

# Phenomics@Lepse

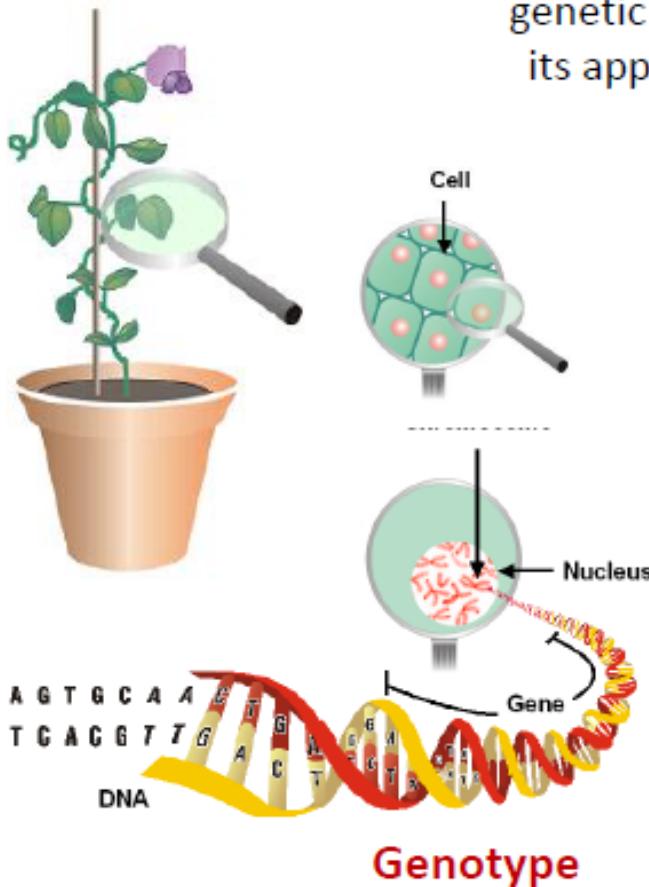


Christian Fournier, Llorenç Cabrera-Bosquet

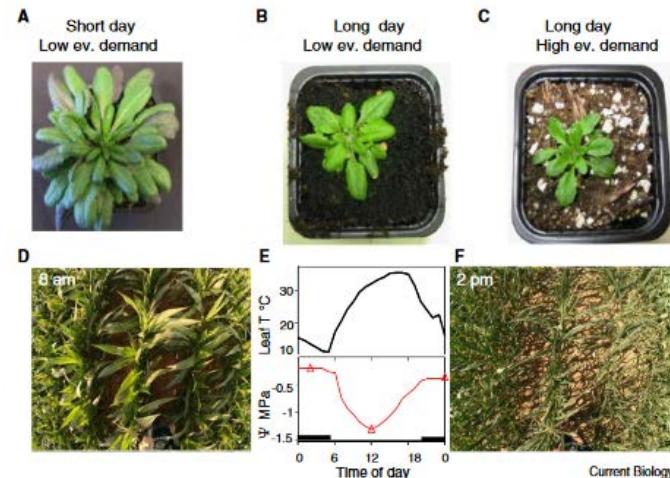


# Phenomics : from genes to phenotype

## Phenotype



**Definition:** Phenomics is the study of how the genetic make-up of an organism determines its appearance, function and performance



