

Delivering innovation to growers: how PIA projects have improved information provided to farmers

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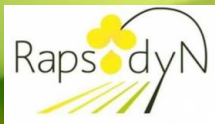
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de la **Betterave**

Fabienne MAUPAS



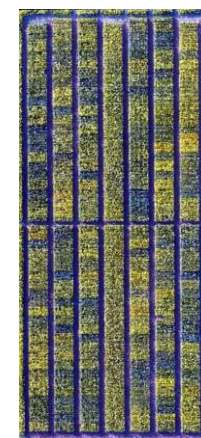
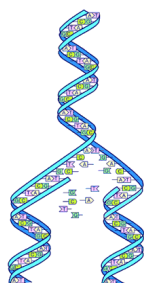
PeaMUST



Main targets to add value for farmers



High throughput and high definition phenotyping tools

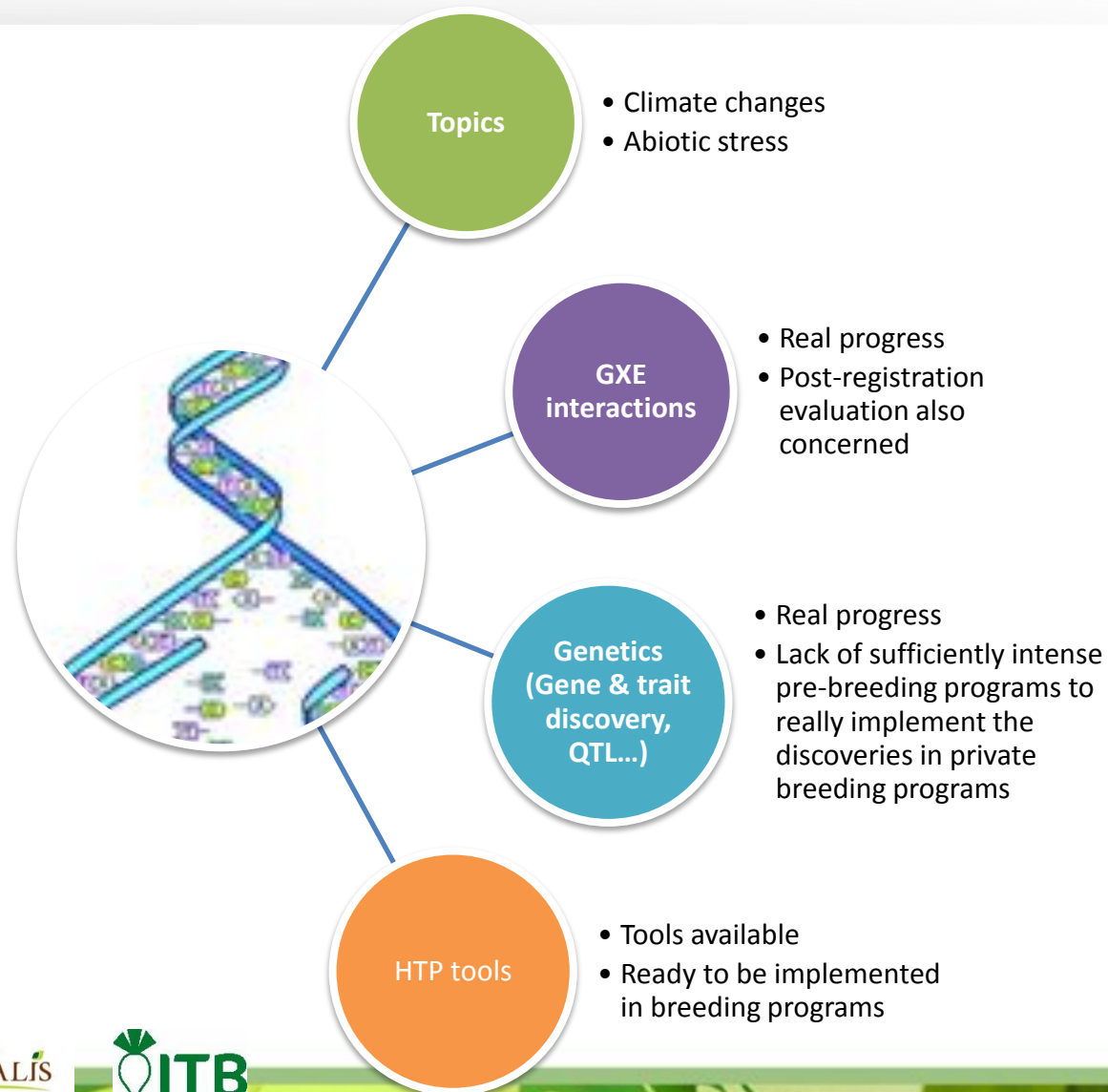


Support of breeding programs

Tools to better characterize & advise registered genotypes

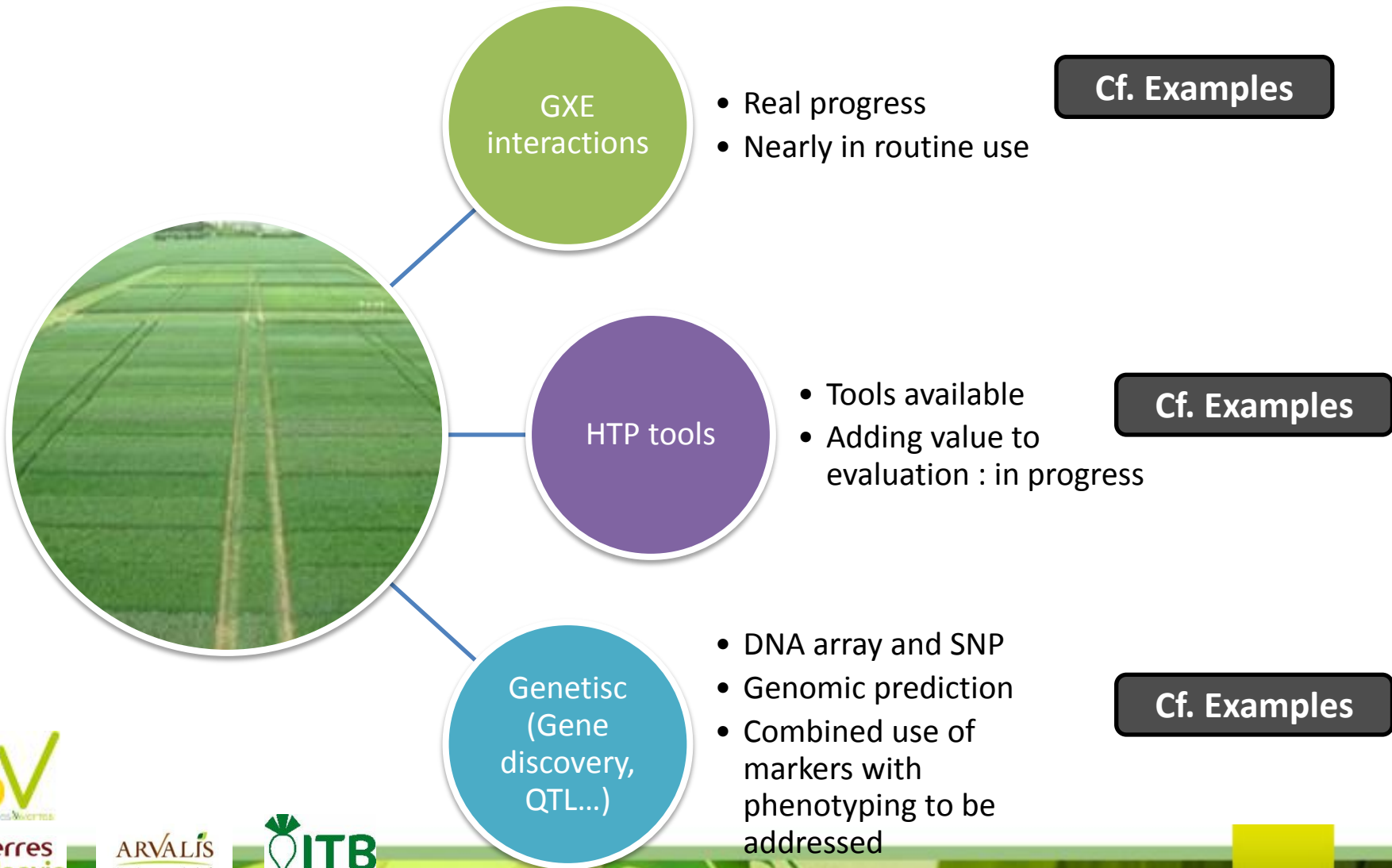


Support of breeding programs



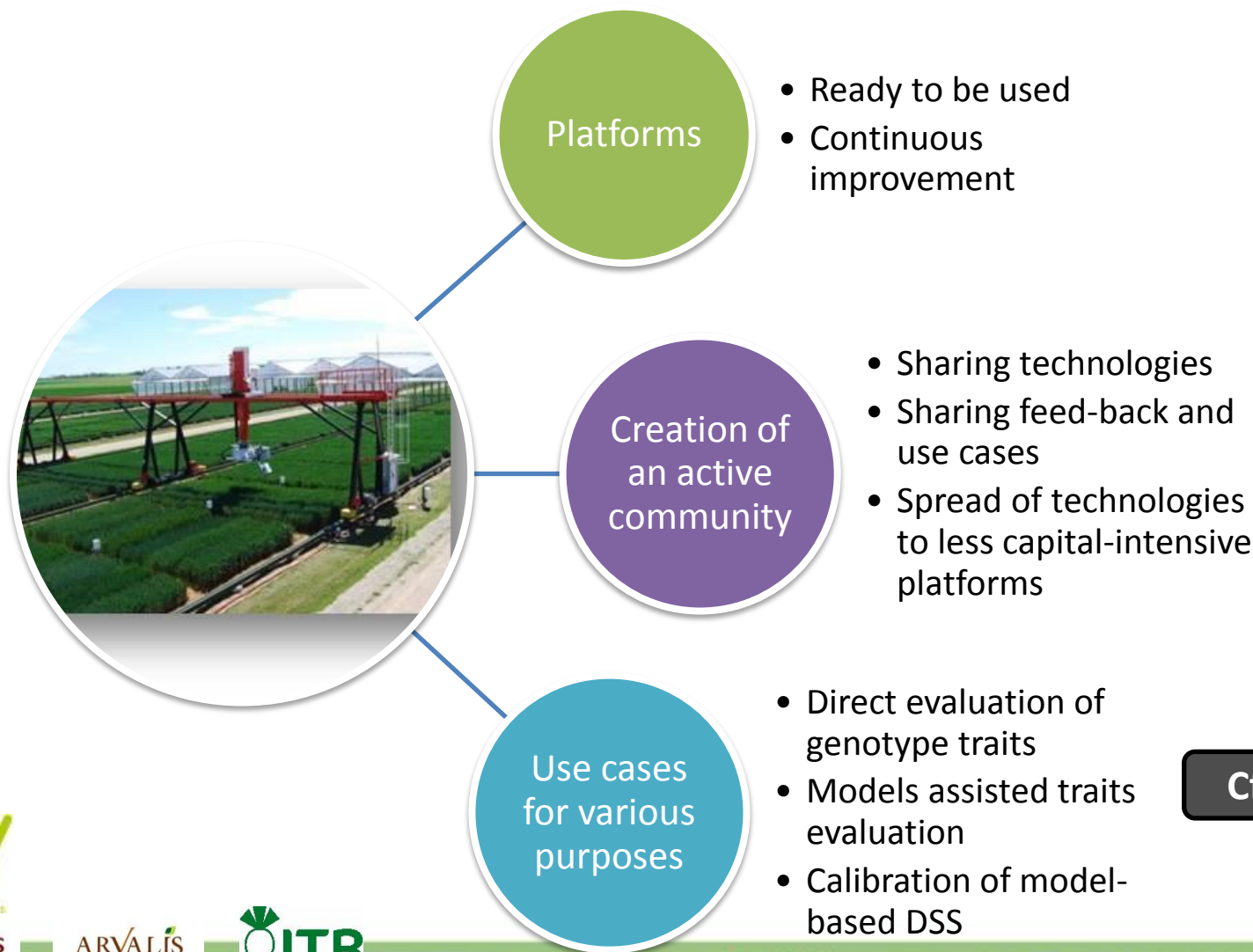


Tools to better characterize registered genotypes





