GENETIC BARCODES FOR IDENTIFICATION OF PURE AND HYBRID *FRAXINUS* SPECIES

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Native populations of species in the genus *Fraxinus* (ash) are being devastated in North America by the emerald ash borer, and in Europe by ash dieback. There is evidence that some Asiatic species of *Fraxinus* have low susceptibility to both of these threats. It is therefore possible that hybridisation between Asiatic species and congeners native to Europe and North America may be one way of retaining ash as a viable forestry species on those continents. We have developed a set of genetic barcodes for the confirmation and identification of ash hybrids. Using whole genome assemblies for 29 individuals from 28 *Fraxinus* taxa (www.ashgenome.org), we identified and aligned putative orthologs from low copy number genes. A subset of 1396 variable gene alignments were analyzed using the statistical programme CONTEXT to identify candidates with a pattern of variability suitable for barcoding the individual species of *Fraxinus*. Primers were designed for the selected barcoding regions, and tested using several example species from the living collection at the Royal Botanic Gardens, Kew, UK and hybrids developed at Ashtown Research Station (Teagasc, Ireland). Sequence data were generated for all regions using Polymerase Chain Reaction (PCR) amplification and Sanger sequencing. The results of this study show that these barcodes are capable of identifying various different *Fraxinus* species, as well as being suitable for both the confirmation and identification of hybrids.

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