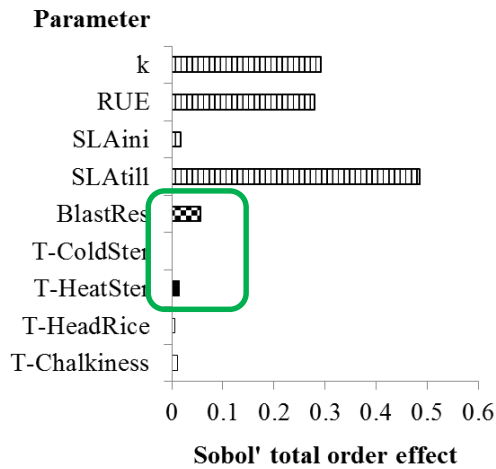




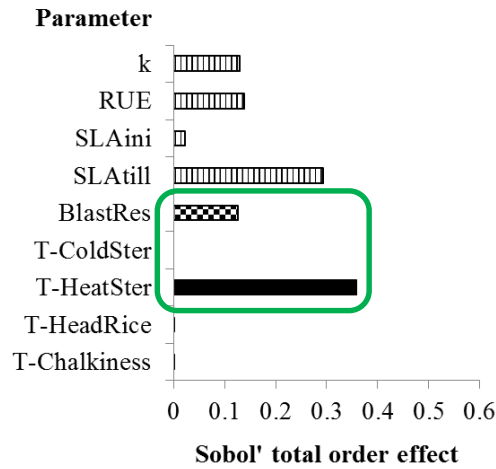
# In silico ideotyping

## Development of crop ideotypes

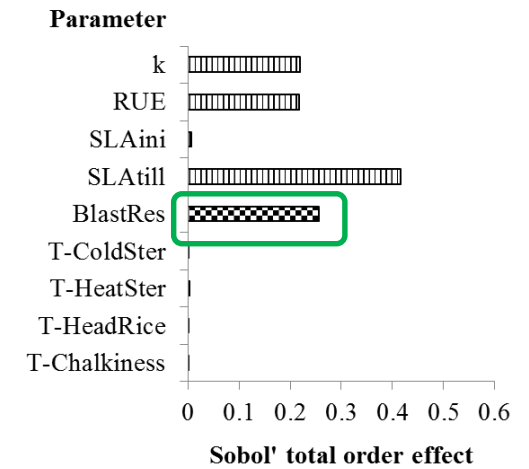
### Los Baños



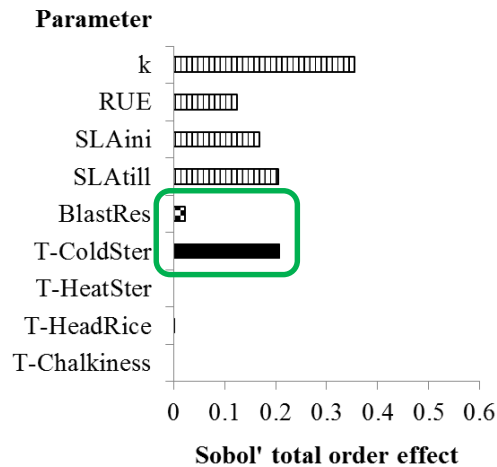
### Ludhiana



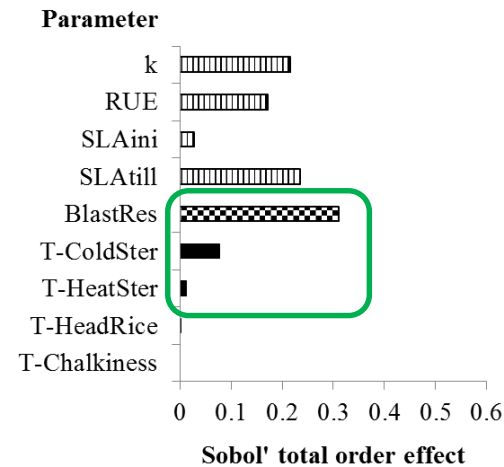
### Nanjing



### Shizukuishi



### Milan

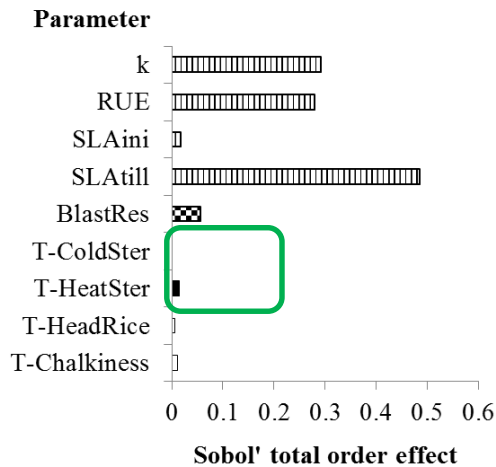




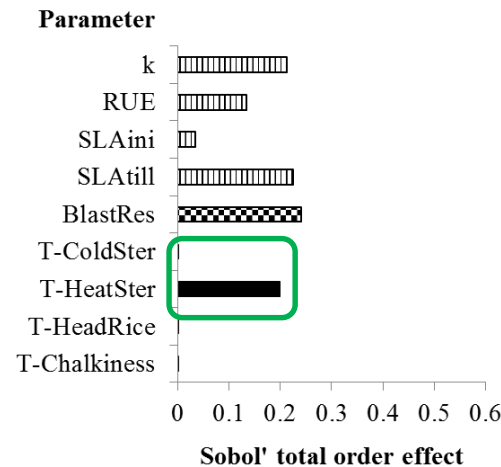
# In silico ideotyping

Development of crop ideotypes

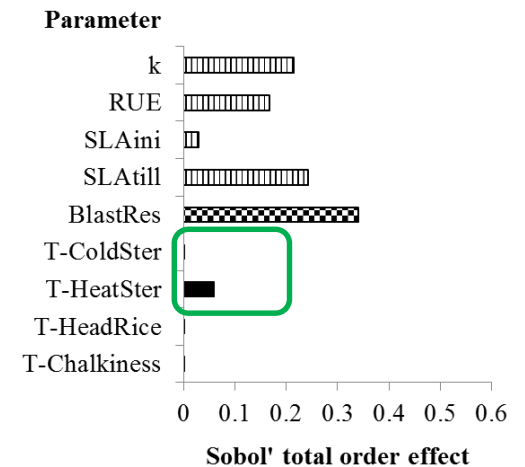
Los Baños



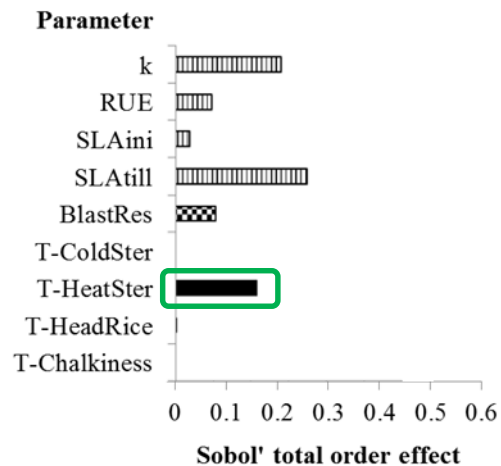
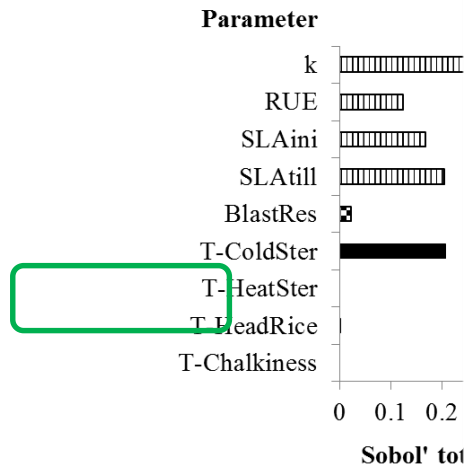
2030 HadGEM\_8.5 Ludhiana