High throughput and high definition phenotyping tools



Cf. Examples

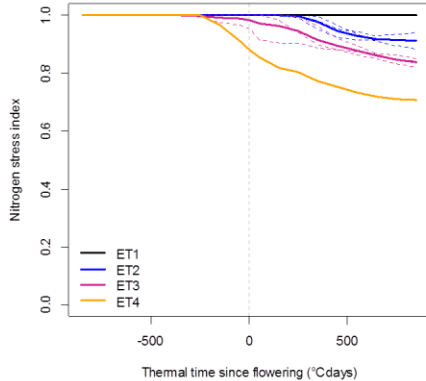
Example 1: characterization of environments in GxE studies



GxE studies



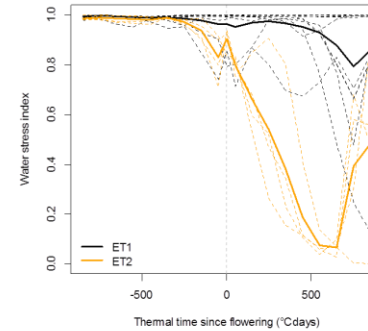
aMaizing trials clustering based on nitrogen stress dynamics



- Four clusters of trials:
 - ET1: no N stress
 - ET2: N stress at SLAG
 - ET3: N stress at flowering
 - ET4: N stress before flowering

- Clustering explains 13% of the total variance (35% of the trial effect)

aMaizing trials clustering based on water stress dynamics



- Two clusters of trials:
 - ET1: no water stress or water stress starting at SLAG
 - ET2: strong water stress starting before flowering

- Clustering explains only 2% of the total variance (4% of the trial effect)

