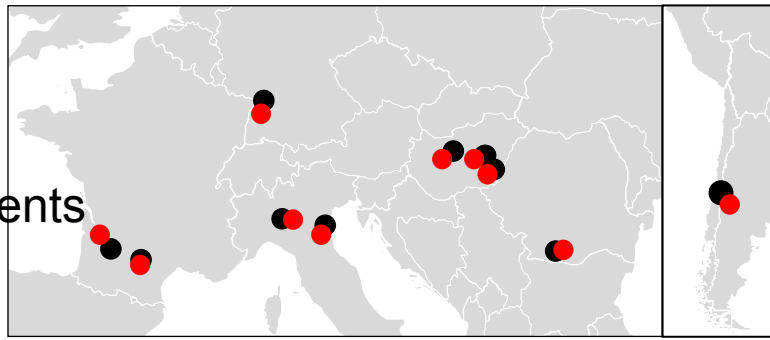
Allelic effects 1 QTL. each square, one scenario

DROPS
 Coll van Eeuwijk
 Charcosset

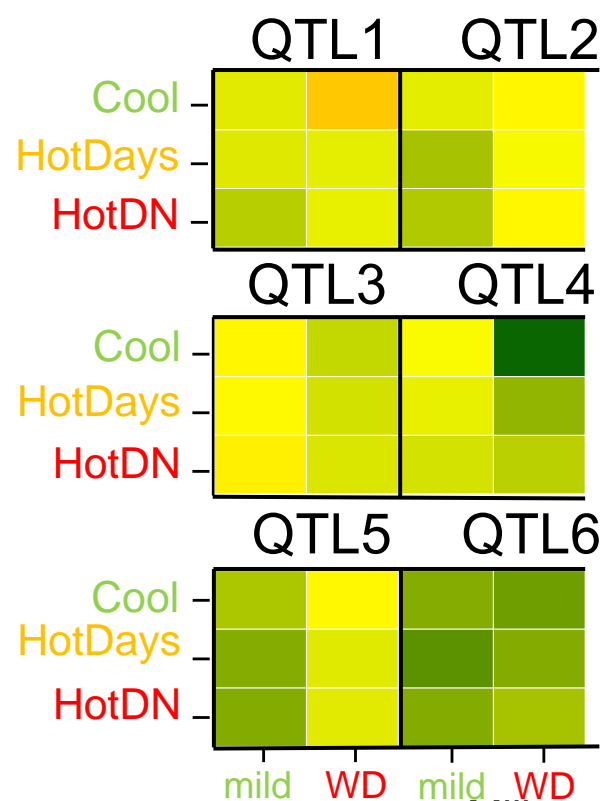
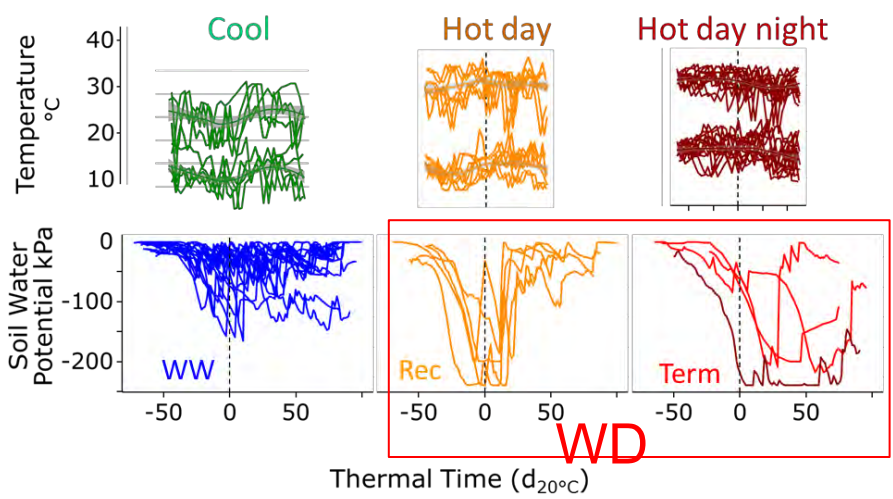


Affordable phenotyping : yield + sensor networks + modelling

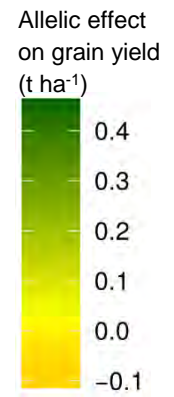
16 fields
 X
 2 years
 X
 2 W treatments