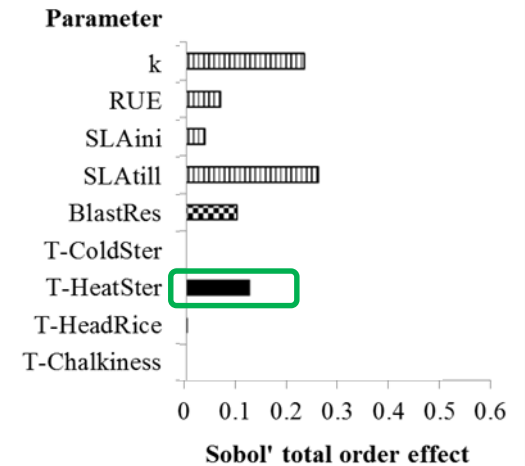
2030 GISS\_2.6 Nanjing



Shizukuishi 2030 HadGEM\_8.5



Milan 2030 GISS\_2.6

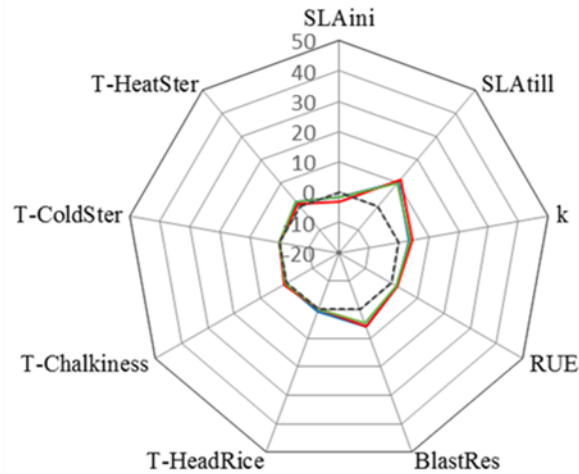




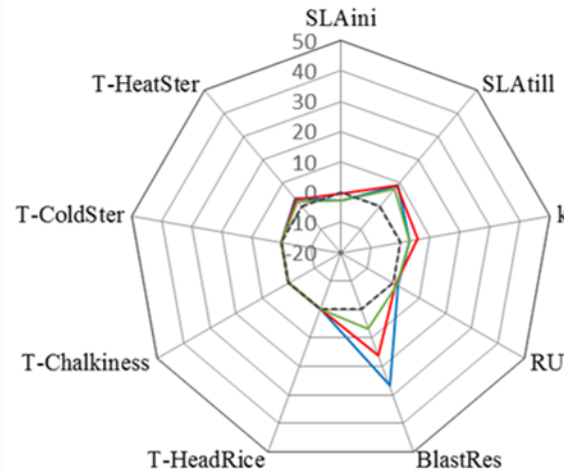
# In silico ideotyping

Development of crop ideotypes

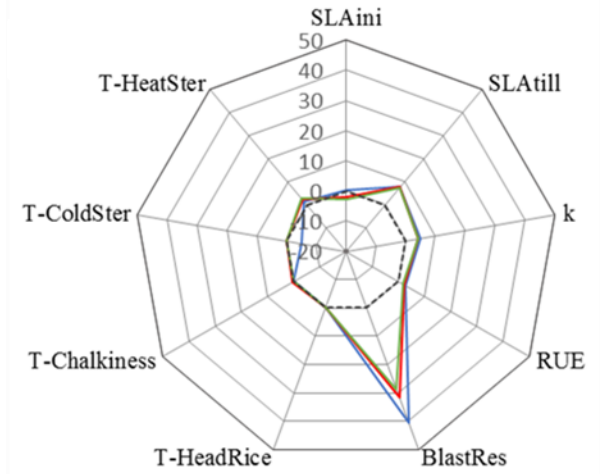
## Los Baños



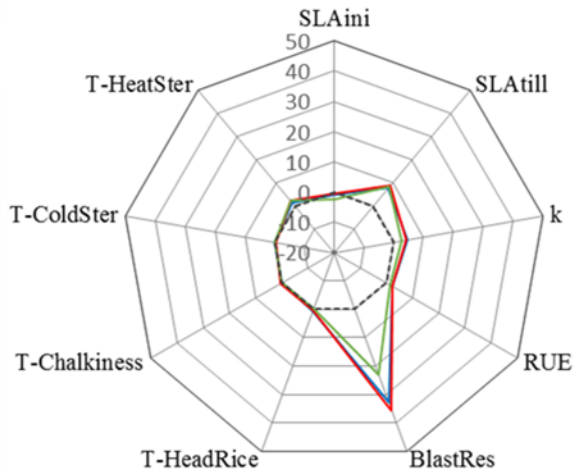
## Ludhiana



## Milan



## Nanjing



## Shizukuishi



--- distribution mean    ■ Baseline  
■ GISS\_RCP2.6  
■ HadGEM\_RCP8.5

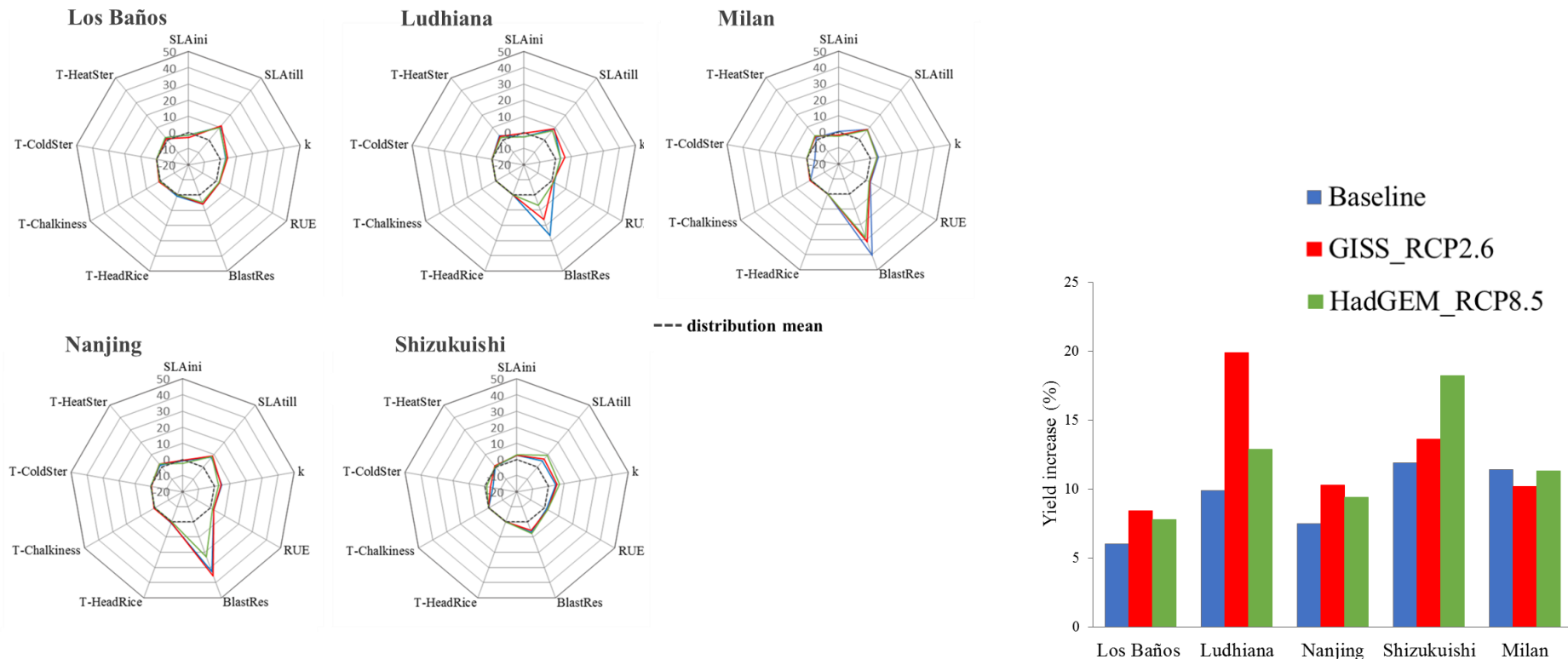
**Ideotype profiles**



# In silico ideotyping

## Development of crop ideotypes

- **After deriving ideotype profiles**, a crucial step is **quantifying the potential benefits** deriving from their adoption
  - ✓ This allows comparing **costs and benefits** of a breeding program based on the ideotypes

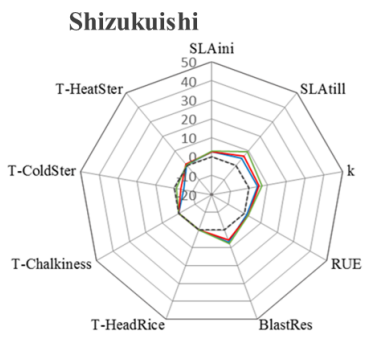
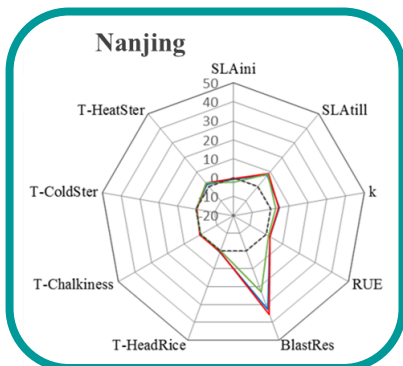
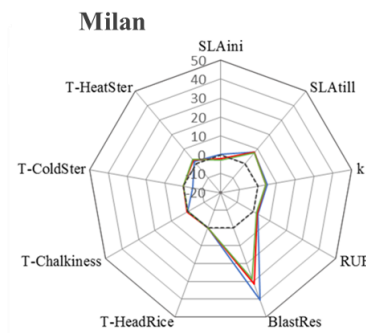
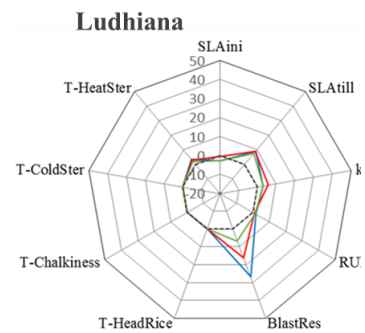
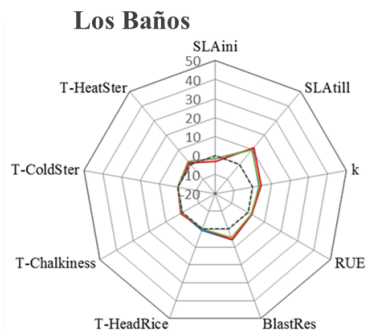