Trial name = loc × year × management

strong water stress starting before flowering

NI14LN
NI14OPT
SO14WD

BL14WD

Modèle CHN
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No water stress or water stress after SLAG

ES14ES
ES14OPT
ES15OPT
SA14WD
SO14OPT

ES14LN
VI14OPT

BL14OPT
ES15LN
RE15ES

VI14LN

No N stress

N stress starting at SLAG

N stress at flowering

N stress before flowering

Bogard et al. WP5

→ Clustering explains 21% of the total variance (55% of the trial effect)





Example 2: DNA array for genomic prediction and functional markers



DNA Arrays (420 K, 35 K)
(BreedWheat WP1)

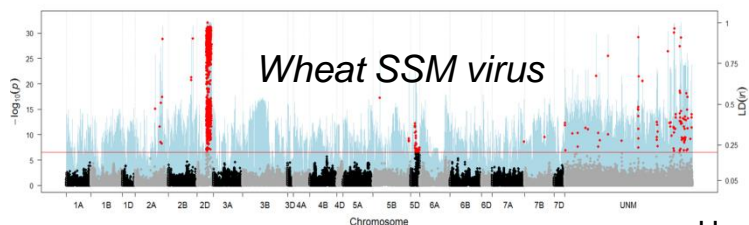


SNP markers

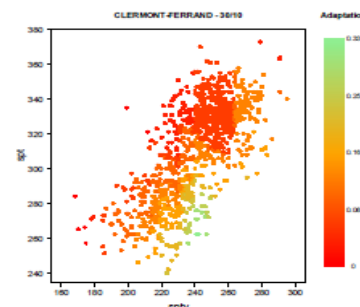
« fonctionnal QTL »
for breeding and
cultivar evaluation