## MAJOR RESEARCH CHALLENGE:

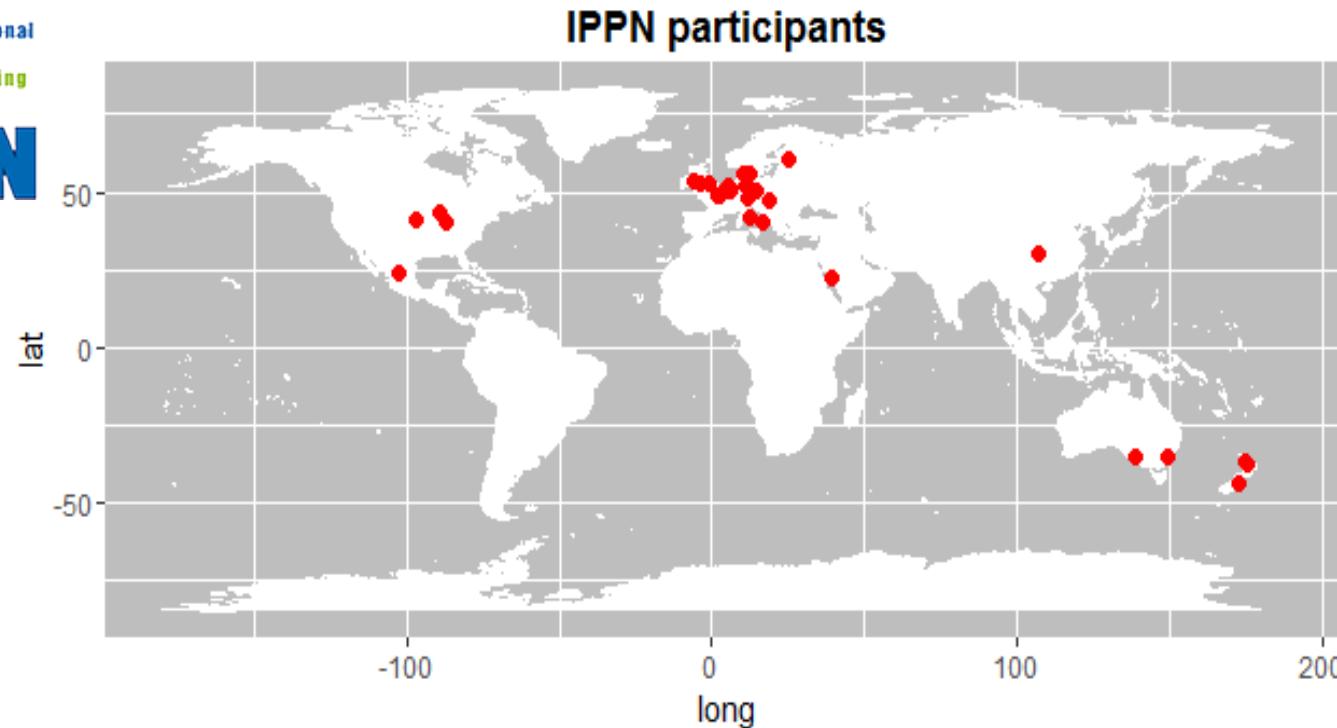
Automating the interpretation and analysis of biological images on an industrial scale

Furbank, R. T., & Tester, M. (2011). Phenomics—technologies to relieve the phenotyping bottleneck. *Trends in plant science*, 16(12), 635-644.

Tardieu, F., Cabrera-Bosquet, L., Pridmore, T., & Bennett, M. (2017). Plant phenomics, from sensors to knowledge. *Current Biology*, 27(15), R770-R783.

## 1. Numerous platforms around the world, numerous tools...

*Good! Big phenotyping community (Phenome, EPPN, IPPN,...)!*



## PHENOARCH is part of the Montpellier Plant Phenotyping Platforms (M3P) facility



# Montpellier Plant Phenotyping Platforms (M3P)

## 1. PHENOPSIS (<http://bioweb.supagro.inra.fr/phenopsis/>)

It allows to weight, irrigate precisely and take a picture of more than 500 individual *Arabidopsis thaliana* plants in rigorously controlled conditions.



## 2. PHENODYN (<http://bioweb.supagro.inra.fr/phenodyn/>)

It measures growth rate and transpiration rate of 420 plants every minute, together with environmental conditions.

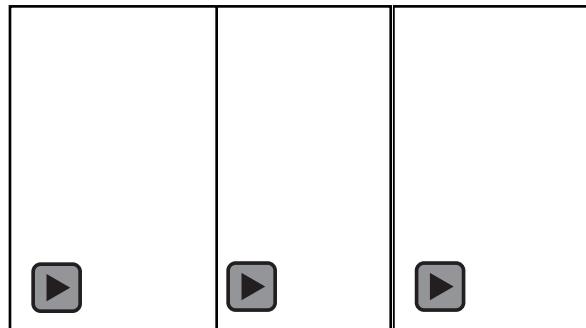


## 3. PHENOARCH (<http://bioweb.supagro.inra.fr/phenoarch/>)

It aims at analysing the genetic determinisms of plant responses to environmental conditions in particular drought, temperature and light (2400 plants).



## PHENOARCH: Growth, architecture and transpiration of large populations in response to environmental conditions



Cabrera-Bosquet et al. 2016 *New Phytologist*

Analyses of **genetic determinisms** of plant **responses to environmental conditions** (drought, temperature and light)

- Capacity for **2400** plants (ca. 300 genotypes)
- Automated high throughput system for:
  - RGB Imaging (side and top view images)
  - Watering and whole-plant transpiration
- Low throughput operations
- Precise environmental characterisation