# In silico ideotyping

## Development of crop ideotypes

- In case the **ideotype differs** from current varieties **for a single trait**, the **evaluation** of its performances can be achieved with an **in silico introgression**



--- distribution mean

Climatic Change (2015) 132:661–675  
DOI 10.1007/s10584-015-1457-4



**District specific, in silico evaluation of rice ideotypes improved for resistance/tolerance traits to biotic and abiotic stressors under climate change scenarios**

L. Paleari<sup>1</sup> • G. Cappelli<sup>1</sup> • S. Bregaglio<sup>1</sup> • M. Acutis<sup>1</sup> •  
M. Donatelli<sup>2</sup> • G. A. Sacchi<sup>3</sup> • E. Lupotto<sup>4</sup> •  
M. Boschetti<sup>5</sup> • G. Manfron<sup>3,5</sup> • R. Confalonieri<sup>1</sup>

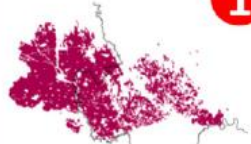


# In silico ideotyping

## Development of crop ideotypes

**Select a district**

Clear selection 1



District name:  
Lombardo-Piemontese

Surface:  
195.545 ha

Relevant biotic injures:  
Blast disease (Pyricularia)  
Brown spot (Helminthosporium)

Relevant a-biotic damages:  
Sterility (warm)

**Defining ideotype traits: an example for blast resistance**

Fungal pathogens

Blast  Brown spot

Resistance coefficient during:	Sporulation	Infectiousness	Latency	Infection
	3	2	3	3

2

**Defining the climate scenario: selecting RCPs, GCMs and time frames**

Representative Concentration Pathways

RCP8.5  RCP2.6

General Circulation Model

HadGEM2  GISS

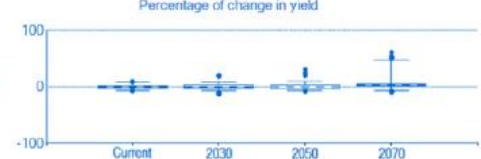
Project the analysis up to:

2030  2050  2070

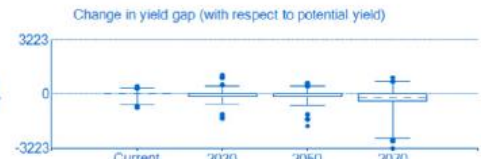
3

**Look at synthetic results, produce reports and save results**

Percentage of change in yield



Change in yield gap (with respect to potential yield)



4

Computers and Electronics in Agriculture 128 (2016) 46–49



Contents lists available at ScienceDirect

**Computers and Electronics in Agriculture**

journal homepage: [www.elsevier.com/locate/compag](http://www.elsevier.com/locate/compag)



Application note

ISide: A rice modelling platform for *in silico* ideotyping

L. Paleari <sup>a,\*</sup>, S. Bregaglio <sup>a</sup>, G. Cappelli <sup>a</sup>, E. Movedi <sup>a</sup>, R. Confalonieri <sup>b</sup>





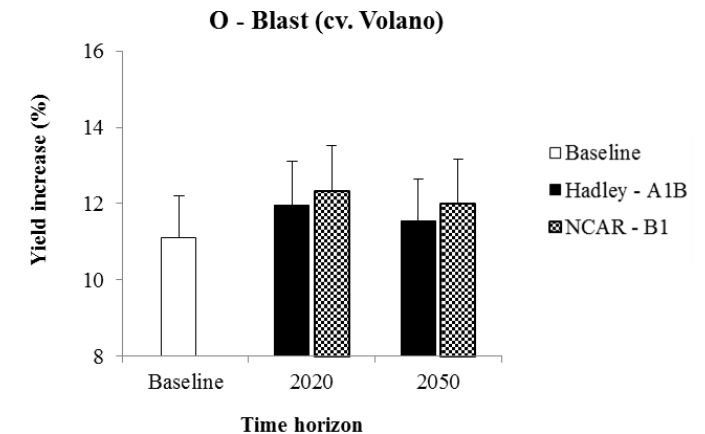
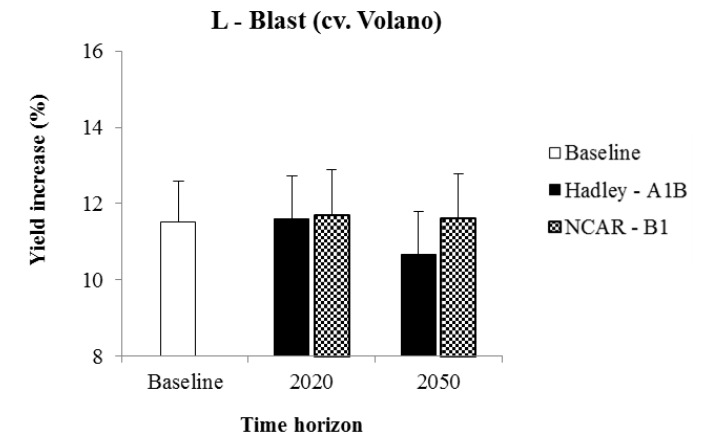
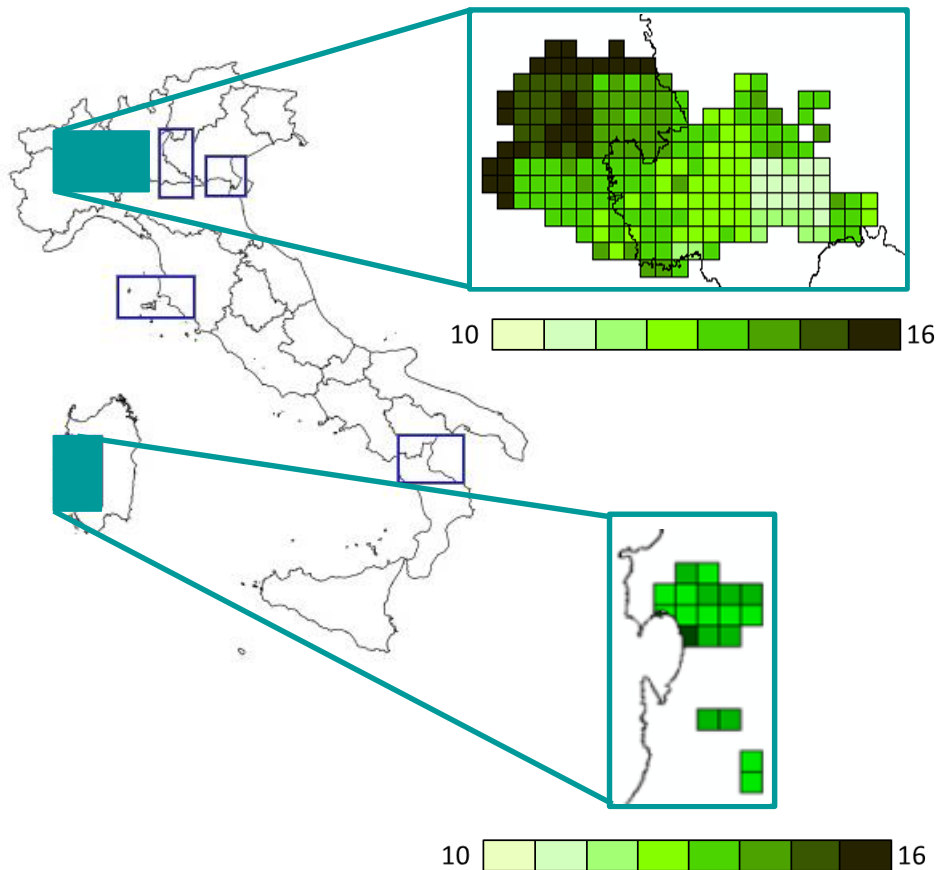
# In silico ideotyping