Genomic prediction models

Wheat phenology



Hourcade *et al.*, 2018
Plant Pathology



Bogard *et al.*, in prep

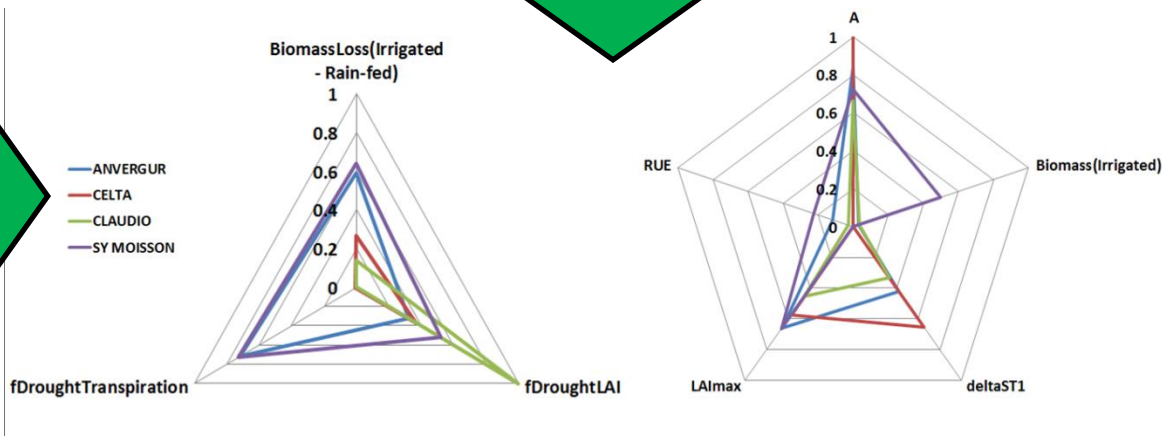
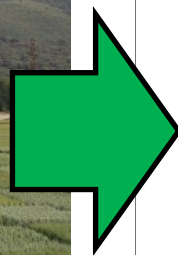
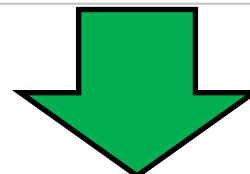
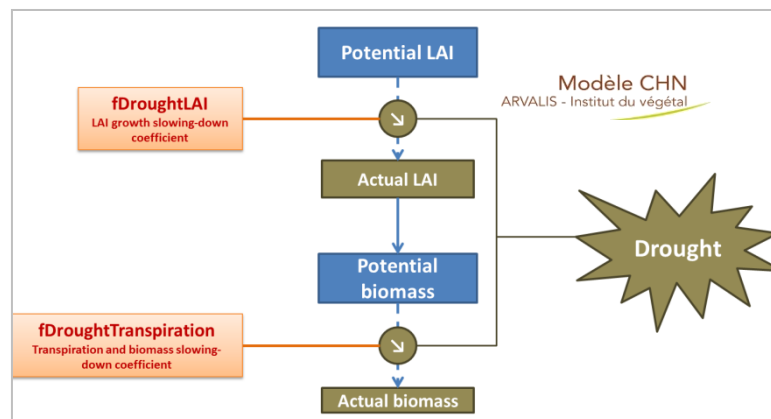
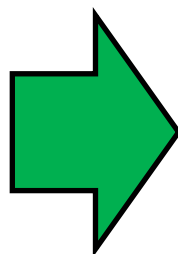
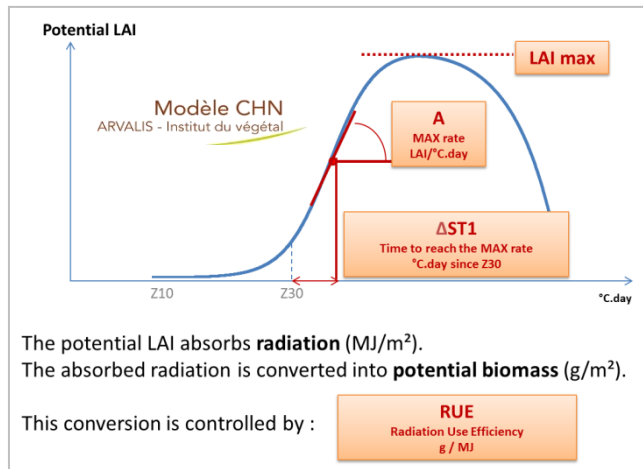




Example 3: Model assisted traits evaluation in wheat



Piquemal *et al.*, 2018 (IPPS)