## PhenoArch platform, Montpellier, FRANCE



*Conveyor belts*



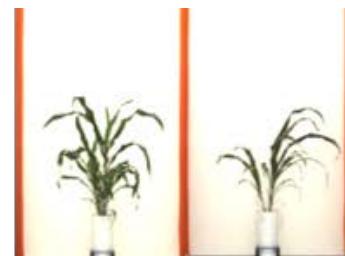
*Watering stations*



=> Evaluate phenotypic diversity within and between species



*Maize*



*Sorghum*



*Rice*



*Grapevine*



*Apple tree*

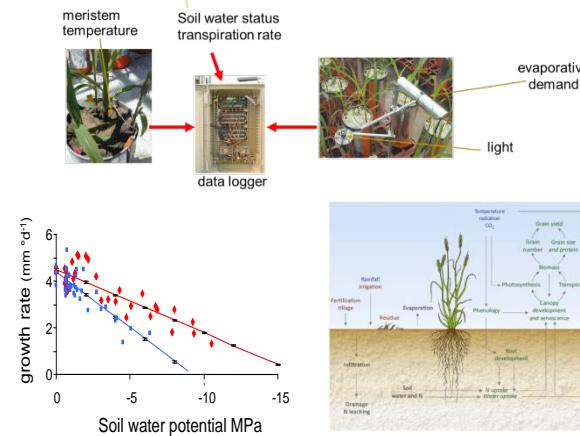
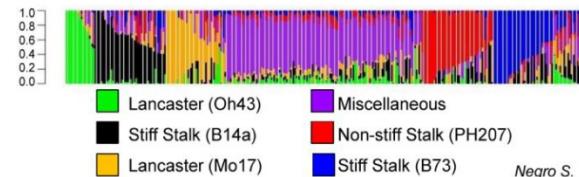


*Wheat*



*Seedrape*

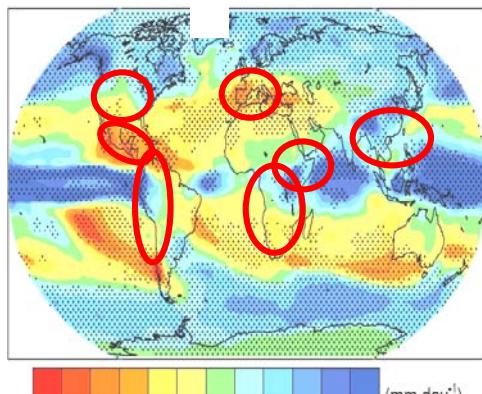
# Phenomics Analysis @ LEPSE



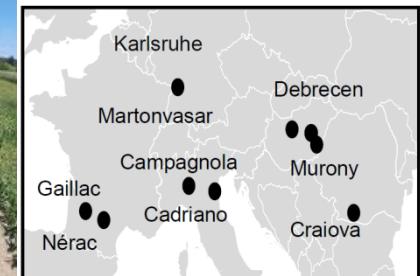
Ecophysiology & modelling of response traits integration in crop models