Allelic effects 6 QTL. each square, one scenario



Coll van Eeuwijk
 Charcosset



Affordable phenotyping : yield + sensor networks + modelling

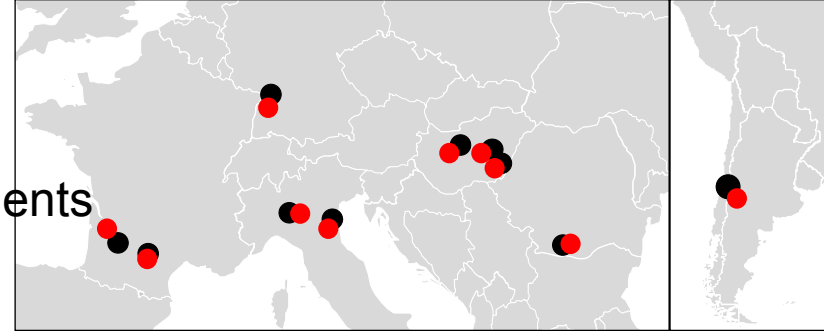
16 fields

X

2 years

X

2 W treatments



***Environmental sensor outputs are part of phenotyping:
Environmental scenarios allow dissecting/predicting the GxE interaction***

***Phenotyping: Sensor networks + yield components + stat analysis
(cheap, but not for data analysis)***

Sensor networks and weather grids are ‘game changers’

- Environment captured in all European fields
- Make sense of simple information (yield, durations) in a range of environmental scenarios if combined with statistical and process-based modelling
- Progress in remote sensing will bring more information

... we are in the era of big data ; breeders already do that.

This is part of EMPHASIS

- *‘Simple phenotyping in field networks’*
- *‘Modelling’*
- *‘Information system’*

‘Proper’ Phenomics needs to bring added value to this
largely the role of the methodological part of EPPN²⁰²⁰

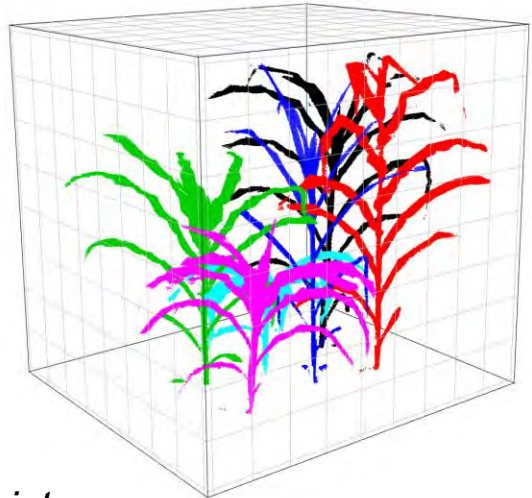
Need to simulate the behaviour of 100s genotypes in 100s scenarios

Genomic prediction : simulation of yield based on genomic info
environment needs to be taken into account

Where is Phenomics ?