## Development of crop ideotypes

- **Sample results**

- ✓ Evaluation of **rice ideotypes** in Italian districts

- Resistance to **blast** disease





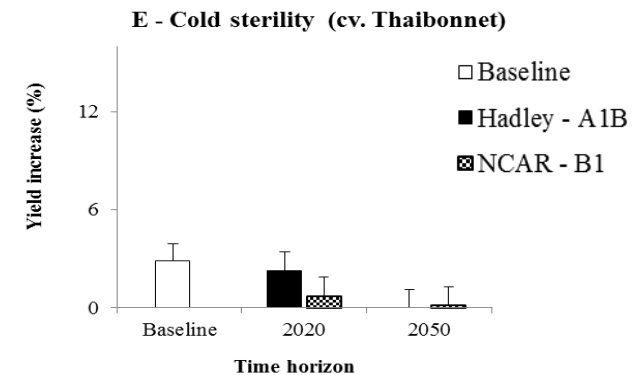
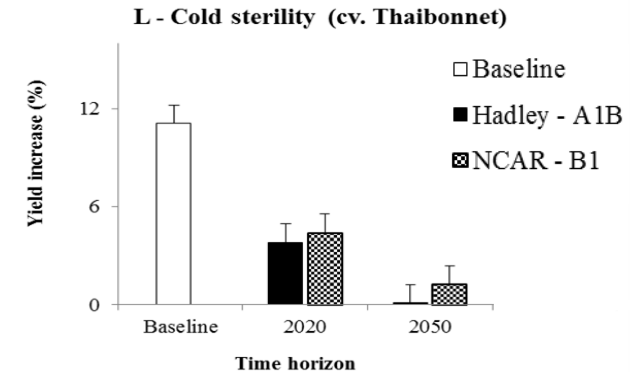
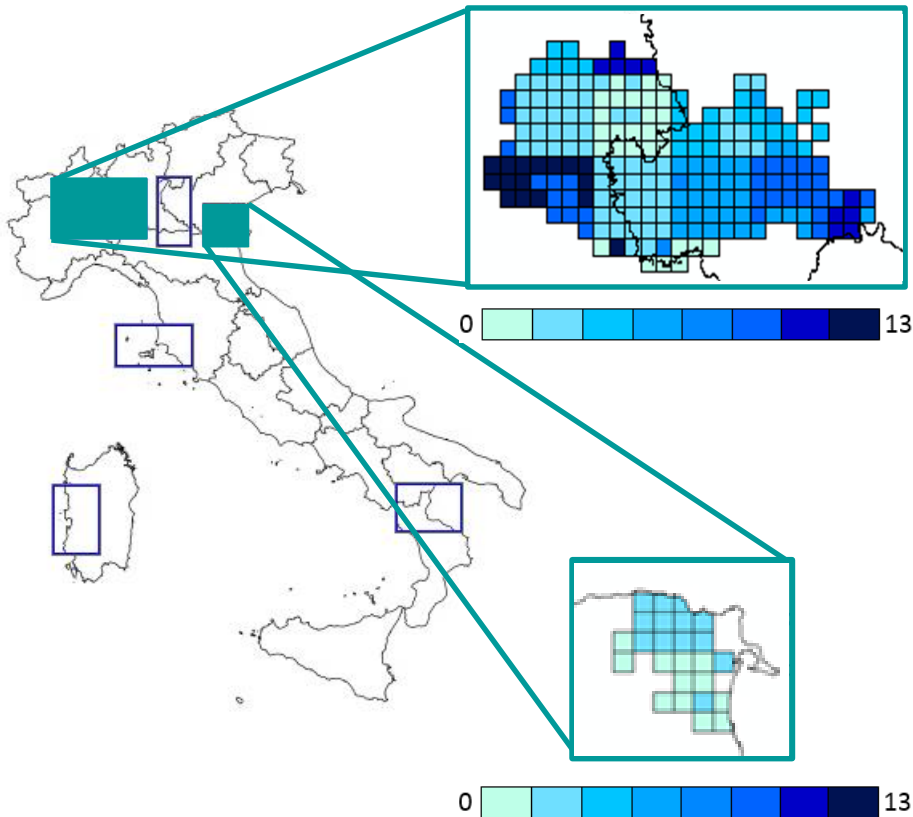
# In silico ideotyping

## Development of crop ideotypes

- **Sample results**

- ✓ Evaluation of **rice ideotypes** in Italian districts

- Tolerance to **cold-induced spikelet sterility**



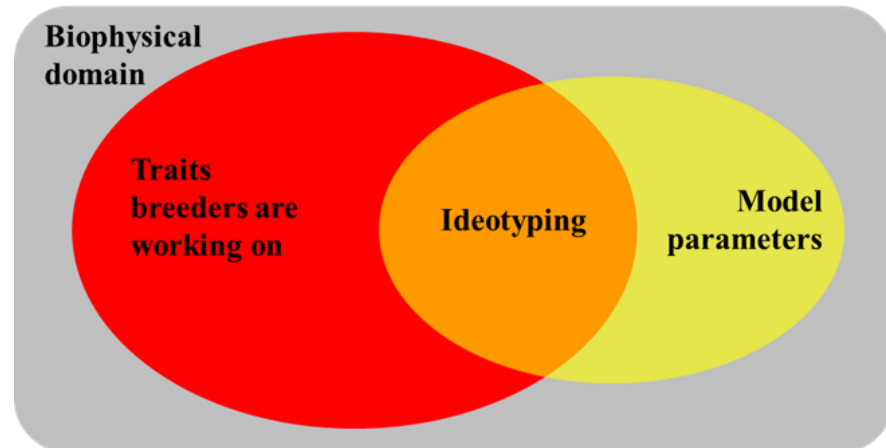




# In silico ideotyping

## Development of crop ideotypes

- As mentioned, **current crop models** are **not completely suitable** to support breeding/genetics
  - ✓ They were **not explicitly developed for** this purpose
  - ✓ The **risk** is to develop ideotypes that **cannot be realized in vivo**
- **Two strategies:**
  - ✓ Mid term





# In silico ideotyping

Development of crop ideotypes

## Mid term strategy

- **Develop new models**, by building models **around traits**
  - ✓ **An example for rice and salinity (toxic effect)**
    - We **defined as “traits”** crop features for which specific breeding programs are ongoing
    - We **developed** a model **starting from** those **traits**

[www.nature.com/scientificreports](http://www.nature.com/scientificreports)

SCIENTIFIC REPORTS 

**OPEN** Trait-based model development to support breeding programs. A case study for salt tolerance and rice

Received: 6 January 2017  
Accepted: 8 May 2017  
Published online: 28 June 2017

Livia Paleari<sup>1</sup>, Ermes Movedi<sup>1</sup> & Roberto Confalonieri<sup>2</sup>

Eco-physiological models are increasingly used to analyze  $G \times E \times M$  interactions to support breeding programs via the design of ideotypes for specific contexts. However, available crop models are only



