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Llorenç Cabrera Bosquet, Christian Fournier, Claude Welcker, Benoit Suard,

Francois Tardieu

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High throughput estimation of incident light, light interception and radiationuse efficiency of thousands of plants in a phenotyping platform

Llorenc Cabrera-Bosquet, Christian Fournier, Claude Welcker, Benoît Suard and Francois Tardieu INRA, UMR759, Laboratoire d'Ecophysiologie des Plantes sous Stress Environnementaux, F- 34060 Montpellier, France

Rationale

A major limiting step in phenotyping is the availability of methods for extracting information from massive phenotypic data, thereby generating variables usable in genetic analyses or in modelling. One of the major difficulty in these analyses is the genotype by environment (G×E) interaction. Experiments in phenotyping platforms can serve to dissect the complex phenotype into traits that have a high heritability and a high reproducibility. For instance, biomass accumulation can be expressed as a function of the incident light, the fraction of light



PHENOARCH platform at LEPSE, Montpellier (http://bioweb.supagro.inra.fr/phenoarch)



platform.

1. A mini-panel of 27 maize (Zea mays L.) inbred lines with tropical origins maximising the genetic variability were used in this study. Two greenhouse experiments were conducted during autumn and winter-spring time.



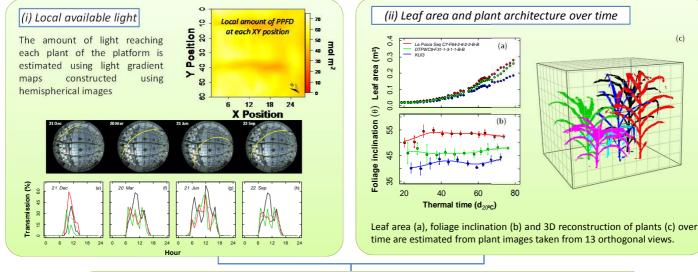
Detail of three contrasted studied maize lines

2. Different models were interfaced in order to calculate the amount of light intercepted by each plant of the platform:

intercepted by the crop and the efficiency in which light is converted to biomass, radiation use

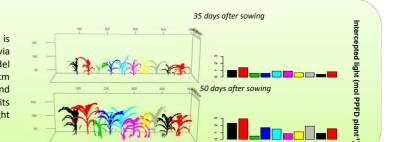
efficiency (RUE)¹. Here we aimed to develop a non-invasive procedure to measure light

interception and RUE in hundreds of maize lines in the PHENOARCH high-throughput phenotyping



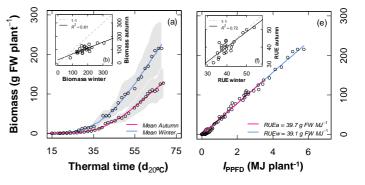
(iii) Intercepted PPFD

The amount of intercepted PPFD per plant is estimated for each plant and each day via the RATP² functional-structural plant model that calculates interception in 20x20 cm voxels of the canopy using leaf area and architecture of each plant and of its neighbours and the local amount of light calculated using the light maps.



Results

- Biomass and leaf area differed between experiments showing • a high G×E interaction. On the contrary, genotypic plant leaf angle values were highly conserved between experiments, showing a high heritability.
- Difference in biomass between experiments was entirely accounted for by the difference in intercepted light. Hence, the mean RUE was common to both experiments and genotypes ranked similarly.



Conclusions

The methods presented here allowed dissecting the differences between experiments into:

- (i) Genotypic traits that did not differ between experiments but had a high genetic variability, namely plant architecture and RUE.
- (ii) Environmental differences, essentially incident light, that affected both biomass and leaf area.
- (iii) Plant traits that differed between experiments due to environmental variables, in particular leaf growth.