

**VARIATION AND GENOMIC BASIS OF *FRAXINUS EXCELSIOR* (COMMON ASH)
SUSCEPTIBILITY TO *HYMENOSCYPHUS FRAXINEUS*
(ASH DIEBACK) THROUGHOUT BRITAIN**

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Ash dieback (ADB), caused by *Hymenoscyphus fraxineus*, has severely damaged a large proportion of ash trees (*Fraxinus excelsior*) in continental Europe. In Britain, the disease was found only 6 years ago in the southeast, and is still spreading. A large-scale screening trial to evaluate ADB damage to provenances of *F. excelsior* sourced from throughout the British Isles was planted in 2013 in the southeast of England. Trees were scored in 2015 and 2016 for their level of ADB damage observed in field. Significant differences were found in average ADB damage among planting sites and seed source provenances in 2016. All provenances contained some healthy trees, so a breeding program to produce genetically variable native ash tree populations with lower ADB susceptibility may be feasible. In 2015, we undertook a pilot project, using Restriction Site Associated DNA sequencing (RADseq) on 95 samples, to search for alleles associated with low susceptibility to ash dieback. We are now sequencing whole genomes from 1,400 individuals sampled across all provenances: 700 high-susceptibility and 700 low-susceptibility trees. Of these 1,250 are placed in 31 pools with 80X coverage per pool, and 150 are being sequenced as individuals with 20X coverage each. This provides data for a genome wide association study, searching for loci associated with low susceptibility, and genomic prediction of trees with low susceptibility.

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