Model assisted phenotyping



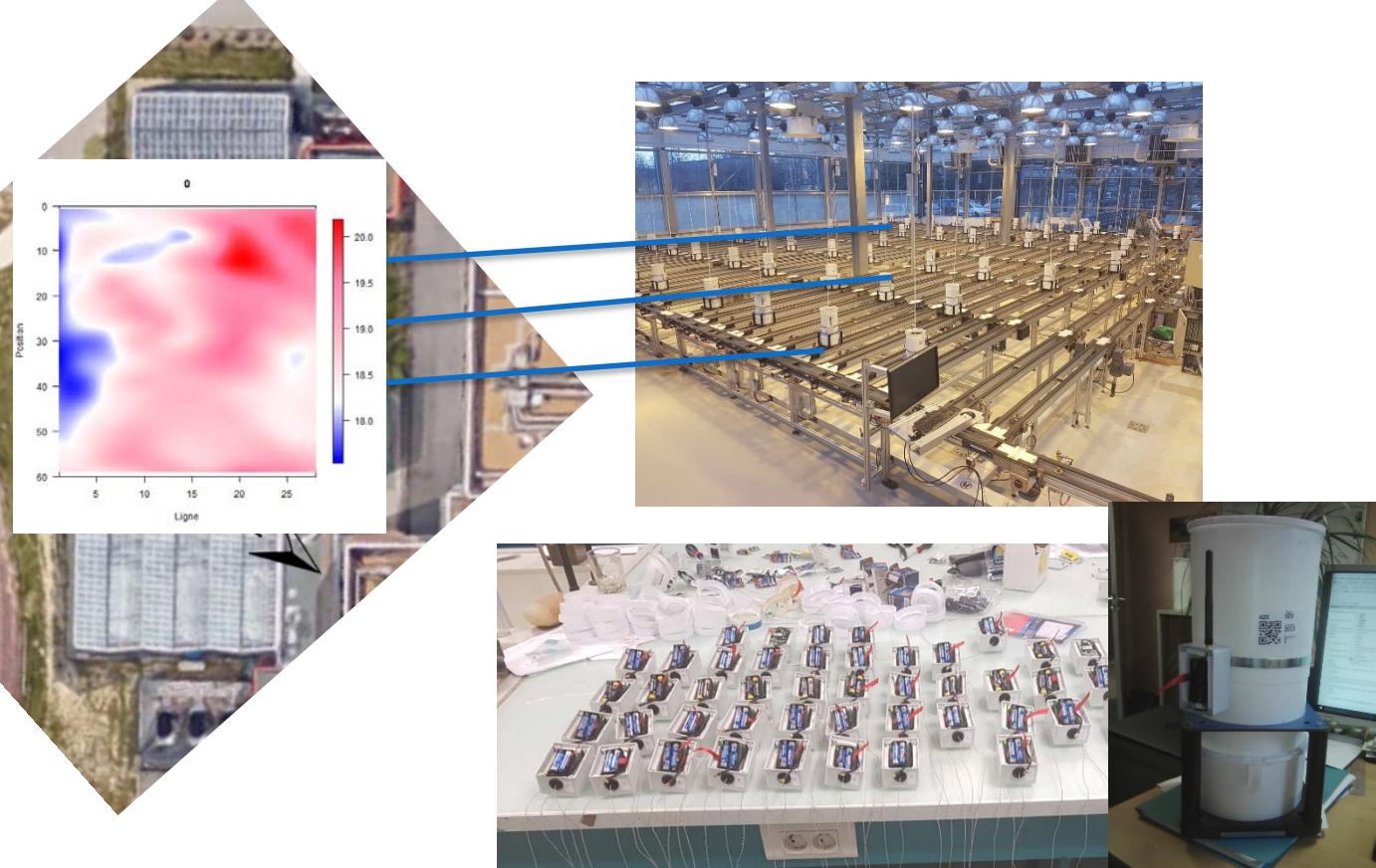
Genomic prediction of adapted genotypes for Current and future environments



