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Envirotyping within a multi-environment trial allowed identifying genetic determinants of winter oilseed rape yield plasticity

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Background:

A main challenge for rapeseed consists in maintaining seed yield while adapting to climate changes and contributing to environmentally friendly cropping systems. Breeding for plasticity and cultivar adaptation is one of the keys to meeting this challenge.

Objective:

Genetic diversity for plasticity is the expression of Genotype x environment interaction. Therefore, we propose to identify the genetic determinant of seed yield G×E interaction for winter oilseed rape using GWAS coupled with a multi-environmental trial and to interpret them in the light of environmental characteristics.

Methods:

173 WOSR was experimented across a multi-environmental trial (MET) constituted of 22 environments resulting from the combination of 8 locations (representative of French growing conditions), 2 growing seasons (2013-2014 and 2014-2015) and two N managements (limiting and non-limiting). An environmental characterization including pedoclimatic indicators (daily temperatures, precipitations, radiation, soil water content), plant status indicators (development stages, nitrogen nutrition index), N-management indicators (quantity of N applied to the crop, soil N content, rainfall before and after fertilization, …) was carried out. The environmental factors that limited seed yield were identified using a PLS regression analysis and used to cluster the individual environments of the MET into envirotypes. GWAS were then carried out for seed yield (SY), at the global MET scale, at the envirotype scale and at the individual environment scale to characterize QTL specificity to environment and QTLx environment interactions.

Results:

The 22 environments were regrouped into 4 contrasting envirotypes (EA, EB, EC, ED). EA presented high SY (3,8 t/ha) and no stress; ED presented the lowest SY (1,9 t/ha), and was mainly affected by vernalization conditions, high temperature during winter, low radiation and temperature during flowering and grain filling. EB and EC presented intermediate SY (2,8t/ha and 2,7 t/ha respectively) and different patterns of limiting factors: low temperature and radiation at flowering as well as a low soil water content for EB, and low N availability combined to low temperatures during bolting for EC. At the MET scale, the SY variation was explained by the genotype (G) (24.7% of SY variation), the environment (E), (55,5%) and the GxE (5.8%). The envirotype effect explained 70% of the environmental variation and 24.6% of GxE. As the whole 19 QTL were detected for SY. Out of these, 4 for were detected either at the MET or envirotype scale. QA09 and QC09a, were stable (detected at the MET scale or for different envirotypes and environments) and QA07a, was specifically detected on the most stressed envirotype (ED).

Conclusions:

The combination of an analysis of the main environmental factors that affected seed yield, combined to GWAS performed in a MET allowed a precise characterization of genomic regions involved in SY plasticity. For instance, the QTL QA07a was only detected in envirotype ED. To go further, we also analysed the molecular diversity at QA07a and showed a lack of genetic diversity within modern lines compared to older cultivars bred before the selection for low glucosinolate content. This open perspective for improving plasticity and rapeseed adaptation within the elite germplasm.