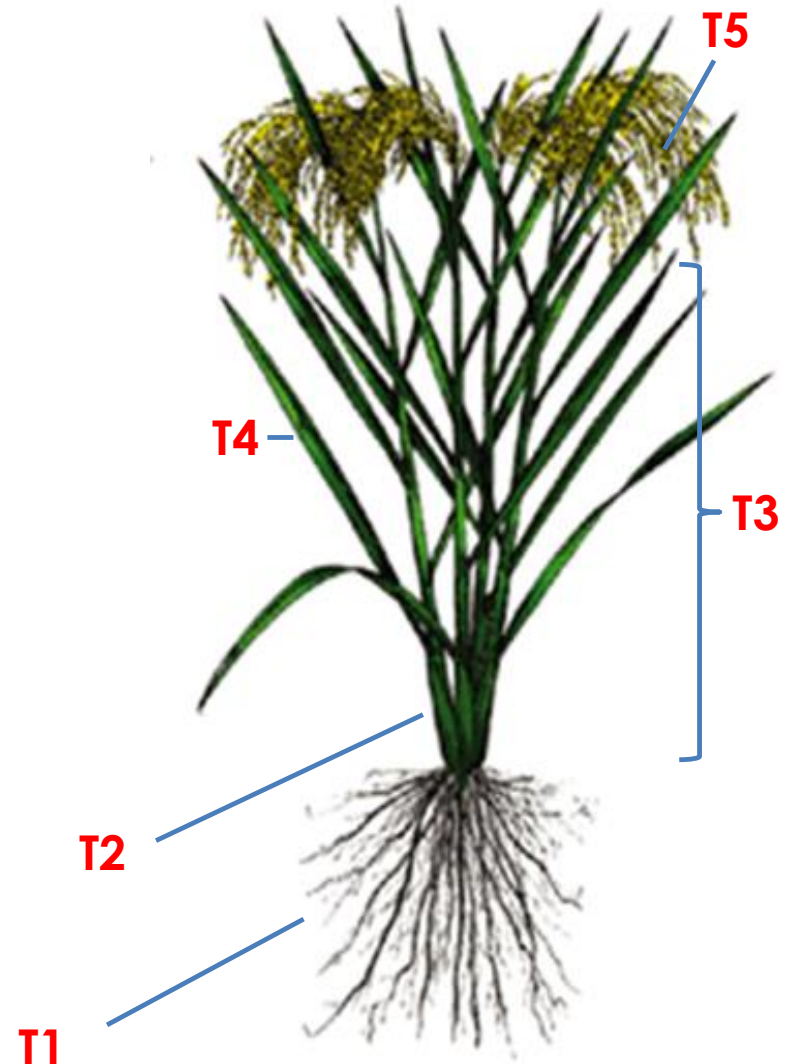
# In silico ideotyping

## Development of crop ideotypes

### Mid term strategy

- **Tolerance traits:**

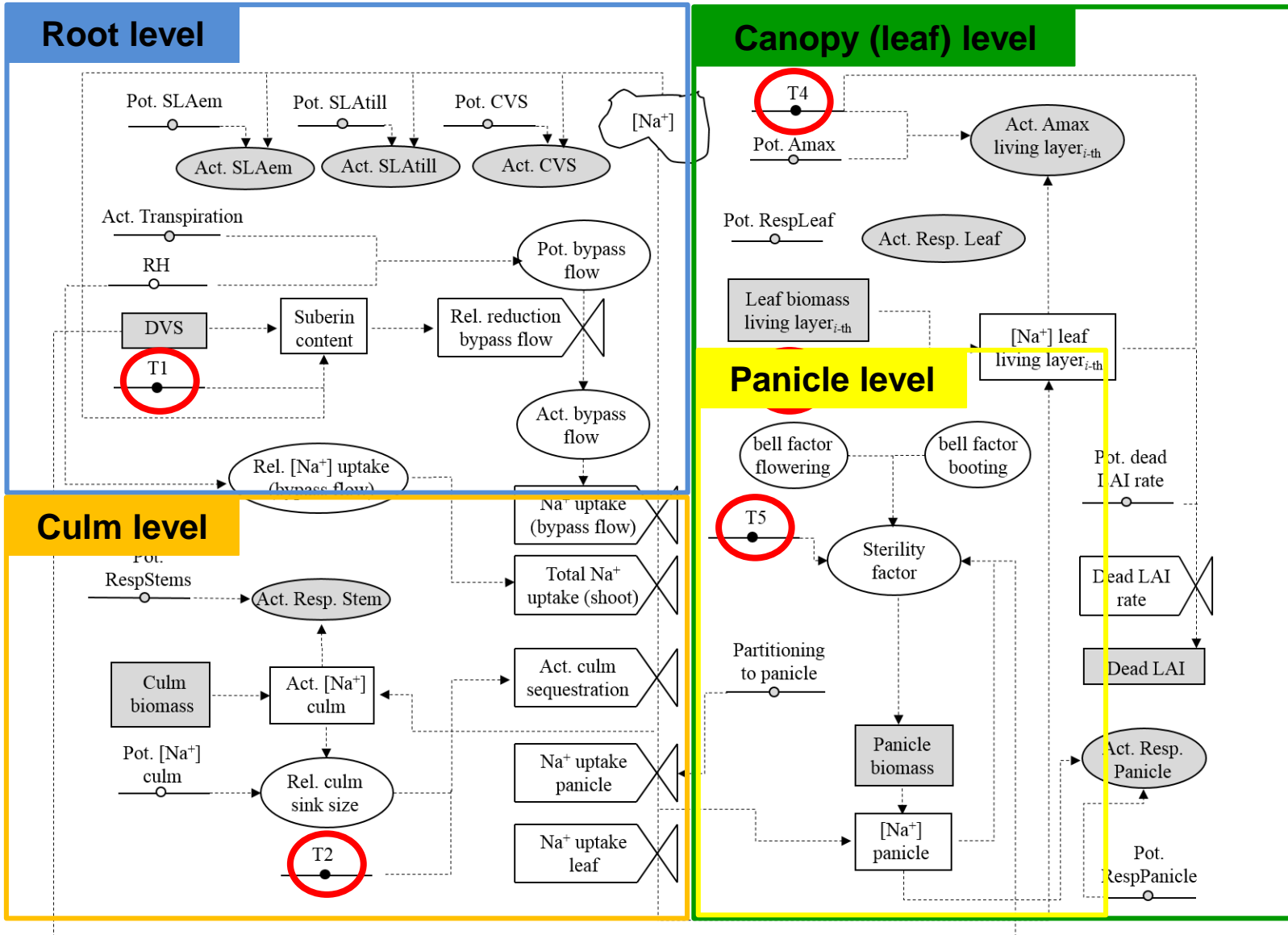
- ✓ Na<sup>+</sup> **uptake** and translocation to the **shoot (T1)**
- ✓ Na<sup>+</sup> sequestration into pseudo-**culm base (T2)**
- ✓ Na<sup>+</sup> compartmentation into **oldest leaves (T3)**
- ✓ Impact of the accumulated Na<sup>+</sup> on **photosynthesis** and leaf **senescence (T4)**
- ✓ Na<sup>+</sup> induced spikelet **sterility (T5)**





# In silico ideotyping

Development of crop ideotypes





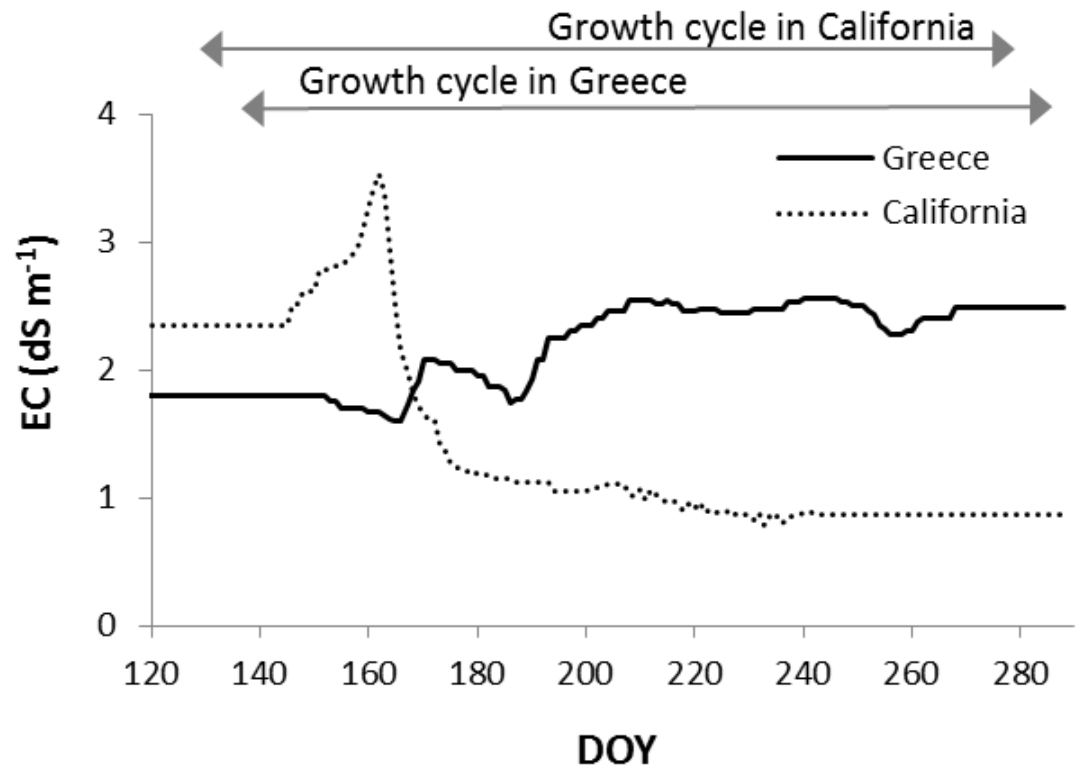
# In silico ideotyping

Development of crop ideotypes

## Mid term strategy

- **Sample results**

- ✓ Rice, salinity, Greece, California

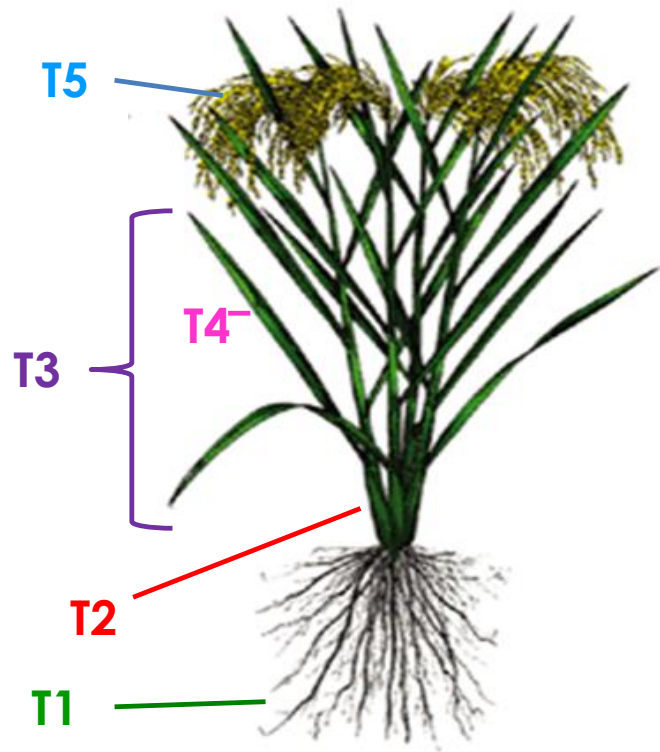




# In silico ideotyping

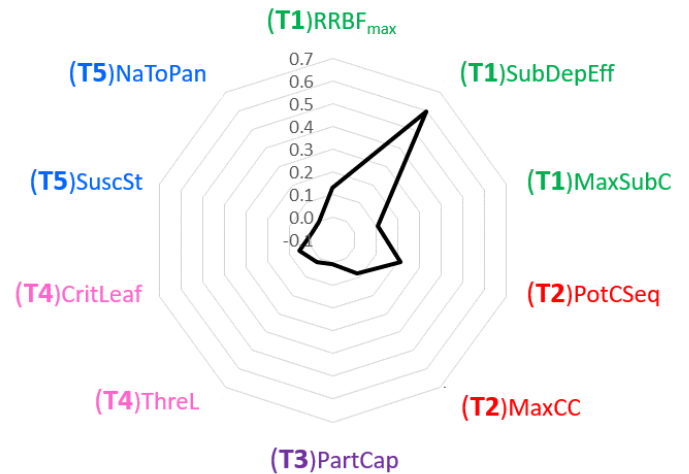
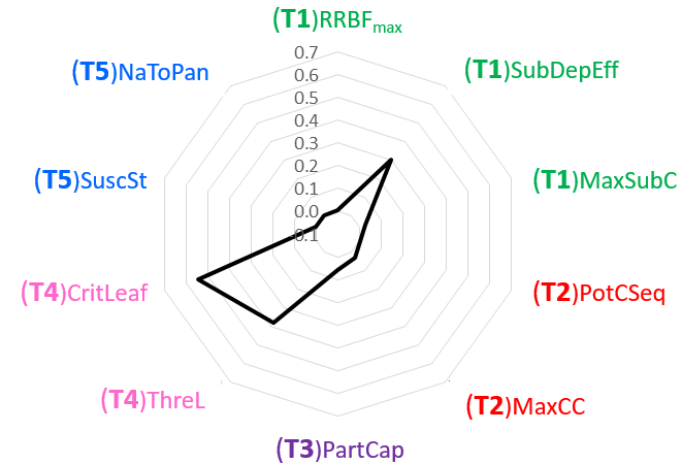
Development of crop ideotypes