Measure genotypic parameters of models

PhenoArch 1680 → 2300 plants



Cabrera et al. 2016 New Phytologist

Combining phenomics and modelling : yields of 100s genotypes

Parameter: Light interception and radiation use efficiency

Images analysis



Individual 3D reconstruction



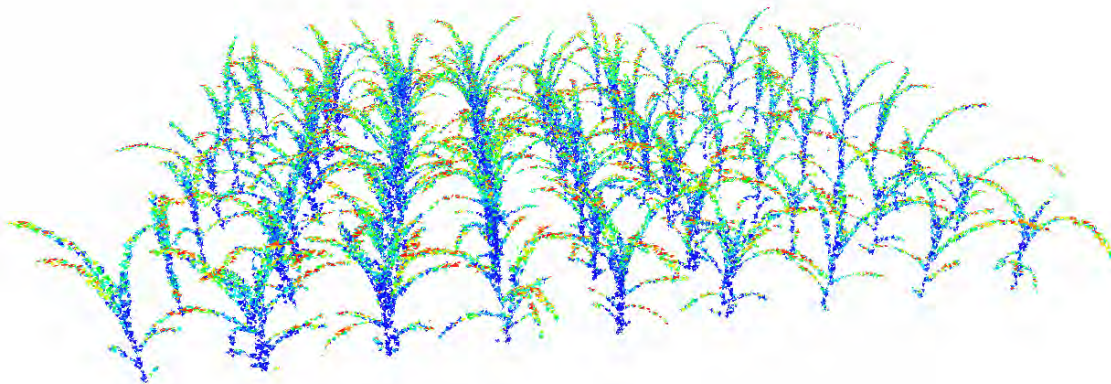
Multi-view RGB images



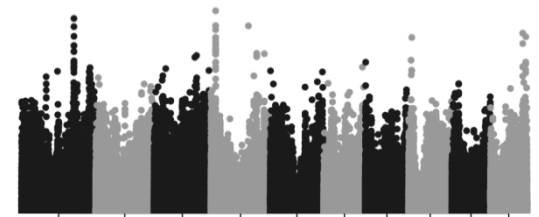
Side image selection



Binarised image



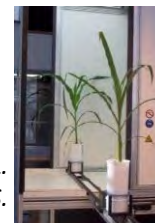
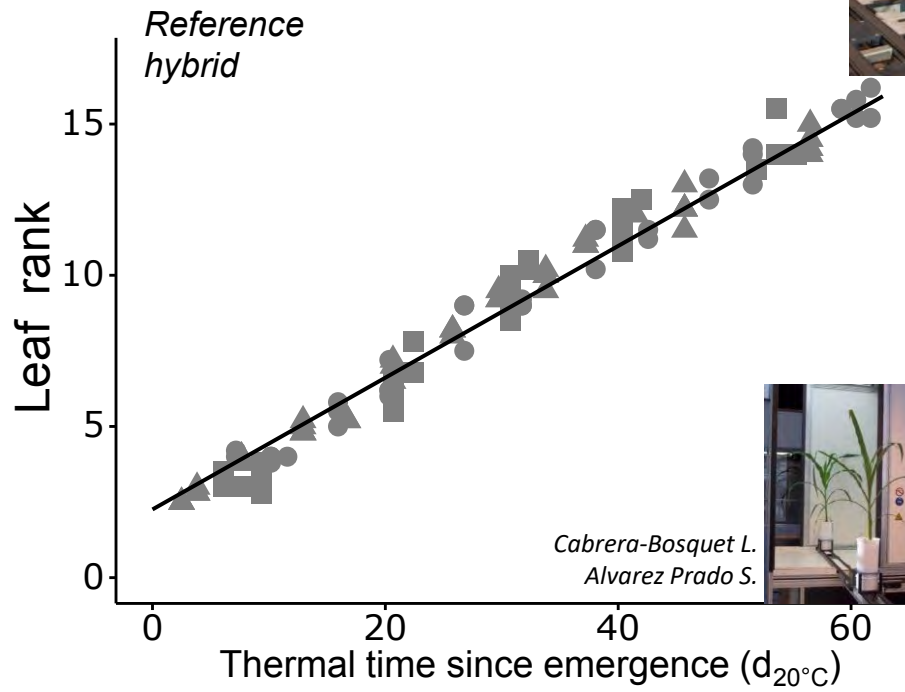
Light interception of the canopy



Genetic dissection

Combining phenomics and modelling : yields of 100s genotypes

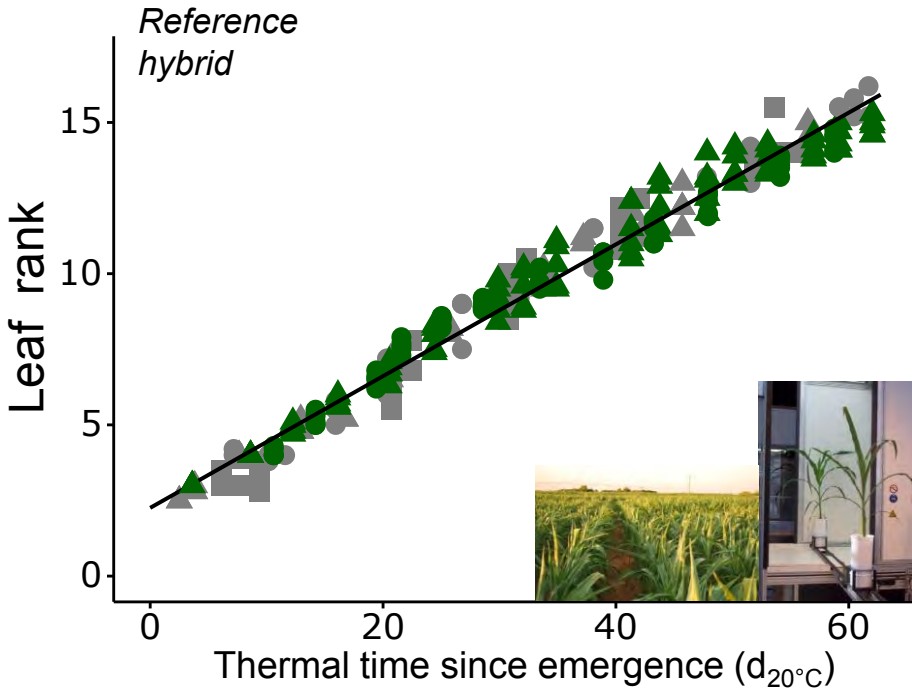
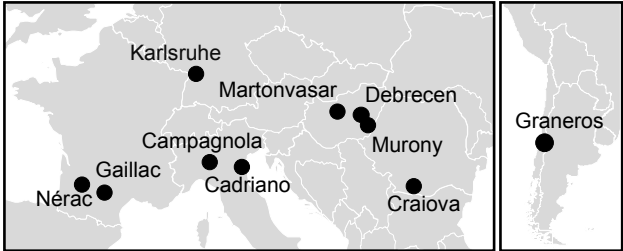
Parameter: phenological stages



