Quantitative Trait Loci for Resistance to Two Fungal Pathogens in *Quercus robur*

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Abstract

Powdery mildew, caused by *Erysiphe alphitoides* (Ascomycete), is the most frequent disease of oaks, which are also known to be host plants for *Phytophthora cinnamomi* (Oomycete), the causal agent of ink disease. Components of genetic resistance to these two pathogens, infecting either leaves or root and collar, were investigated in a full-sib family of *Quercus robur* L, that was vegetatively propagated by cuttings.

Resistance to powdery mildew was assessed by two methods. First, inoculations with *E. alphitoides* were performed under controlled conditions on excised leaves removed from cuttings grown in the greenhouse. The level of host-pathogen compatibility was assessed by recording infection success and mycelial growth. Second, the progeny, planted in a comparative test, were assessed for susceptibility to powdery mildew using field evaluation under natural infection conditions over 3 years. Resistance to ink disease was estimated by inoculating *P. cinnamomi* on stems of 2-year-old cuttings grown in the glasshouse, and by measuring the length of the induced lesion in two experiments.

Preliminary results showed that quantitative trait loci (QTL) associated with the response to both pathogens were located on the genetic linkage maps available for the two parents of the F1 family. However we could not identify QTL involved in both diseases.

Although the genetic architecture of resistance to *E. alphitoides* varied between years and infection conditions, stable QTL were detected. Because infection by this fungus is strongly dependent on the phenological status of its host, co-locations between QTL for resistance and QTL for phenology were studied.

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