## Mid term strategy



**California**  
Sobol' total order effect

**Greece**  
Sobol' total order effect



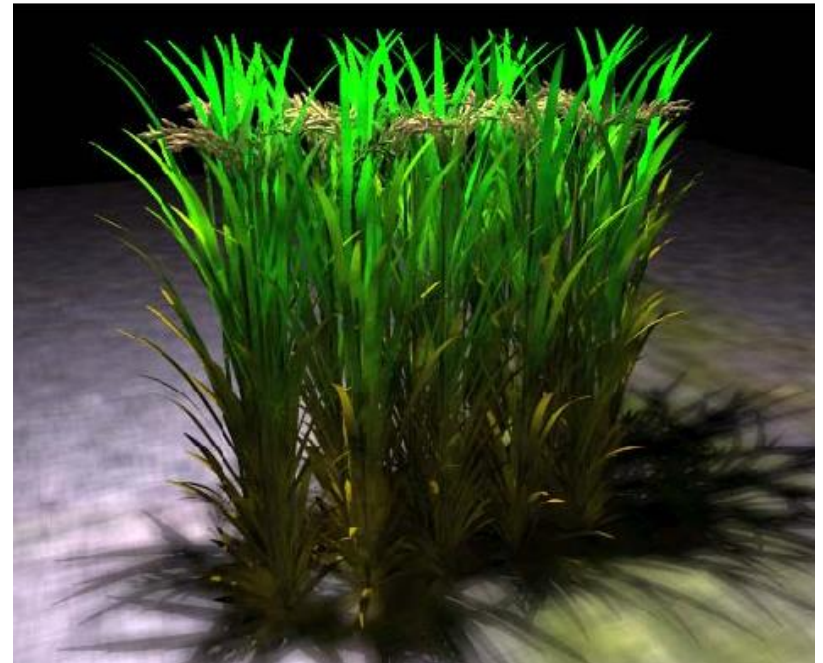
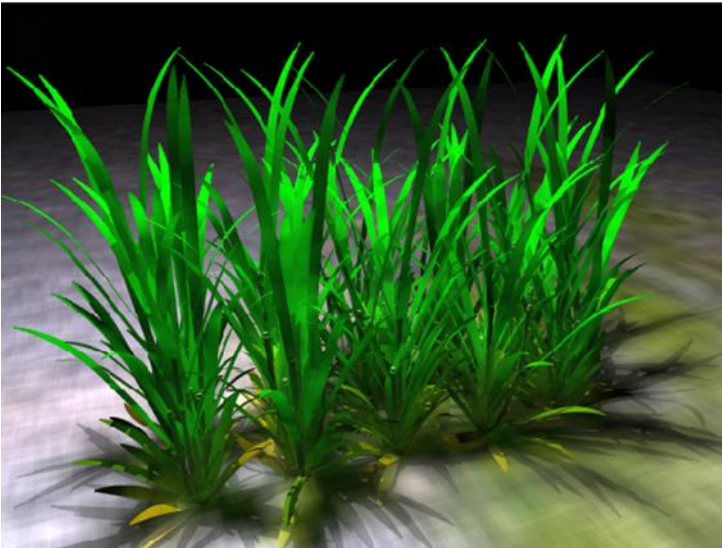


# In silico ideotyping

Development of crop ideotypes

## Mid term strategy

- Develop new models, by building models around traits
  - ✓ **Not only salinity...**
    - **Canopy structure**



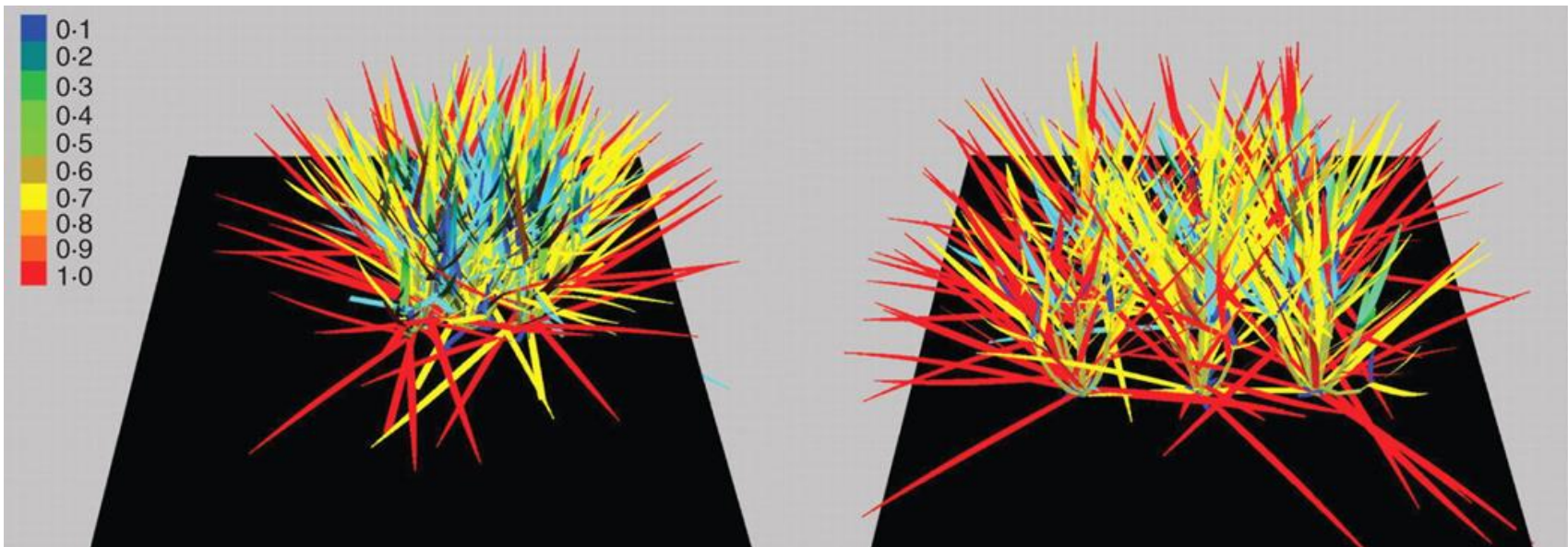


# In silico ideotyping

Development of crop ideotypes

## Mid term strategy

- Develop new models, by building models around traits
  - ✓ **Not only salinity...**
    - **Canopy structure**







# In silico ideotyping

Development of crop ideotypes

## Mid term strategy

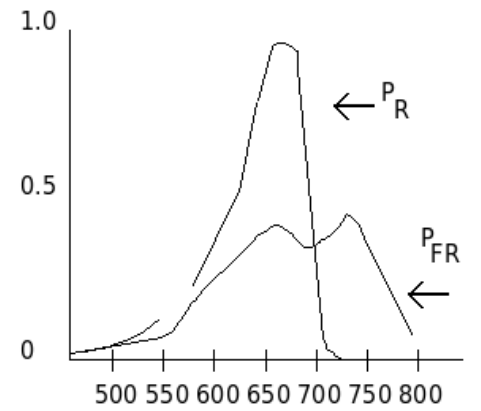
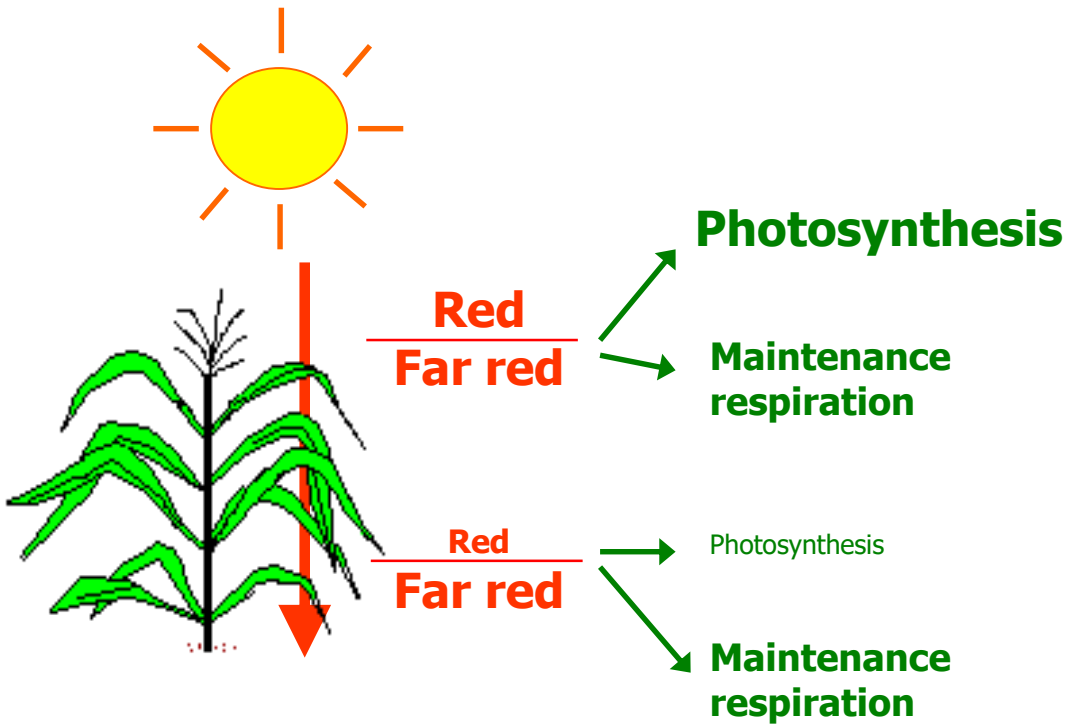
- Develop new models, by building models around traits
  - ✓ **Not only salinity...**
    - **Multi-spectral photosynthesis**
      - **Available crop models** simulate photosynthesis **without considering efficiency** in different **wavelengths**
      - **Saturation** to light of enzymatic chains is **mostly** simulated at the level of **whole canopy**
      - **Phytochrome A**



