

QTL mapping of carrot resistance to leaf blight with connected populations: stability across years and consequences for breeding

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QTL mapping of carrot resistance to leaf blight with connected populations: stability Titre

across years and consequences for breeding

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ISSN 1432-2242 Combining biparental and multiparental connected population analyses was useful for the identification of 11 QTLs in two new genetic backgrounds of carrot resistance to Alternaria dauci and for breeding recommendations.

Leaf blight due to the fungus Alternaria dauci is the major carrot foliar disease worldwide. Some resistance OTLs have been previously identified in one population, but the evaluation of additional genetic backgrounds with higher level of resistance would give opportunities for breeders to combine them by pyramiding. For this purpose, two segregating populations were evaluated twice across 4 years in the same environment (1) to compare the efficiency of the single vs. the connected populations approach for characterizing the new sources of carrot resistance to Alternaria dauci; (2) to evaluate the stability of QTLs over the years; and (3) to give recommendations to breeders for marker-assisted selection. Single and connected analyses were complementary; their combination allowed the detection of 11 QTLs. Connected analyses allowed the identification of common and specific QTLs among the two populations and the most favorable allele at each QTL. Important contrasts between allelic effects were observed with four and five most favorable alleles coming from the two resistant parental lines, whereas two other favorable alleles came from the susceptible parental line. While four QTLs were consistent across years, seven were detected within a single year. The heritabilities for both populations PC2 and

PC3 were high (75 and 78 %, respectively), suggesting that the resistance of carrot to *A. dauci* was little affected by these environmental conditions, but the instability of

Résumé en anglais

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QTL over years may be due to changing environmental conditions. The complementarity between these parental lines in terms of interesting allelic

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- [1] http://okina.univ-angers.fr/publications?f[author]=167
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combinations is also discussed.

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