Check / calibrate field prediction in multi-site genetic trial

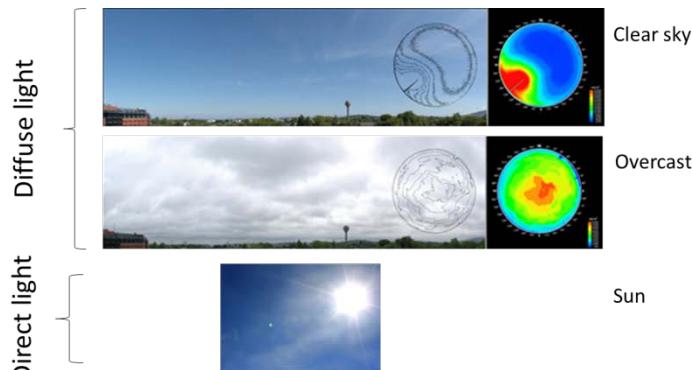
# Temperature maps: network of sensors

*Temperature map using a network of wireless sensors (ZigBee protocol)*

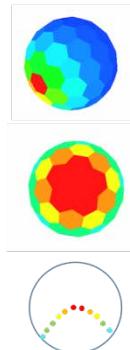


# Incident light map within greenhouse using FSPM tools

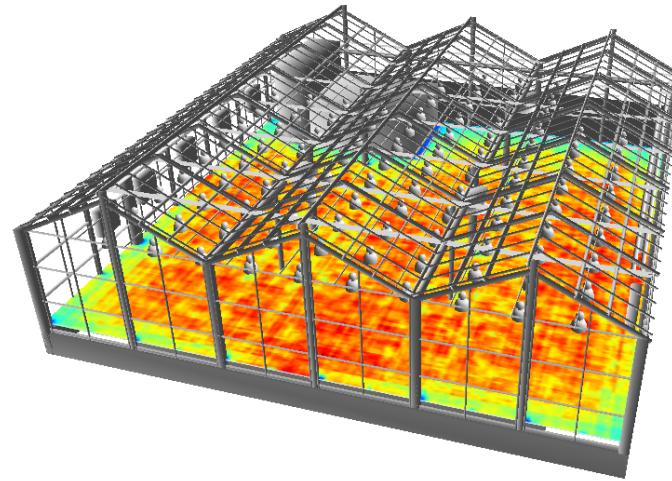
## Sky luminance model



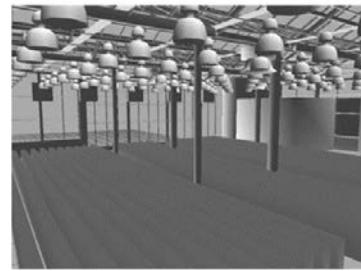
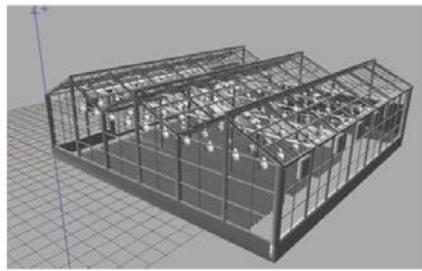
<https://github.com/openalea-incubator/astk>



## Raytracing



## GreenHouse reconstruction

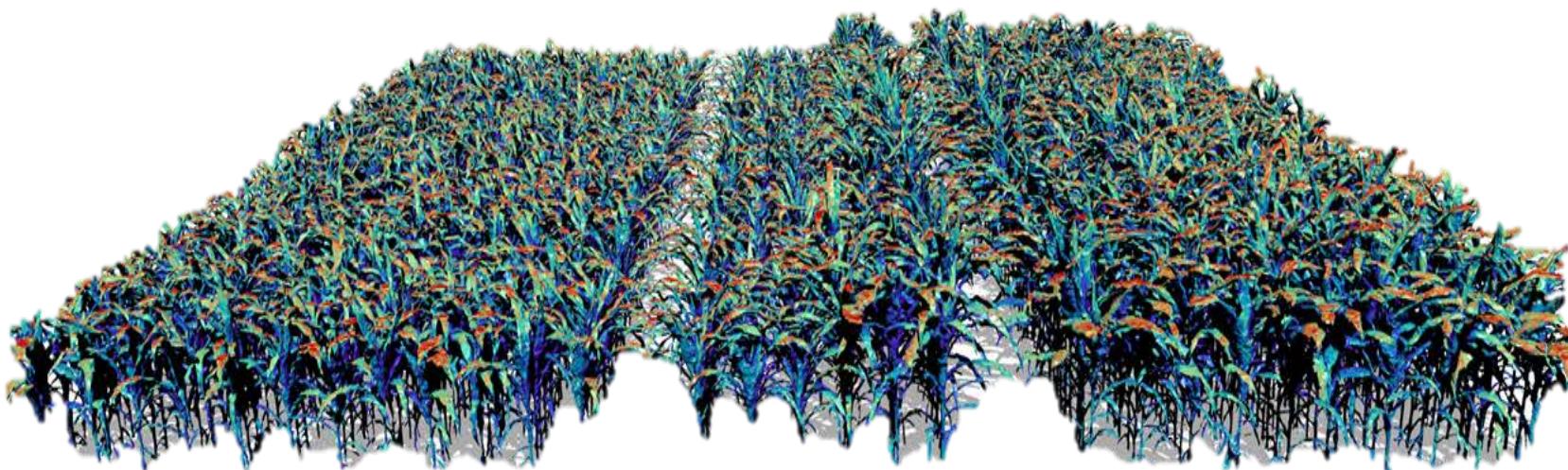


<https://github.com/openalea/plantgl>

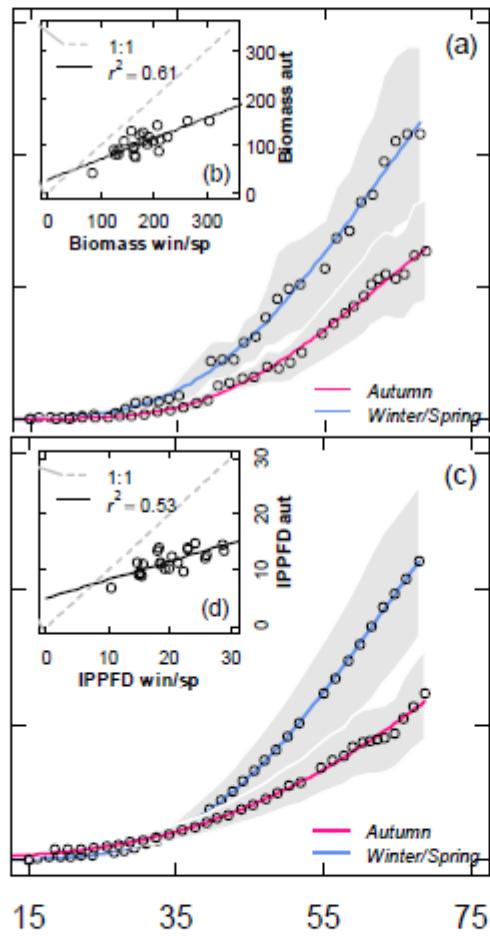
<https://github.com/openalea-incubator/caribu>

