

Accelerating Dynamic Genetic Conservation Efforts: Use of FT-IR Spectroscopy for the Rapid Identification of Trees Resistant to Destructive Pathogens¹

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A strong focus on tree germplasm that can resist threats such as non-native insects and pathogens, or a changing climate, is fundamental for successful genetic conservation efforts. However, the unavailability of tools for rapid screening of tree germplasm for resistance to critical pathogens and insect pests is becoming an increasingly serious bottleneck. Here we present the development of a new technique that can potentially revolutionize genetic conservation efforts. Fourier-transform infrared (FT-IR) spectroscopy is a chemical fingerprinting technique that has been recently shown to be suitable for the rapid identification of oaks resistant to *Phytophthora ramorum* (cause of sudden oak death) prior to infection (Conrad, A.O.; Rodriguez-Saona, L.E; McPherson, B.A.; Wood, D.L.; Bonello, P. 2014. Identification of *Quercus agrifolia* (coast live oak) resistant to the invasive pathogen *P. ramorum* in native stands using Fourier-transform infrared (FT-IR) spectroscopy. *Frontiers in Plant Science*. 5: 521.). The aim of this study was to determine if FT-IR spectroscopy can be used for the rapid identification of resistant trees in other pathosystems as well, such as Port-Orford-cedar (*Chamaecyparis lawsoniana*)/root disease (caused by *P. lateralis*), and whitebark pine (*Pinus albicaulis*)/white pine blister rust (*Cronartium ribicola*). For both pathosystems, we collected and analyzed plant material that had been previously characterized in terms of resistance/susceptibility to its specific pathogen. Soft independent modeling of class analogy was used to discriminate between resistant and susceptible trees, while partial least squares regression was used to predict mortality rates or severity of symptoms in the progenies. Preliminary results strongly indicate that FT-IR can discriminate between different phenotypes, and predict resistance-associated traits in the progenies of sampled trees in these pathosystems. Our results also suggest that this technique can be expanded to the rapid phenotyping of hosts in many other pathosystems, including tree crops, e.g., cacao, coffee, or eucalypts. This technique could also be developed for rapid identification and separation of morphologically similar tree taxa, further contributing to genetic conservation efforts worldwide.

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