- ▲ Phenoarch Winter13
- Phenoarch Spring13
- Phenoarch Spring12

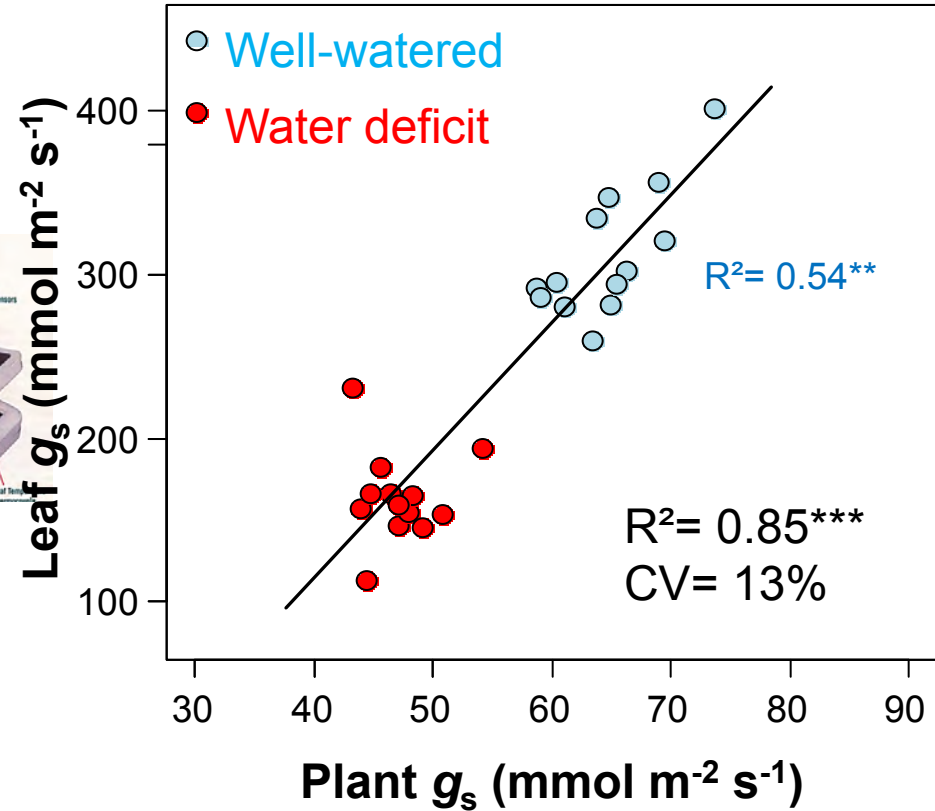
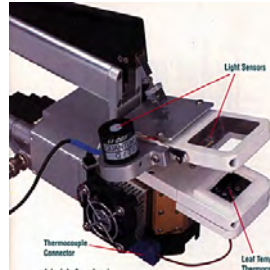
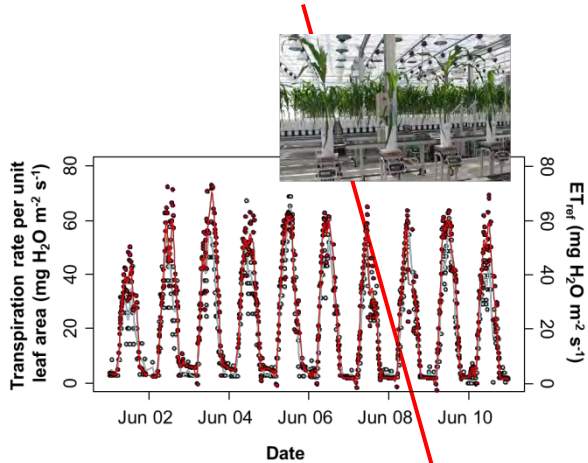
Combining phenomics and modelling : yields of 100s genotypes

Parameter: Phenological stages



Combining phenomics and modelling : yields of 100s genotypes

Parameter: Stomatal control



$$J_w = \frac{s (\Phi_n - G) + \rho_a c_p VPD_{air} g_a}{\lambda [s + \gamma(1 + g_a / g_s)]}$$

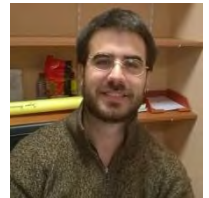
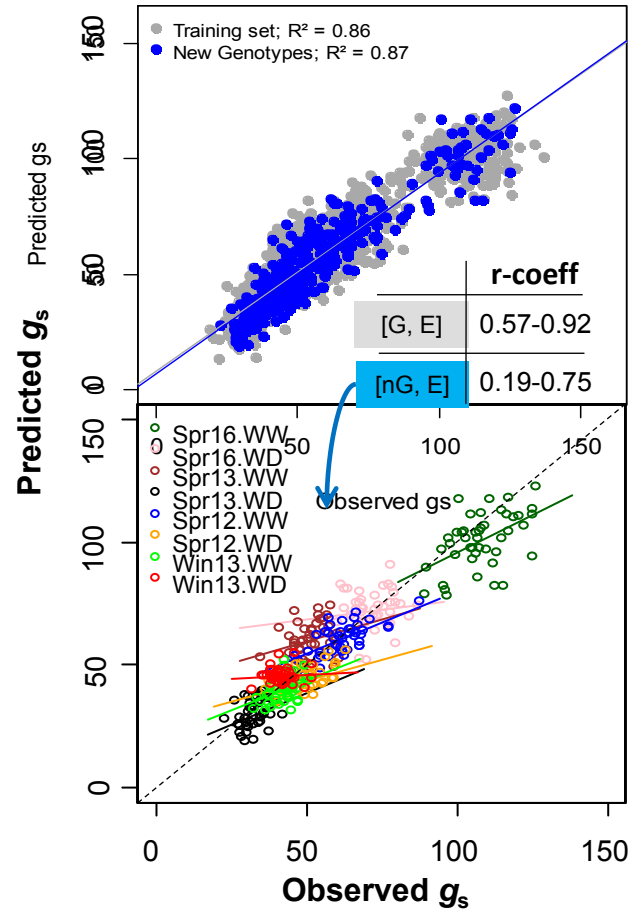