## *Virtual canopy illumination*

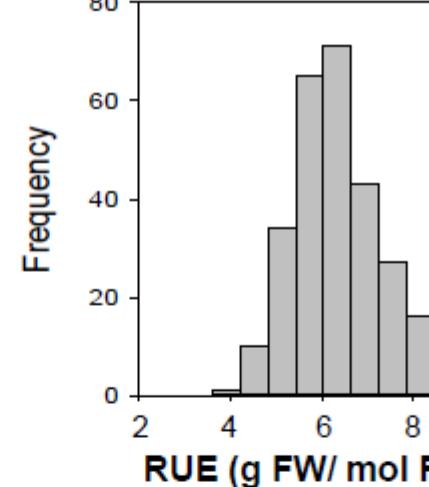
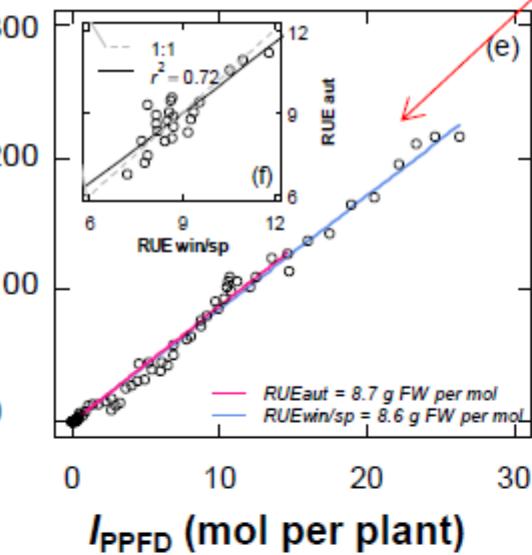
*Artzet et al. 2019*



$$\text{Biomass} = \int \text{Incident light} \times \text{Intercepted light} \times \text{RUE}$$



Biomass (g FW per plant)



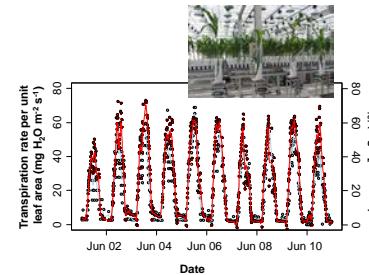
Tsu-Wei Chen (LEPSE,

Cabrera-Bosquet et al., 2016 *New Phytologist*

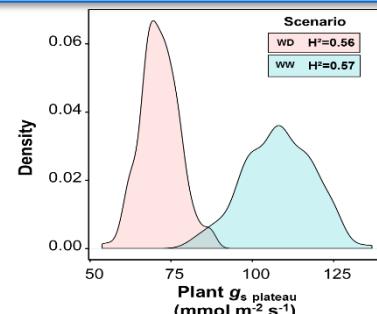
# Combining experiments and environments (and scales)

A method for high throughput estimation of maize **stomatal conductance**, based on transpiration, leaf area and micro-meteorological conditions ([Alvarez Prado et al. PCE 2018](#))

Stomatal conductance from water flux in 250 genotypes  
(Inversion of Penman-Monteith's equation):  
$$g_s = g_a \frac{Tr | g}{(s Rn + r Cp VPD g_a - Tr | (s+g))}$$

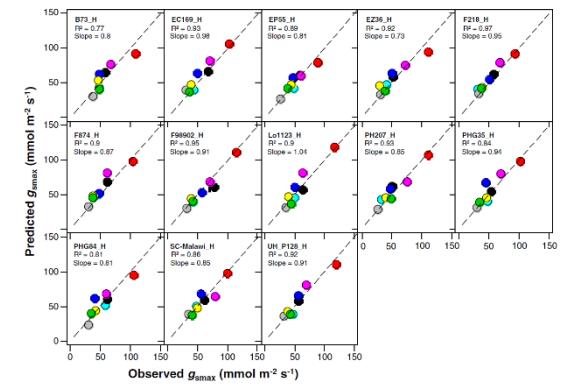


Genotypic variability and heritability of stomatal conductance



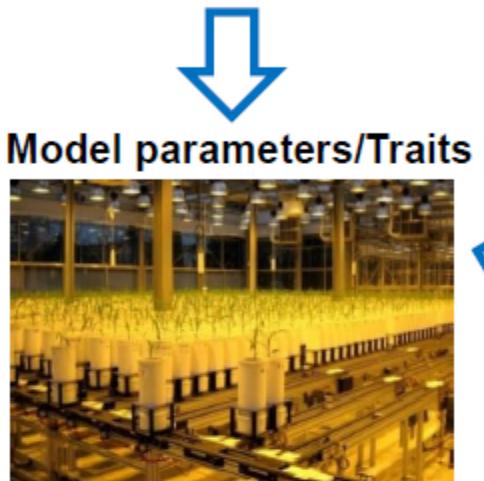
S. Alvarez Prado

Genetic dissection of  $g_s$   
and prediction by considering detected QTL and local micro-environmental conditions

