

High-throughput phenotyping and genetic analysis to promote breeding for enhanced nitrogen use efficiency in winter oilseed rape

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Objectives

- Development high-throughput multispectral sensor-based method for determining nitrogen use efficiency of new winter oilseed rape genotypes in the field
- Compilation of a phenotypic database for analyzing growth dynamics under low nitrogen fertilization
- Improve genetic predict genotypic performance leverage and selection models

High-throughput phenotyping to capture crop dynamics



PARROT BLUEGRASS™ quadcopter PARROT analyses; Integrated agricultural SEQUOIATM multispectral sensors

Multispectral sensor records sunlight reflection at the crop canopy.

The GPS-controlled periodically drone captures multispectral images to precisely monitor the development of each genotype.

Vegetation indices (VI) provide information on canopy biomass, leaf area, and nitrogen status.

Translating sensor information into plant nitrogen status

In a calibration trial of different varieties under of nitrogen fertilization treatments, multispectral data and plant samples were collected across developmental stages. Samples were analyzed for nitrogen content and the mass laboratory. were calculated the multispectral data and correlated with nitrogen content data.

A multispectral orthomosaic (left) provides localized information on reflectance at multiple wavelengths. The reflectance data are extracted with a plot raster (right) in QuantumGIS.

Statistical models fitted on calibration data predict crop parameters from VI:

 $Y(c_{Nitrogen}) \sim BBCH \ stage + VI_1 + VI_2 + VI_3$ $(R_{adi}^2 = 0.92; p < 0.001)$ $Y(Dry\ mass) \sim BBCH\ stage + VI_1 + VI_2 + VI_3$

 $Nitrogen\ uptake = c_{Nitrogen} * Dry\ mass$

 $(R_{adi}^2 = 0.82; p < 0.001)$

minimum 50 % quantile

maximum

Prediction of

performance

low

genotypic

under

input

nitrogen

Predicted nitrogen concentration [%] (left) and shoot dry mass [g/m²] (right) values for each plot. The color scale indicates genotypic differences and spatial trends.

Screen microNAM population for highly nitrogen-efficient genotypes in field Common "father" line n = 50

5 elite mother lines

Genome-wide marker data of elite mothers, common father, and double haploid lines

Phenotypic data of parents and experimental hybrids

5 families of 50 DH lines

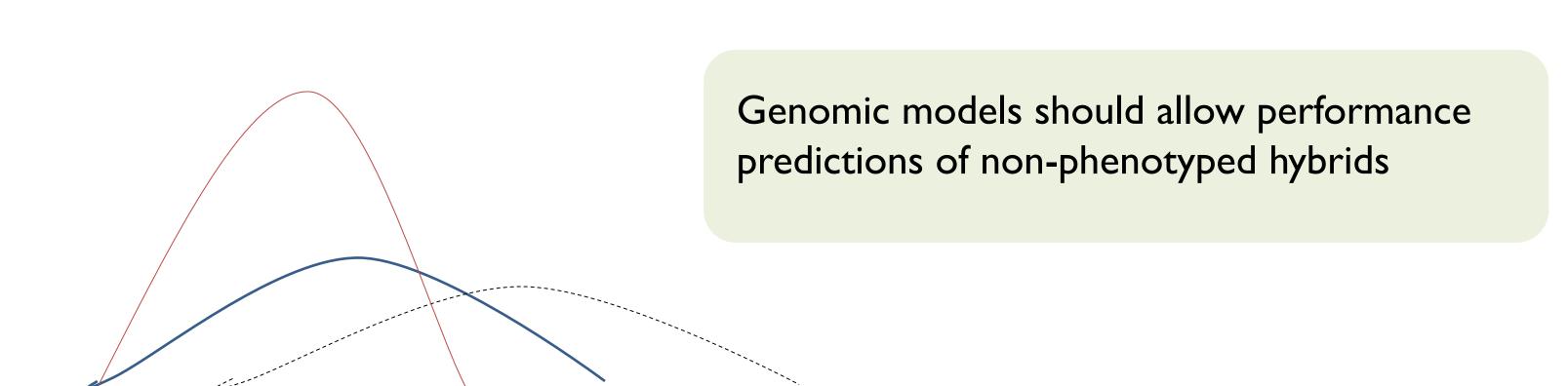
2 male-sterile testers

500 test hybrids

Evaluation of yield and quality parameters Oil, protein,

SCA / glucosinolate content proxyGCA

Modelling genotypic performance under low N-fertilization



Examining the genomic basis of heterosis

- Mapping of haplotypes associated with heterotic effects
- Genome-wide association studies
- Identification of nitrogen-use efficiency candidate QTL

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