Combining phenomics and modelling : yields of 100s genotypes

Parameter, maximum stomatal conductance

Genomic prediction

[G, E] Training set (200 hyb)
 [nG, E] Testing set (46 hyb)



S. Alvarez Prado

Yield prediction

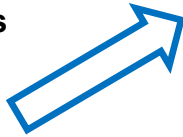
Genomic prediction



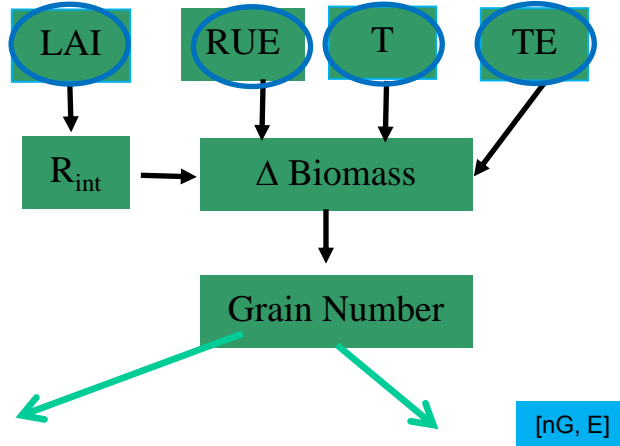
Model parameters/Traits



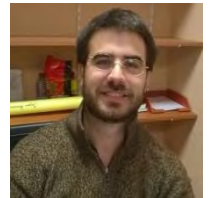
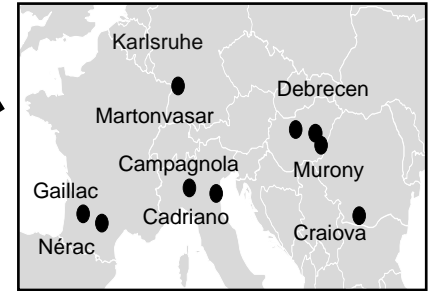
[G, E]



APSIM



Climatic and soil data from 15 field experiments



S. Alvarez Prado

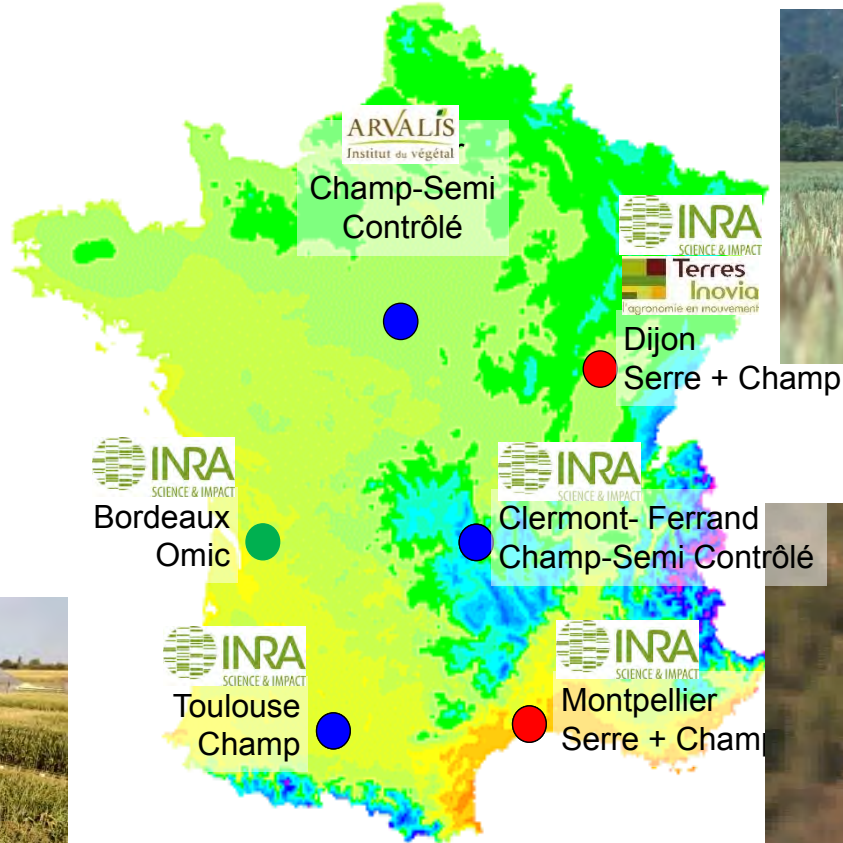
Controlled conditions



Semi controlled fields



fields



+ imaging, information system and models



2017-2020

Access to 31 installations in Europe

<https://eppn2020.plant-phenotyping.eu/>



Calls every 6 months (next, February 2019)