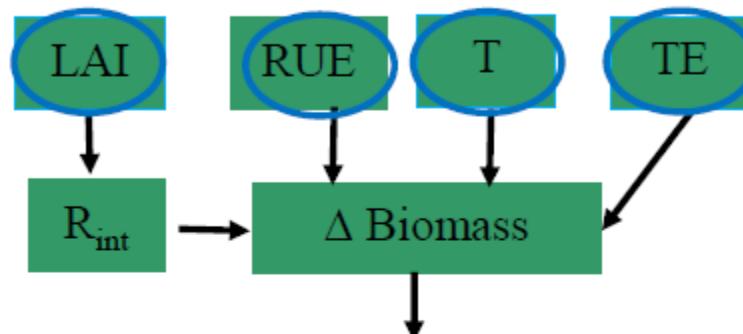


# Prediction of grain number combining genomic prediction with dynamic models

## Genomic prediction



## APSIM



## Climatic area/field



Training Set

predicted grain number

**CV = 15%**  
r-coef: 0.36-0.73

6000

4000

2000

0

predicted grain number

**CV = 16%**  
r-coef: 0.36-0.59

6000

4000

2000

0

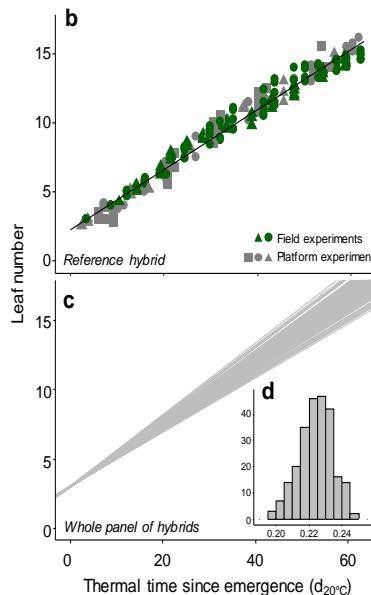
New genotype

# Combining platform and field data

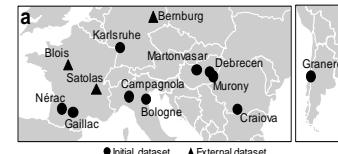
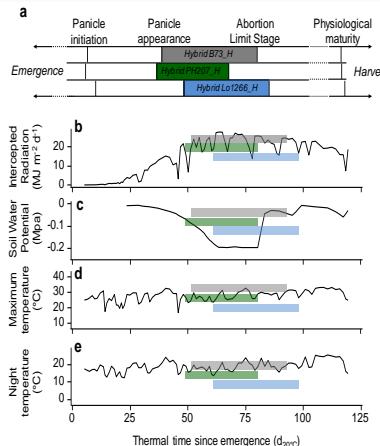
Leaf appearance measurements performed in the platform combined with environmental records in the field allow predicting yield in hundreds of genotypes in a network of fields

## Leaf appearance rates in the platform

(↑heritable, easy to measure)



## Phenology and critical window period in the field



Millet et al. 2019 Nature Genetics

$$GY_{ij} = (\mu + e_j + g_i + T_{night,i,j} \beta_{1,i} + R_{i,j} \beta_{2,i} + \Psi_{soil,i,j} \beta_{3,i} + \varepsilon_{ij}) \times GW_i$$

$$GY_{ij} = (\mu + e_j + g_i + \sum_{l=1}^s \beta_{l,i} cov_{l,i,j} + \varepsilon_{ij}) \times GW_i$$

