ADVANCED PHENOTYPING USING FT-IR DISTINGUISHES DISEASE RESISTANCE IN *FRAXINUS EXCELSIOR* AGAINST *HYMENOSCYPHUS FRAXINEUS*

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The invasive ascomycete fungus *Hymenoscyphus fraxineus* has caused large scale population decline of European ash (*Fraxinus excelsior*) throughout much of its distribution range in Europe. Large genotypic variation in susceptibility to the pathogen exists in the natural population, albeit resistance occurs at a low level. Damage traits associated with the pathogen are strongly genetically controlled, which suggests that considerable gain can be achieved through selection and breeding. Large potential exists for utilizing modern approaches or tools that can quantitatively identify phenotypes and help explain the genetic basis of important plant traits, such as disease resistance. One main obstacle to making such advances is the lack of viable tools for rapid resistance phenotyping. Vibrational spectroscopy is one approach that has been used successfully for rapid phenotyping for plant resistance. In this study, we used Fourier-transform Infrared (FT-IR) spectroscopy coupled with a chemometric model to discriminate between resistant and susceptible European ash genotypes. Non-infected leaves and stem samples from known susceptible and resistant *F. excelsior* genotypes were collected from six European countries. Purified phenolic extracts were analyzed on a FT-IR spectrometer and soft independent modeling of class analogy (SIMCA) was used to discriminate between resistant and susceptible trees. The model built with stem samples, and subsequently validated using random blind samples, gives powerful evidence that FT-IR can clearly discriminate between susceptible and resistant genotypes. These results suggest that spectroscopic phenotyping tools may allow for superior genotypes to be quickly identified and employed in restoration efforts.

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