# In silico ideotyping

Development of crop ideotypes

## Phytochrome A



Energy balance in different canopy layers



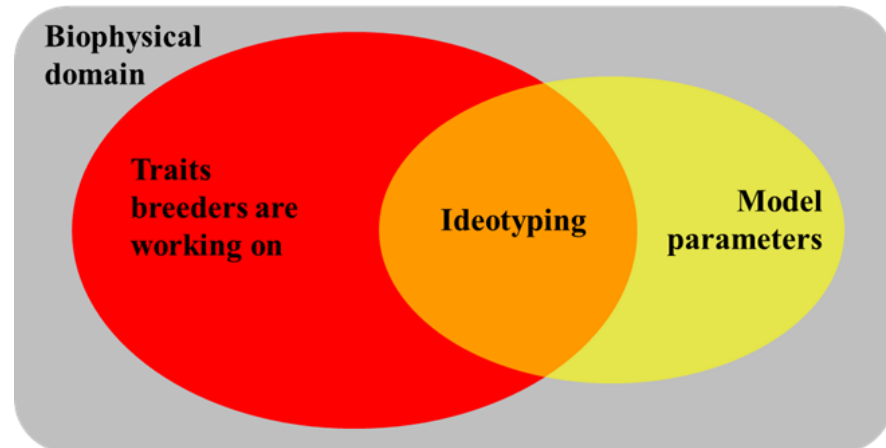
Leaf senescence



# In silico ideotyping

## Development of crop ideotypes

- As mentioned, **current crop models** are **not completely suitable** to support breeding/genetics
  - ✓ They were **not explicitly developed** for this purpose
  - ✓ The **risk** is to develop ideotypes that **cannot be realized in vivo**
- **Two strategies:**
  - ✓ Mid term
  - ✓ Short term





# In silico ideotyping

## Development of crop ideotypes

### Short term strategy

- What can we do **while new models are developed?**
- Try to **reduce the risk** of defining **in silico varieties** that **cannot be realized in vivo**
- How?
  - ✓ Selecting the **most suitable model** according to the specific objective
  - ✓ Pay attention to the **biophysical meaning** of **parameters** (which parameters, ranges, distributions)
  - ✓ **Multi-model** ideotyping?



# In silico ideotyping

Development of crop ideotypes

## Multi-model ideotyping

- **Assumptions:**

- ✓ Models are **partially unsuitable** for ideotyping **for different reasons** (ways processes are represented)
  - **Each** having **imperfect relationships** between **parameters** and **traits**
- ✓ **The effects** of those imperfect relationships **will be diluted**
- ✓ **The impact** of the **(over)responsiveness** of different models **to the uncertainty in the distributions** for the same parameters (or of parameters with a very similar meaning) **will be decreased**

→ We are leading an **international activity** on this within **AgMIP-Rice**



# In silico ideotyping

## Development of crop ideotypes

### Short term strategy

- What can we do **while new models are developed?**
- Try to **reduce the risk** of defining ***in silico* varieties** that **cannot be realized *in vivo***
- How?
  - ✓ Selecting the **most suitable model** according to the specific objective
  - ✓ Pay attention to the **biophysical meaning** of **parameters** (which parameters, ranges, distributions)
  - ✓ **Multi-model** ideotyping?
  - ✓ **Interaction** between modellers, breeders, geneticists, physiologists



# Crop models and breeding

## Development of crop ideotypes

### Two main strategies

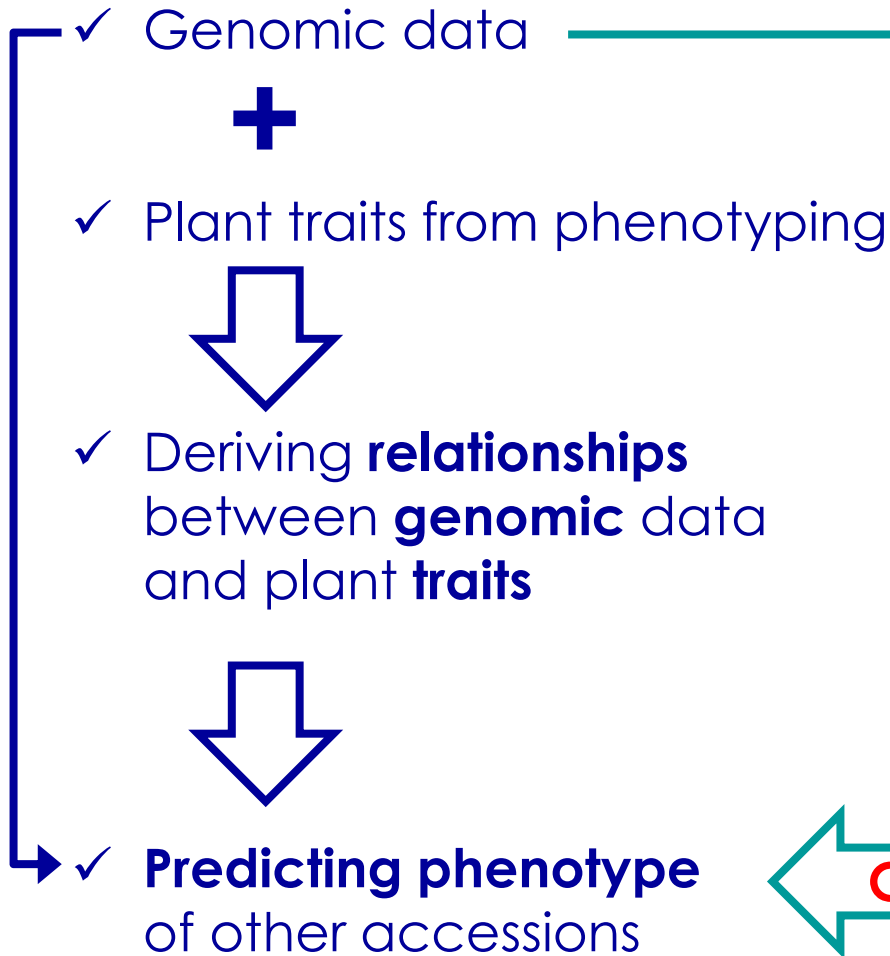
1. **Identifying most promising traits** (and trait values), also targeting “future” conditions
  - Estimating **potential benefits**  
...in silico **ideotyping**
2. **Extending** the potential of **genomic prediction (GP)**
  - ...in silico **phenotyping?**
  - Very few attempts at the moment  
Currently, focus on **phenology**