## Genomic prediction



Emilie Millet

# Model assisted pipeline !



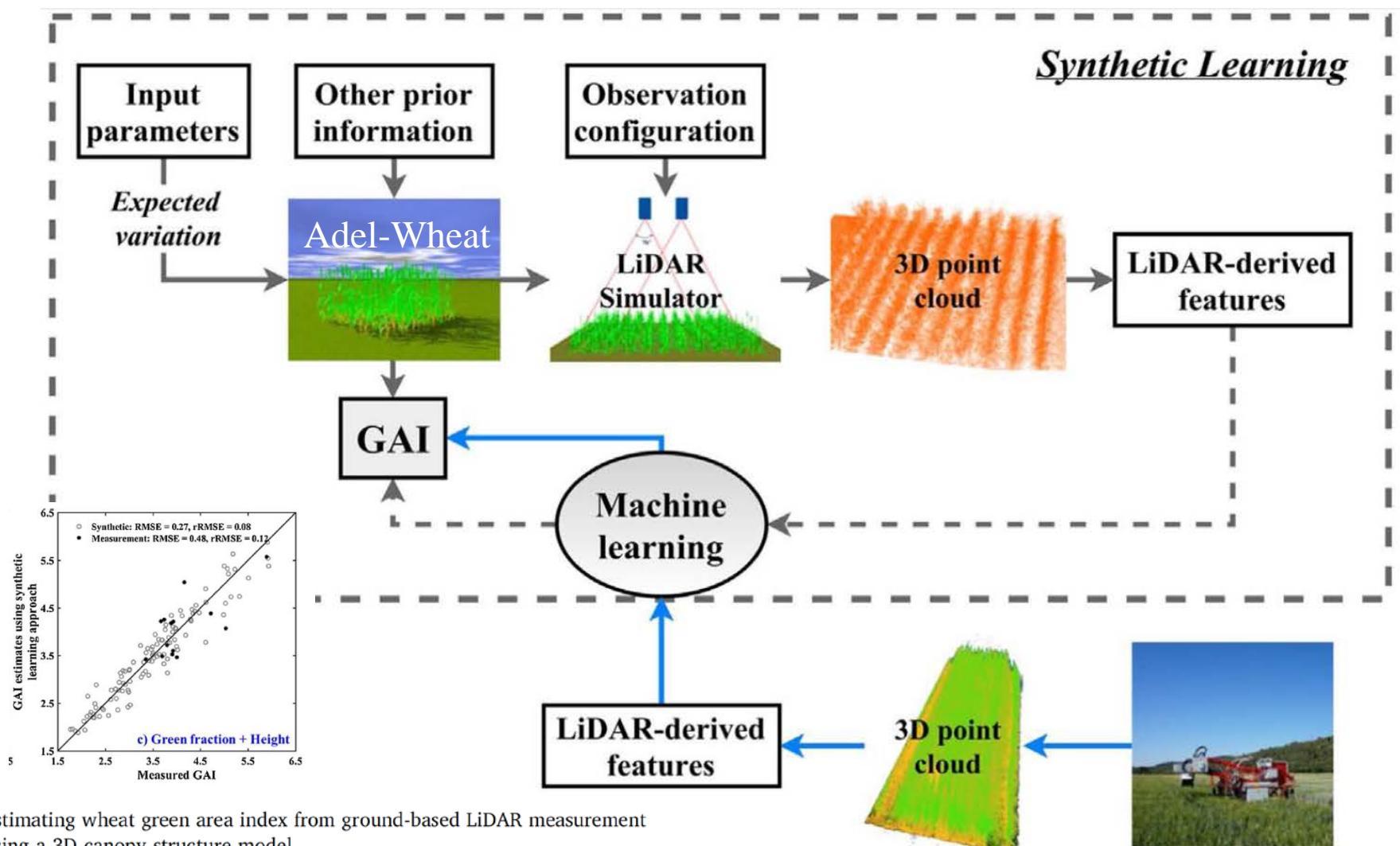
Phenomenal output

Fit FSPM model (ADEL)

Annotated output

Fournier et al, IcropM

# Predict, (machine) learn & estimate



Estimating wheat green area index from ground-based LiDAR measurement using a 3D canopy structure model

Shouyang Liu<sup>a,\*</sup>, Fred Baret<sup>a</sup>, Mariem Abichou<sup>b</sup>, Fred Boudon<sup>c</sup>, Samuel Thomas<sup>d</sup>,  
Kaiguang Zhao<sup>e</sup>, Christian Fournier<sup>f</sup>, Bruno Andrieu<sup>b</sup>, Kamran Irfan<sup>a</sup>, Matthieu Hemmerle<sup>g</sup>,  
Benoit de Solan<sup>d</sup>

# Summary

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**Model assisted phenotyping for HT automated acquisition**

Field

Platform

**Plant phylloclimate**

Simulation local environment

New co-variables

**Dissecting plant responses**

Test/validate FSPM process model <-> 'productive FSPM'

Extract traits / response traits

**Gene to phenotype upscaling**

Extend / Link to crop models



Thanks for your  
attention!