Common effort towards a European community

- A European information system
- Sensors and imaging
- Statistical applications

The cheapest experiment is the one in a database

... but data must be organized in such a way that they can be reused


*BRAPI and ELIXIR (G.Valle yesterday) help reusing data,
not organizing them*

(common work under progress)

Tracking/ontology of all objects in experiments (plants, pots, sensors...)
Where were they (spatial variability), calibrations, samples of which plants ?

In field and controlled conditions

Prefix m3p: `<http://phenome-fppn.fr/m3p>` (a)



URI of plant:
`<m3p:arch/2017/c17000118>`

URI of pot:
`<m3p:arch/2013/pc13001542>`


URI of cart:
`<m3p:arch/2013/ct1300123>`

URI of cabin:
`<m3p:arch/2018/ac180015>`

URI of camera:
`<m3p:arch/2018/ac180019>`

URI of image:
`<m3p:arch/2017/ic17002295855>`

Prefix diaphen: `<http://phenome-fppn.fr/diaphen>` (b)



URI of plot:
`<diaphen:2017/o1700029>`

URI of plant:
`<diaphen:2017/17000147>`

URI of leaf:
`<diaphen:2017/117000590>`

URI of camera:
`<diaphen:2018/ac180002>`

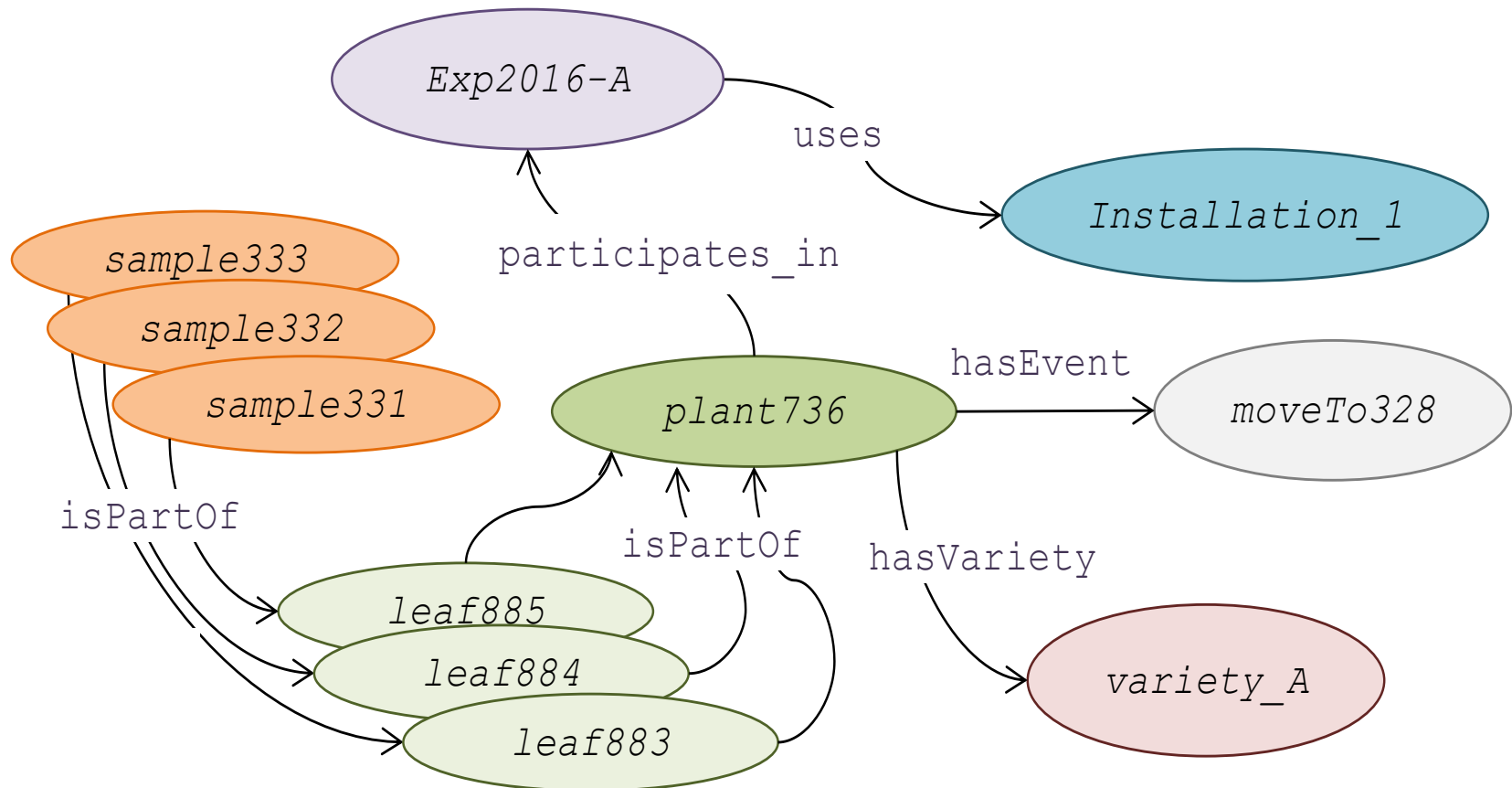
URI of image:
`<diaphen:2017/ic14001480237>`



