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Connecting rapeseed plant architecture to yield via 3D-imaging

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Background:

Increasing seed oil content and seed yield are major aims of rapeseed breeding. Seed yield is a highly quantitative trait influenced by many genetic and physiological factors. An improved ability to capture the complexity of the rapeseed plant architecture and more easily collect data on key yield-determining traits like the number, length or angle of siliques and primary/secondary branches could potentially play a vital role in prediction and selection for biomass and seed yield.

Objective:

Here, we sought to assess and reveal relationships between the complex plant architecture of rapeseed and seed yield under low Nitrogen fertilization, in order to collect detailed data about how primary yield components impact the formation of yield. Furthermore, we benchmark methods to automatically dissect and evaluate rapeseed canopy architecture via 3D scans of field-grown plants, representing a novel alternative to potentially reduce the need for labour-intensive manual phenotyping.

Methods:

To evaluate the impact of different architectural traits on seed yield, we used correlations and importance scores from the machine learning method extreme gradient boosting. Furthermore, genome wide association studies were conducted to identify key regions for architectural traits.

To automate the phenotyping process for architectural traits, we utilized 3Dimage scans of manually phenotyped plants to train machine learning-based prediction models. Since 3D data is not directly usable in most prediction pipelines, we first extracted properties of the 3D data (various surface and volume measures) as proxies for plant architecture. Alternatively, we directly used the 3D image data in a complex deep learning framework.

Results:

Trait correlations revealed that the number of siliques on the side branches were more important in formation of seed yield than the silique number on the main branch. Furthermore, the number of siliques at intermediate sections of the branches were more highly correlated to overall yield than the number of siliques on lower or higher sections of branches. Interestingly, genome wide association studies indicated that silique number on different side branches was controlled by different genetic loci. Although total plant height did not show a noteworthy correlation to overall yield, the side branch height correlated positively with yield.

Predictions of plant architectural traits from 3D scans showed good prediction accuracy for silique number, plant height, the side branch height and seed yield, respectively. Generally, the use of extracted features for predictions resulted in higher prediction accuracies compared to the use of deep learning methods directly on 3D data.

Conclusions:

Plant architecture seems to be highly related to seed yield and Nitrogen utilisation efficiency, and the consideration of architectural traits in breeding programs can potentially help to identify genotypes with superior seed yield potential, especially in early generations. We established and benchmarked novel methods to automate assessments of rapeseed architectural traits. In future, these techniques could help replace labour-intensive manual phenotyping.