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Genetic control of germination-related traits in rapeseed and the potential of genomic and phenomic selection to predict fast germinating ability

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Background:

Fast and uniform seed germination is essential for successful establishment in any crop species. Several studies have explored the genetic bases of germination speed and very early post-germination growth in rapeseed populations, providing candidate genes and potential markers for fast-germinating accessions. However, germination is a complex character that could hardly be resumed by a discrete number of markers.

Objective:

Germination is often approximated by the final germination rate (GR) and the germination speed. This study aims to (i) provide a comprehensive overview of the processes underlying these traits and the related genetic factors and (ii) examine the potential of genomic and phenomic calibrations to predict seed germination capacity.

Methods:

A population of 242 genetically diverse *B. napus* inbred lines was phenotyped for seed germination parameters using a high throughput phenotyping facility. It included 135 winter (WOSR) and 91 spring oilseed rape (SOSR), 14 winter fodder and 2 rutabagas. Germination was estimated by GR and a proxy for germination speed: its uniformity. The related traits were measured during 96h from the start of seed imbibition: (i) pre-germination processes (imbibition speed), (ii) germination dynamics (area under the curve (AUC), time to reach 50% of germination (T50), GR, GR at 36h (GR36), uniformity) and (iii) post-germination processes (radicle elongation speed (ES)). Near infrared spectra (NIRS) and thousand seed weight (TSW) were acquired on the same seeds lots. Relationships between those traits were studied using PCA and random forest. A GWAS was then conducted to identify the main genomic regions controlling germination-related traits. The ability of genomic (GP) and phenomic (PP) predictions was compared to predict seed germination. Several models were tested: ridge-regression BLUP, genomic/hyperspectral BLUP and Bayesian lasso.

Results:

Our results highlighted AUC, T50 and GR36 as key processes involved in germination. On the contrary, imbibition related-traits, ES and TSW did not contribute to germination rate or uniformity. Three germination patterns were identified within the population: the slowest lines (high uniformity, low GR), intermediates lines (medium uniformity and GR) and the fastest lines (low uniformity, high GR). Deciphering the genetic control of the key processes allowed to identify 32 QTL. These traits being polygenic, we compared the GP and PP abilities to predict them. Predictive abilities were higher for the process-based traits than for the germination integrative traits. Indeed, GP and PP abilities ranged between 0.50 and 0.60 for AUC, T50, and GR36 and between 0.35 and 0.45 for GR and uniformity. Furthermore, PP performed slightly better than GP (0.50>GP>0.55) for GR36, AUC and T50, highlighting the potential of NIRS spectra to predict complex traits.

Conclusions:

These results bring more knowledge on traits underlying germination as well as their genetic bases. Our study highlights that PP is particularly adapted to predict germination related-traits and open a door to the integration of this character in breeding. The next step will be to evaluate the germination ability under sub-optimal conditions, (e.g., low water potential) to investigate germinative vigour and to study the link between germination ability and seedling vigour to improve crop establishment.