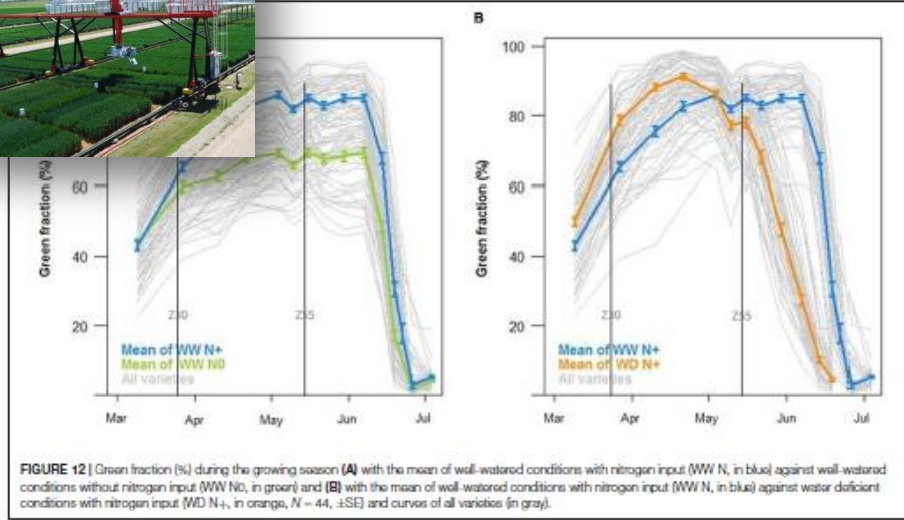
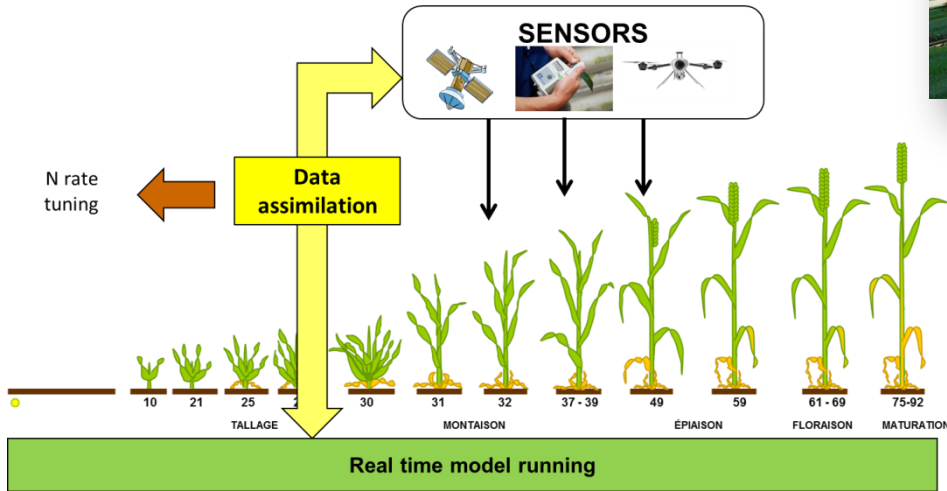




Example 4: Use of HTP tools to calibrate model-based DSS

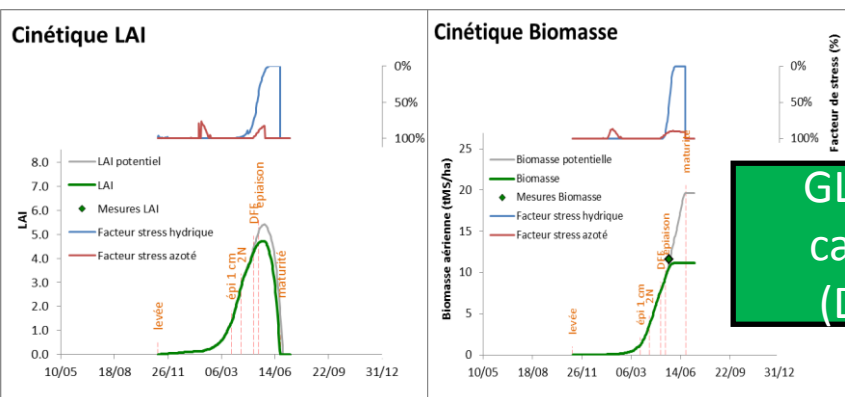


A model is not perfect → need to mix simulation and sensor measurements → more accurate DSS