P. Neveu LI Cabrera

Relating/ontology of objects via semantic web

'samples, belong to plants, leaves, genotypes, experiments...'



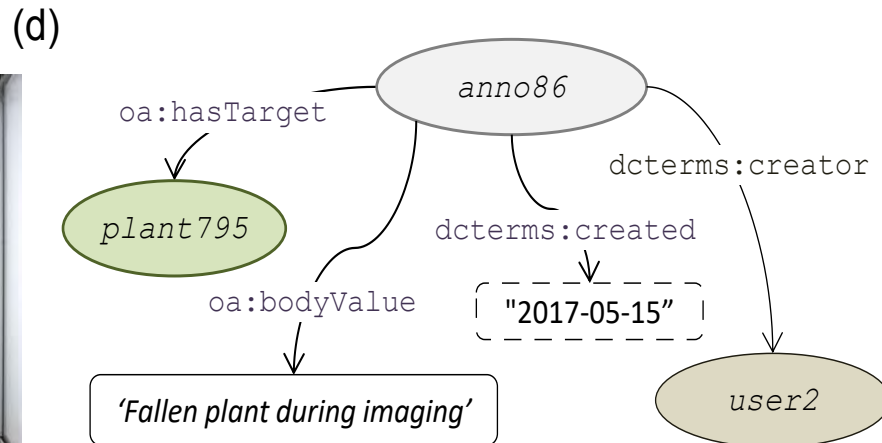
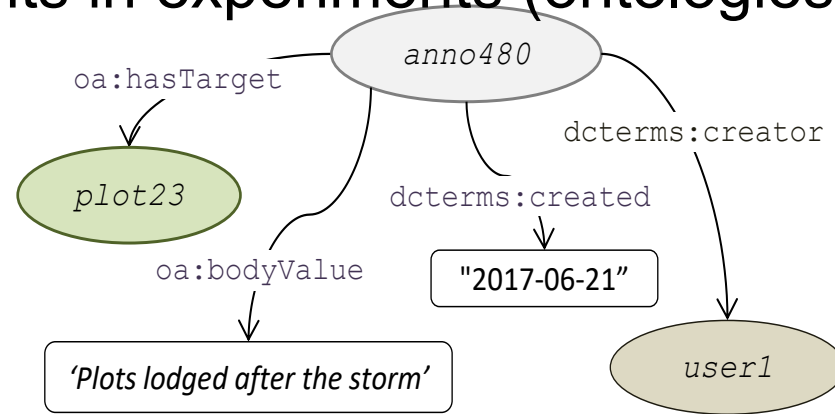
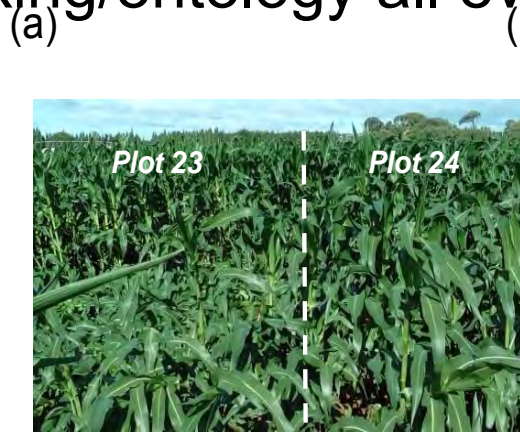
Creates the metadata in a parsimonious way (transitivity)

Neveu et al 2018 New Phyt

#URIs of the different objects

'Installation_1' = <http://www.nationalinfrastructure/Installation_1/>

Tracking/ontology all events in experiments (ontologies)