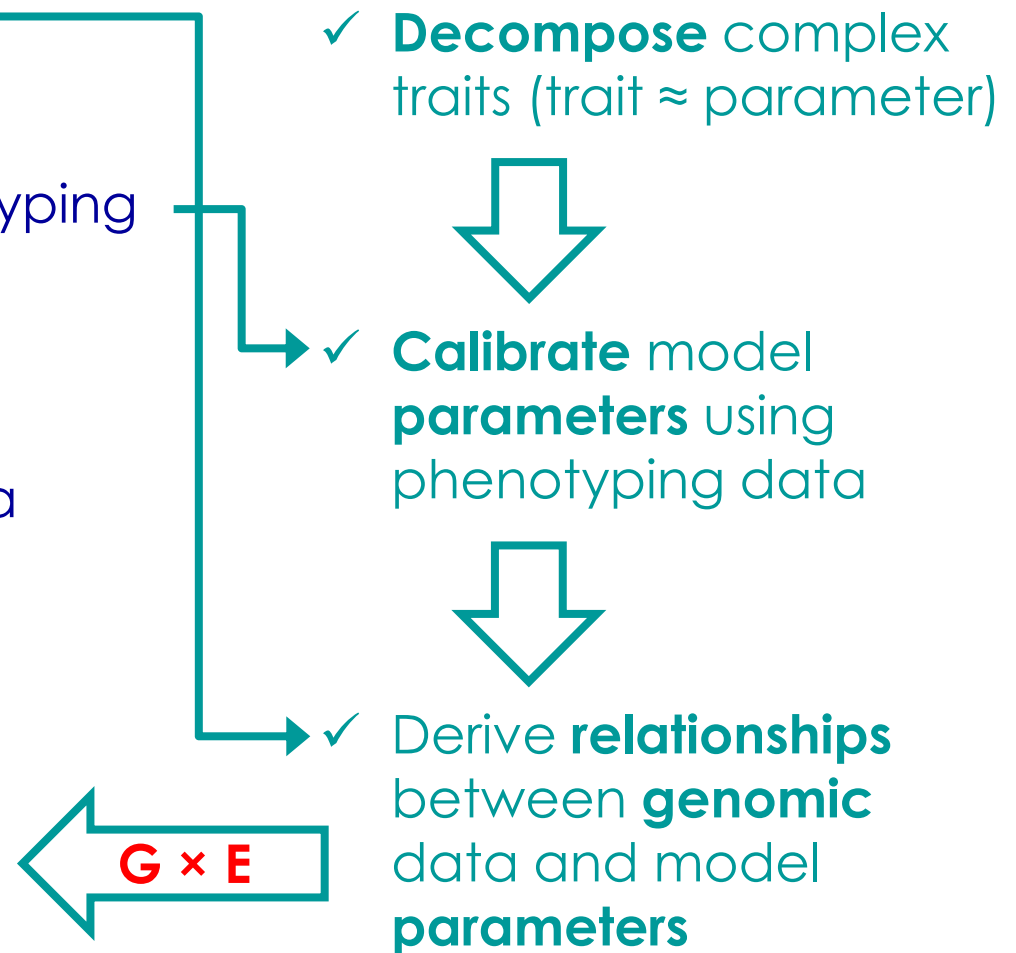
# In silico phenotyping

Development of crop ideotypes

- “Standard” GP



- “Model-based” GP







# In silico phenotyping

Development of crop ideotypes

## Why crop model-supported GP?

### ✓ **Standard GP:**

- **Statistics** is used to derive **relationships** between genotype and phenotype
  - relationships are **not explicit**
  - relationships **valid** only under the **same conditions** for which they were developed

### ✓ **Model-supported GP:**

- The **model** is used to **interpret  $G \times E$**  interactions
  - **relationships** between genotype and phenotype are more **explicit**
  - relationships should be **valid** under **conditions different** from those they were developed for



# In silico phenotyping

Development of crop ideotypes

- **Sample results:**

- ✓ **169** rice **accessions** (rice diversity panel)
- ✓ **Genomic data** (SNPs) consisting of **700,000 SNPs** from the high-density rice array (IRRI)
- ✓ **Trait: days from sowing to flowering**
  - 3 sites (2 in Madagascar, 1 in Senegal)
  - 10 planting dates (on 2 years)
- ✓ Number of **observations for each genotype: 8 to 10**



# In silico phenotyping

## Development of crop ideotypes

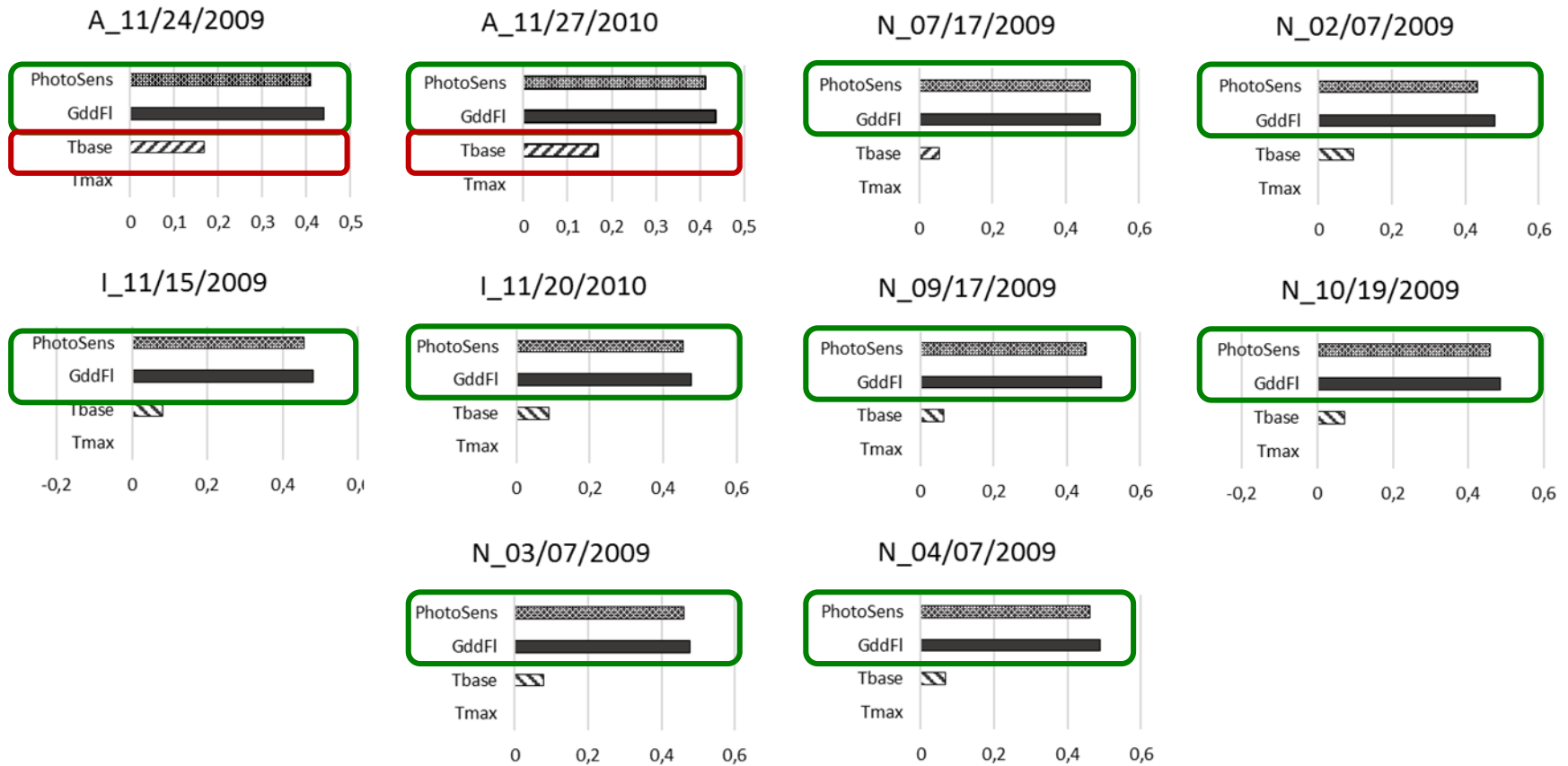
- **Sample study**, step 1:
  - ✓ **Decomposition** of the **complex trait**
  - ✓ **Crop models** {in case of WARM}:
    - Base temperature for thermal time accumulation
    - Maximum temperature for thermal time accumulation
    - Sensitivity to photoperiod
    - Growing degree days from sowing to flowering
  - ✓ **Minimize** the **risk** of **losing robustness** during **calibration**
    - **Sensitivity analysis** to identify most relevant parameters (those to focus on during calibration)



# In silico phenotyping

Development of crop ideotypes

- **Sample study, step 1:**





# In silico phenotyping

## Development of crop ideotypes

- **Sample study**, step 1:
  - ✓ **Decomposition** of the **complex trait**
  - ✓ **Crop models** {in case of WARM}:
    - Base temperature for thermal time accumulation
    - Maximum temperature for thermal time accumulation
    - Sensitivity to photoperiod
    - Growing degree days from sowing to flowering
  - ✓ **Minimize** the **risk** of **losing robustness** during **calibration**
    - **Sensitivity analysis** to identify most relevant parameters (those to focus on during calibration)



# In silico phenotyping

## Development of crop ideotypes

- **Sample study**, step 2
  - ✓ **GP** on calibrated model parameters
    - R package **rrBLUP** (Endelman, 2011) for GP
    - RR-BLUP can directly handle **multi-environment data** and allow running **GWAS** and **GP** with a **one-step** approach
    - **Training dataset**: 135 accessions
      - **Relationships** between **SNPs** and model **parameters**
    - **Validation dataset**: 34 accessions
      - **SNPs-derived model parameters** to simulate flowering date



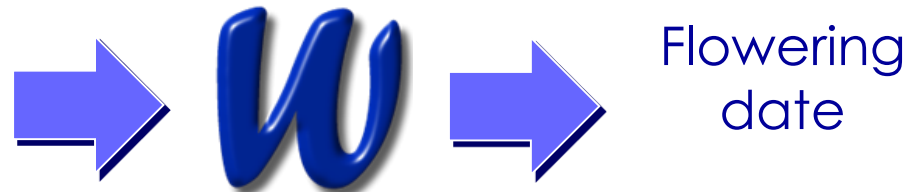
# In silico phenotyping

Development of crop ideotypes

- **Sample study**, step 3

- ✓ Prediction of **flowering date** by running the crop models with **genomic-predicted model parameters** (validation dataset)

Parameter 1 - GDDFlo	
Genomic-	
Accession	Parameter 2 - PhotoSens
	Genomic-predicted value
1	
2	
3	1 0.72
...up to 34	2 0.99
	3 0.97
	...up to 34 0.71



- ✓ **Evaluation** through comparison with **observed flowering date**