

Genome wide association analysis reveals candidate genes controlling an antagonistic effect of biotic and osmotic stress on *Arabidopsis thaliana* growth

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Abstract

While the response of *Arabidopsis thaliana* to either drought, herbivory or fungal infection has been well-examined, the consequences of exposure to a series of such (a)biotic stresses are not well studied. This work reports on the genetic mechanisms underlying Arabidopsis response to single osmotic stress, and to combinatorial stress, either fungal infection using *Botrytis cinerea* or herbivory using *Pieris rapae* caterpillars followed by an osmotic stress treatment. Several small effect genetic loci associated with rosette dry weight (DW), rosette water content (WC), and the projected rosette leaf area (PLA) in response to combinatorial stress were mapped using univariate and multi-environment genome wide association approaches. A SNP associated with *DROUGHT INDUCED 19 (DI19)* was identified by both approaches, supporting its potential involvement in the response to combinatorial stress. Several SNPs were found to be in linkage disequilibrium with known stress-responsive genes such as *PEROXIDASE 34 (PRX34)*, *BASIC LEUCINE ZIPPER 25 (bZIP25)*, *RESISTANCE METHYLATED GENE 1 (RMG1)*, and *WHITE RUST RESISTANCE 4 (WRR4)*. An antagonistic effect between biotic and osmotic stress was found for the *prx34* and *arf4* mutants, which suggests *PRX34* and *ARF4* to play an important role in the response to the combinatorial stress.

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