High-throughput field phenotyping: bridging scales from gene to canopy for trait discovery

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Wheat & nitrogen response in France
4 trials, 225 genotypes x N+/N- (-100 kgN/ha)

- Equivalent progress in N+ and N-
- Positive yield trend without losing % protein
- NUE increase

Wheat & nitrogen response in France
4 trials, 225 genotypes x N+/N- (-100 kgN/ha)

- No improvement in tolerance to N deficit
- NUE improvement in 10 years = 7 kg N/ha saved
- Compensating N:wheat price volatility would require 40 years breeding

The scale issue for functional genomics and crop improvement

Relevant scale for impact in breeding

What could high throughput field phenotyping contribute?
What mechanisms are behind what breeding has been empirically ameliorating?

The PhénoBlé project phenotyping system

A semi-automatic system for high throughput phenotyping wheat cultivars in-field conditions: description and first results

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The PhénoBlé project phenotyping system

2010 → 2013: Technology readiness level: 2 → 6

Sensor
Raw data
Calculated data
Functional data

The PhénoBlé project phenotyping system

Technology readiness level: 2 → 6

Incoming radiation
Interception efficiency (RIE)
Leaf area (and angle)
Chlorophyll related traits
Conversion efficiency (RUE)
Nitrogen stress
Harvest index
Yield components

The trial

- 208 genotypes x 2 reps x 2 treatments N+/N-) + 4 checks x 2 reps x 2 treatments x 6 sub-blocks
- N+ = standard; N- = standard – 100 kg/ha
- Yield loss: 12.4 q/ha = 16.4%

- Protein loss: 11.8% → 10.9%
- NNI flowering: 0.88 → 0.67

Data analysis

- Phenotypic:
  - Adjusted means, including heading date effect
  - Correlation between agronomic traits and sensor traits
  - For N+, N- and difference between N+ and N-
  - Yield tolerance to N computed with 9 additional trials

- GWAS

Results: sensor phenotypes

- Canopy chlorophyll at mid-grain fill → yield
- Canopy chlorophyll loss at mid-grain fill → yield loss
- (Green area loss at mid-grain fill → yield loss)
- (Similar results for biomass at flowering)
Results: GWAS

1 zone: B2
1 zone: B3

1. also associated with chlorophyll
2. also associated with mid-grain SE
MTCI

Further steps: functional mapping

\[ LAI = K \left( \frac{1}{1 + e^{-a(x-x_m)}} \right) \]

Consider a graph showing normal and low N supply effects on LAI over a range of chlorophyll levels.

Further steps: Improving technology

TRL
4
5
6
7
8
9

2011
2012
2013
2014
2015
2016
2017

Consider a TRL ladder diagram with arrows indicating progression.

Conclusions & perspectives

- Developing high-throughput phenotyping in the field is a long & painful process, but it looks like it should pay!
- We should be able to learn about how canopy function mediates yield and nitrogen deficit tolerance
- This should help us identifying relevant candidate genes directly at the canopy scale
- This could help us in understanding effects of candidate genes in field settings
- A 1st proof of concept with technologies at intermediate TRL
- We should move our technologies further up the TRL ladder if we want them to have broad impact

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