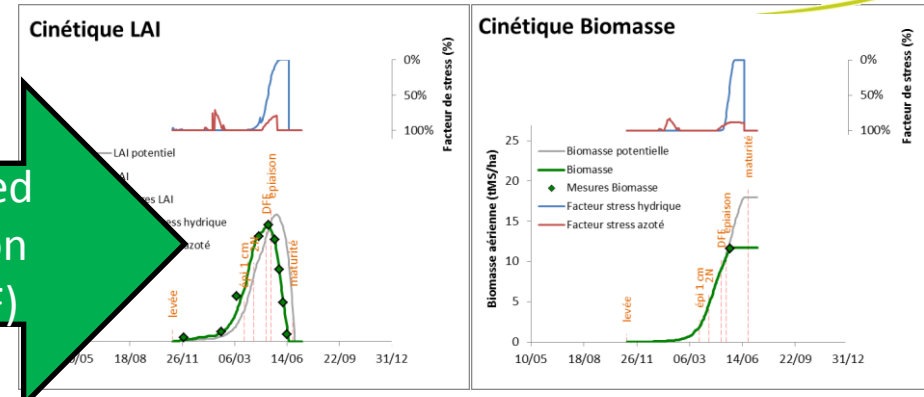


Beauchêne et al. 2019- FPS

Modèle CHN
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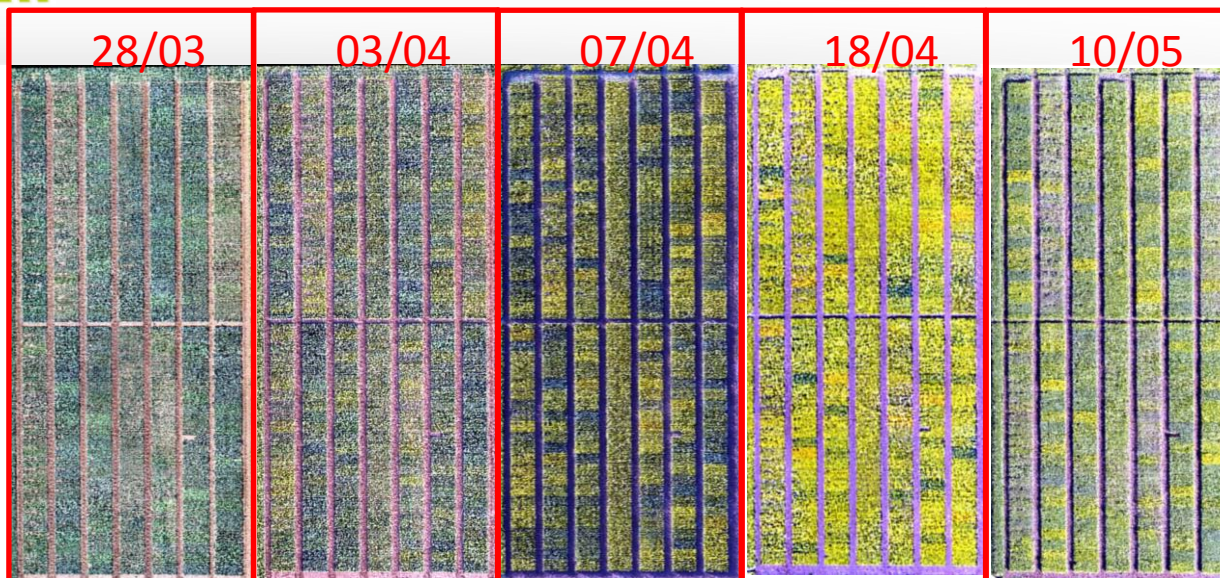


GLAI based calibration (DRM-KF)

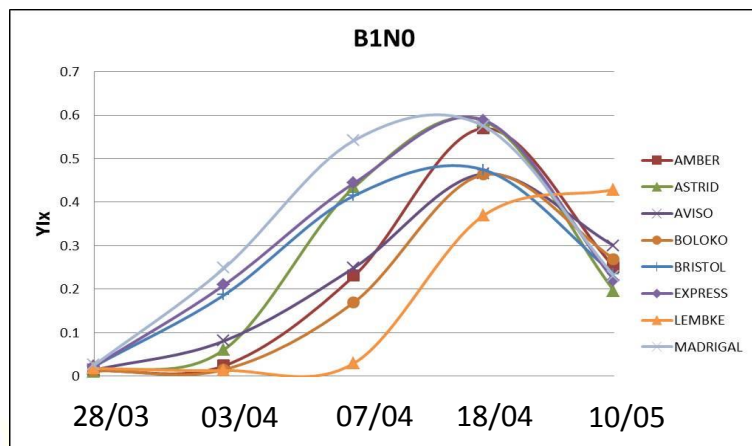
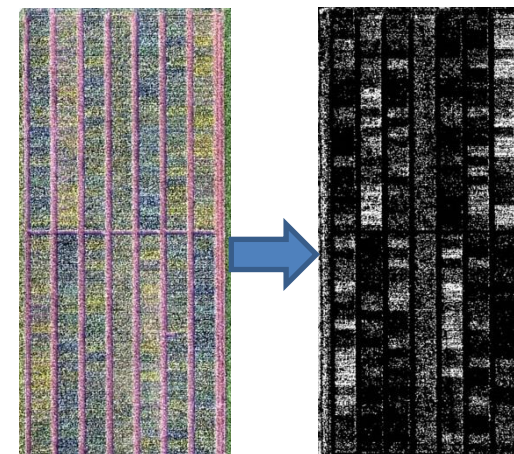


Piquemal et al. unpub.

Example 4bis: Use of drone to assess OSR flowering



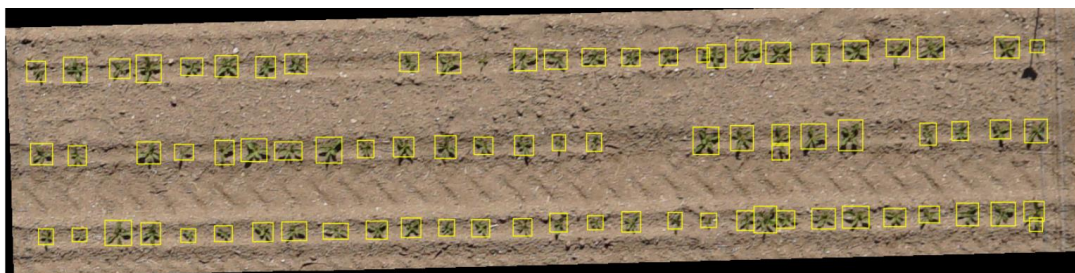
2017



- Rapeseed models : poor phenology models w/ 0 genotypic variability
- Approach → potential for massive data acquisition to calibrate :
 - Breeding/variety trials
 - Remote sensing / big data : Planet satellite constellation

