

**GENOME-WIDE EXON-CAPTURE APPROACH IDENTIFIES GENETIC VARIANTS  
ASSOCIATED WITH SUSCEPTIBILITY OF NORWAY SPRUCE TREES  
TO *HETEROBASIDION PARVIPORUM* INFECTION**

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In boreal forests the root and butt rot caused by members of the *Heterobasidion annosum* species complex is the most economically important disease of conifer trees. In the infected trees, the wood decay dramatically decreases their value and causes considerable losses to forest owners. Trees vary in their susceptibility to *Heterobasidion* infection, but the genetic determinants underlying the variation in the susceptibility are not well understood. We performed the identification of Norway spruce genes associated with the resistance to *Heterobasidion parviporum* infection using genome-wide exon-capture approach. Sixty-four clonal Norway spruce lines were phenotyped, and their responses to *H. parviporum* inoculation were determined by lesion length measurements. Afterwards, the spruce lines were genotyped by targeted resequencing and identification of genetic variants (SNPs). Genome-wide association analysis identified 36 SNPs located within 34 genes as significantly associated with the larger necrotic lesions in response to *H. parviporum* inoculation. The genetic variants identified in our analysis are potential marker candidates for future breeding programs.

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