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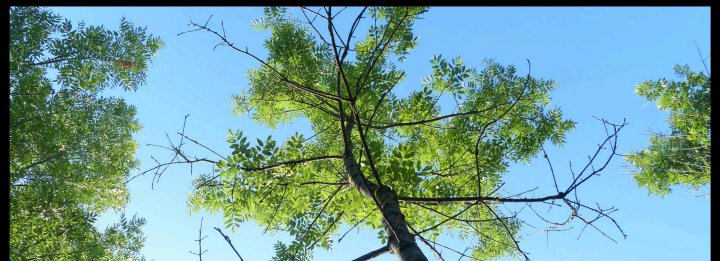
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Genetic variability for susceptibility to the invasive ascomycete *Hymenoscyphus fraxineus* in a common Ash (*Fraxinus excelsior*) provenance and progeny trial indicates significant potential for breeding

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Severe dieback of European common ash (*Fraxinus excelsior*) was first reported in Poland and Lithuania in the early 1990s. It was fourteen years after the first reports that an ascomycete, now referred to as *Hymenoscyphus fraxineus* (Queloz et al. 2011), was finally identified as the primary causal agent (Kowalski 2006). Several findings pledge for the species being of Asian origin and acting as an invasive pathogen in Europe (Husson et al. 2011, McKinney et al. 2012, Bengtsson et al. 2012, Zhao et al. 2013). Detailed quantifications are scarce, but consequences of the disease can be severe. In Lithuania, 10 years after the first report, over 30,000 ha of common ash stands were reported to be affected and mortality was estimated to be 60% state wide while in some parts of the country only about 2% of the trees remained visually healthy (Juodvakis and Vasiliauskas 2002). First detection of the disease in France occurred in 2008, in the North-Eastern part of the country. Since then, the disease has been progressing southwestwards at a pace of approximately 50 km per year. The fungus now occupies half of the country. Eventhough millions of *Fraxinus excelsior* trees died from the disease, recent results from clonal or progeny trials raised hopes that resistant/tolerant trees could be selected. Significant heritability estimates and provenance and/or family effects seem to indicate that breeding programs could be implemented against the disease (Pliura et al. 2011, Kjaer et al. 2012). The present study is only third to analyze the genetic variability of common ash for resistance/tolerance to *H. fraxineus* using open-pollinated progenies. It is based on a 20-year old field trial with 23 half-sib families from 3 French provenances. The trial is located very close to the place where the disease was first detected in France. Because the stand has been monitored every year since 2010 for disease incidence, spatio-temporal components of disease spread could be taken into account to avoid confounding disease escape and resistance. Contrary to previous studies, a Bayesian approach was used instead of the classical frequentist analysis. Bayesian methods accommodate spatio-temporal structures in a more straightforward way. They are also more suitable for modelling data which deviates from normality as commonly observed during early stages of disease spread. This study is also the first to report on genetic parameters for collar lesions and on the genetic correlation with crown defoliation. Collar lesions due to *H. fraxineus* have been described in France only recently (Husson et al. 2012) and this symptom has certainly been overlooked in countries with a longer infection history.

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Keywords

Fraxinus excelsior, European Ash dieback, resistance, tolerance, breeding, progeny trial, genetic variability.