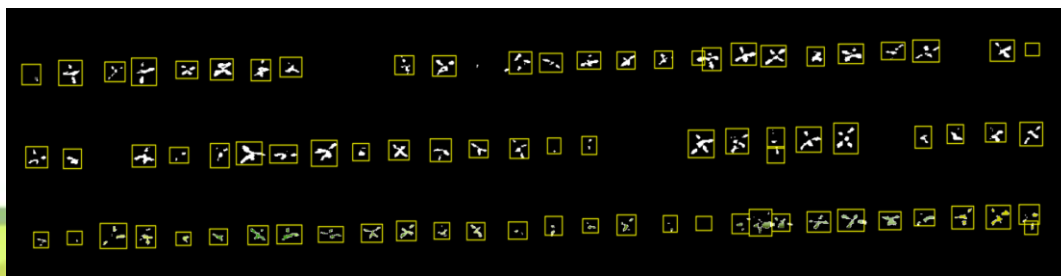


Example 5: Individual sugar beet detection for heterogeneity measurements



Drone image

1st step :
Beet detection
& green pixels segmentation
Performance : 98%





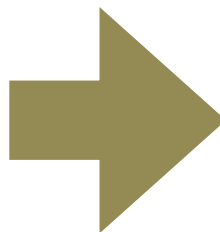
Example 5: Individual sugar beet detection for heterogeneity measurements



2nd step :

Computing coefficient of variation

$CV = \text{std} / \text{mean}$ for each plot

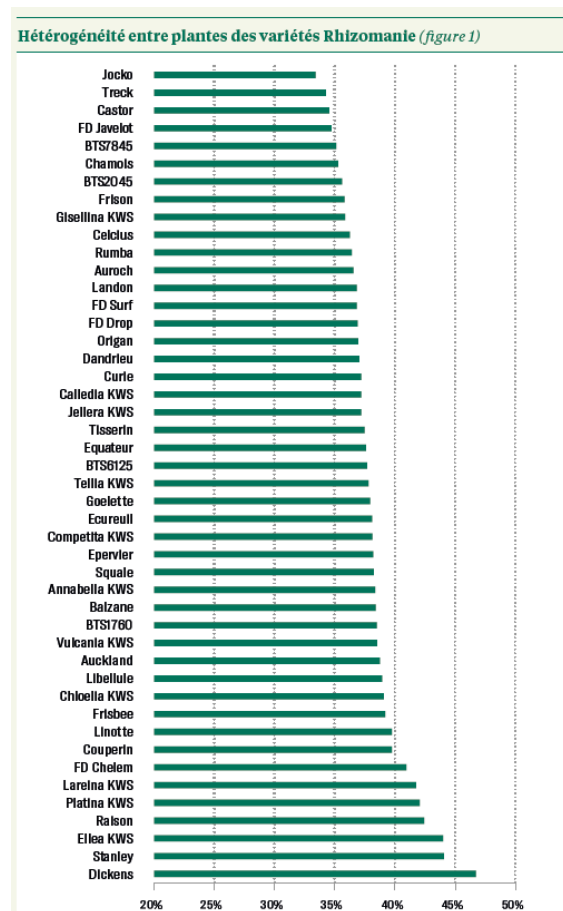


Choosing a uniform variety

Homogeneous development

→ Simplier harvester set-up

→ Easy weed control



Varietal ranking

→ Advices to growers



Example 6: Use of drone to assess OSR early vigor



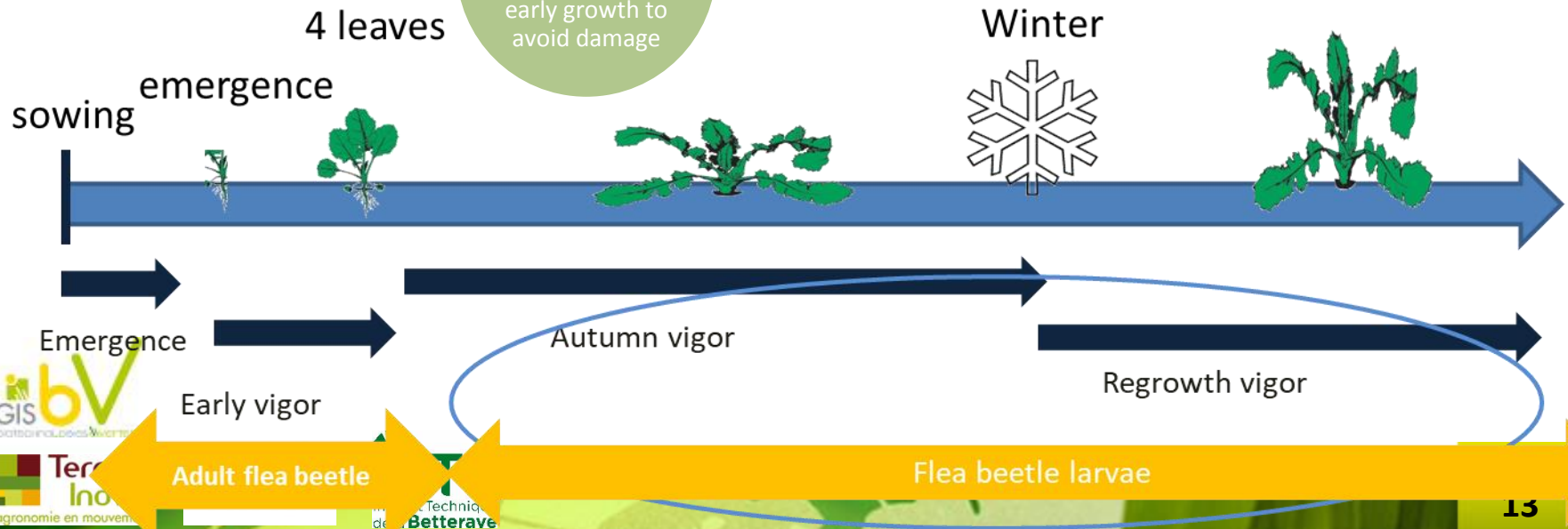
Phenotyping
for a trait
linked to
agroecological
production