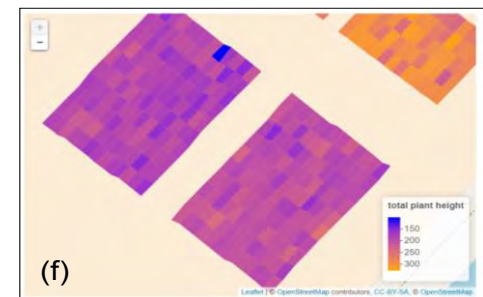
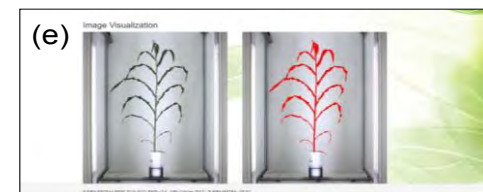
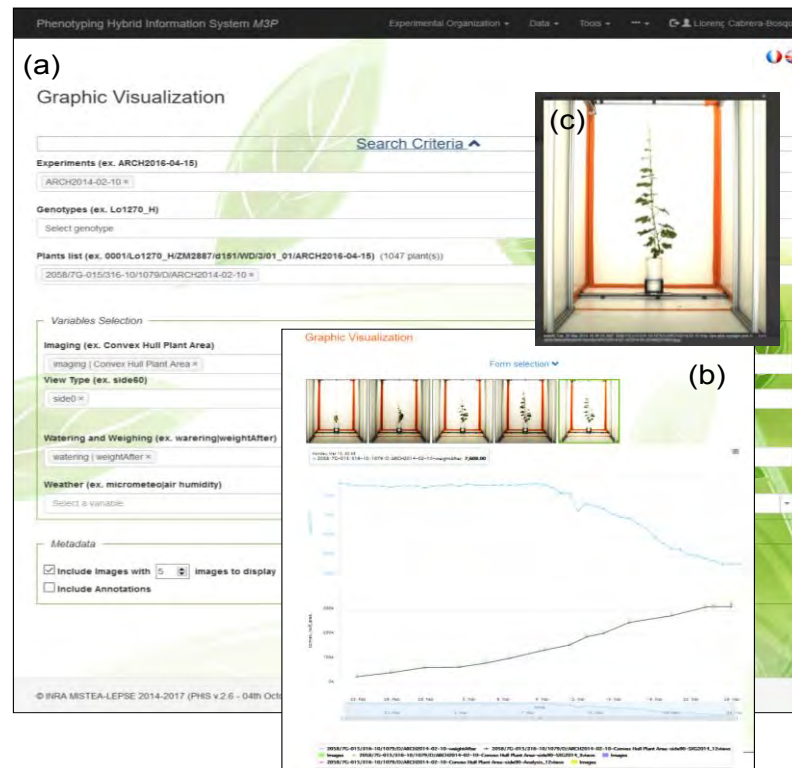


Allows organizing event reports, lost in lab books otherwise
Neveu et al 2018 New Phyt

Available upon demand

- Under implementation in French infra + Wageningen,
- Linked to other information systems via 'Emphasis layer', Ghent and Julich
- Interfaced with ELIXIR information systems and BRAPI

MIAPPE: a common initiative ELIXIR and EMPHASIS



Phenomics in the era of big data

Sensor networks are the first element of phenomics adopted by breeders
Phenomics *stricto sensu* needs added value

Combination of genomic prediction, phenomics and modelling
Potentially allows yield prediction 100s genotypes 100s sites

Phenotyping is an expensive exercise per se

if everything taken into account management, sensors, data management)
similar costs for field (even affordable) and controlled conditions,

Plant Science xxx (xxxx) xxx-xxx

What is cost-efficient phenotyping? Optimizing costs for different scenarios

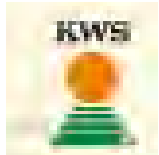
Daniel Reynolds^{a,1}, Frederic Baret^{b,1}, Claude Welcker^{c,1}, Aaron Bostrom^{a,1}, Joshua Ball^a,
Francesco Cellini^d, Argelia Lorence^e, Aakash Chawade^f, Mehdi Khafif^g, Koji Noshita^h,
Mark Mueller-Linowⁱ, Ji Zhou^{a,j,*}, François Tardieu^{c,*}

The cheapest experiment is the one from information systems
+ modelling

Acknowledgements



Field experiments



T. Presterl



S Praud



N. Ranc

RAGT, Euralis
MaisAdour



Genetic analyses



*Moulon,
A Charcosset
S Nicolas*



*Wageningen
F van Eeuwijk
Willem Kruijer*



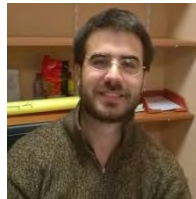
Platform experiments, modelling, GWAS



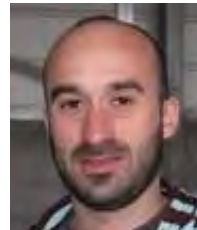
C Welcker



B. Parent



*S. Alvarez
Prado*



LI Cabrera



O. Turc

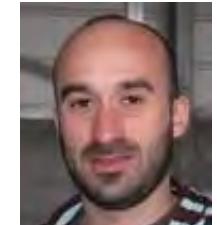


E. Millet

Information system



P. Neveu



LI Cabrera

