

Correlation between line *per se* and testcross performance for rye: Multi-cross QTL analysis results

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Abstract

The genotypic correlation between line *per se* and testcross performance is an important quantitative-genetic parameter to design hybrid breeding programs. The two main goals were to study (1) the association between line *per se* and testcross performance in two segregating winter rye populations (A, B) with each of 220 progenies tested in six environments and (2) the advantage of QTL mapping in single analysis and across populations (multiple cross) for plant height, thousand-kernel weight, test weight, total pentosan, and starch. The segregating progenies were genotyped with single nucleotide polymorphism (SNP), simple sequence repeat (SSR), and DArT markers (2176 for population A and 1072 for population B, respectively) to generate the consensus map. High heritabilities were found for all traits for line *per se* and testcross performance ($H^2=0.7-0.9$). The only exception was pentosan content with moderate heritabilities throughout ($H^2=0.6$). Genotypic correlations between line *per se* and testcross performance were high for most comparisons ($r_g=0.7-0.8$) except for pentosan content ($r_g=0.4-0.7$). Selection of these traits for line *per se* performance in early generations will save field plots in further testing testcross performance.

By single QTL analysis we detected 19 QTL for line *per se* and 43 QTL for testcross performance across all traits in population A, and for line *per se* and testcross performance each of 16 QTL in population B, respectively.

In the multi cross QTL analysis we detected 49 QTL for line *per se* and 44 QTL for testcross performance. The highest explained phenotypic variance across all QTL was found for starch for line *per se* (51.6%), and for plant height for testcross performance (54.2%). For plant height, test weight, total pentosan, and starch contents we detected five, three, two, and four QTL overlapping for line *per se* and testcross performance, respectively.

In contrast, the other traits did not show any overlapping QTL. This can be explained by epistasis and/or masking dominance effects of the tester. For plant height and most quality traits, the higher heritability for line *per se* than for testcross performance and the large congruency of QTL results clearly suggests selection on line *per se* performance should be successful and increase efficiency of hybrid breeding.

Keywords

DArT marker, heritability, hybrid breeding, *Secale cereale*

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