Climate change
→ august-septembre
drought → poor
establishment
conditions

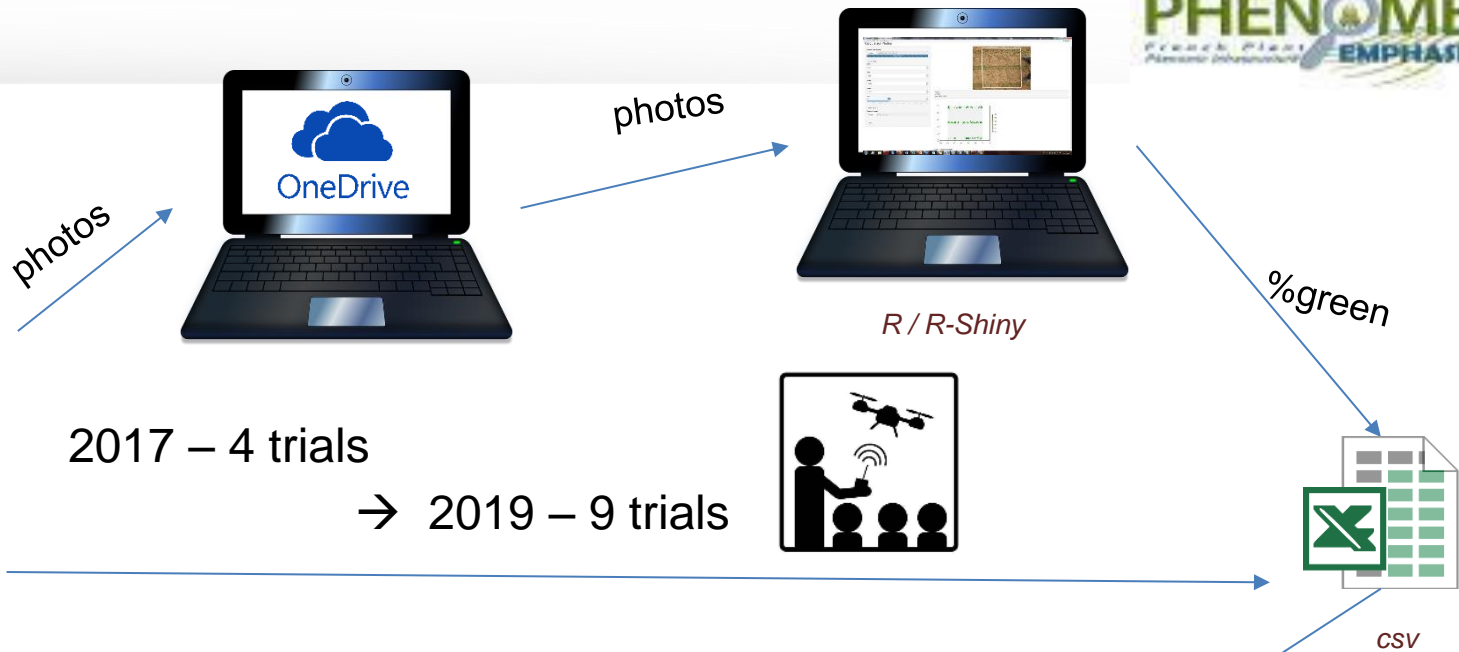


New agronomic paradigm
for establishment & early
growth to avoid
insect(icide)s : towards
direct seeding, companion
cropping, early
fertilization... AND
vigorous, continually
growing varieties

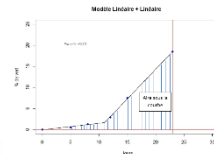
Extension of
highly resistant
autum insects →
need continuous
early growth to
avoid damage



Example 6: Use of drone to assess OSR early vigor



Analysis & recommendation



```

Autoregressive.R x  Utis.R x
Source on Save  Run  Stop  Source
6
7- # glist Functions -----
8
9- glist <- function(...) {
10-   gl <- list(...)
11-   if (length(gl) == 0L ||
12-       all(sapply(gl, okGlistelt, simplify=TRUE))) {
13-     # Ensure glist is "flat"
14-     # Don't want glist containing glist ...
15-     if (all(sapply(gl, is.grob)))
16-       gl <- do.call("c", lapply(gl, as.glist))
17-     class(gl) <- c("glist")
18-     return(gl)
19-   } else {
20-     stop("Only 'grobs' allowed in 'glist'")
21-   }
22- }
    
```

Script-R

And now ? ITA priorities to...

Topic	... continue progress in breeding	... continue progress in delivering advice to growers
HTTP tools	Scale up & scale out : democratize tools	
GxE	- Support environmental & agronomic characterization	- Maize example → sunflower, all crops
Trait-QTL-Gene discovery	<ul style="list-style-type: none"> - Abiotic <u>and</u> biotic stress - Gene editing - Pre-breeding → Largely out of ITA hands (at the moment): are French public & private sector doing what it takes ?	<ul style="list-style-type: none"> - Pea root rot - Combined use of trials & markers for variety evaluation → new traits & more efficient use of resources
Model-based DSS	- Use in GxE studies	<ul style="list-style-type: none"> - Sugar beet diseases - Wheat example → rapeseed - Genomic prediction of model parameters



**Thank you for your attention
Thanks to all our colleagues
involved in PIA projects !**

