METABOLOMICS APPROACHES FOR TRACKING BIOTIC AND ABIOTIC STRESS PERFORMANCE IN TREE IMPROVEMENT PROGRAMS

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With the development of higher throughput platforms for qualifying and quantifying metabolite composition, it is now possible to obtain a snapshot in time and space of the general and/or specific metabolite composition of plant tissues. This information coupled with phenotypic evaluation of plant performance can be used to identify biomarkers that may have utility for rapidly monitoring plant stress performance in improvement programs. This is particularly relevant for tree species where improvement programs have expensive labor and space requirements; therefore, rapid earlier monitoring and elimination of potentially poor performers at the seedling stage is desirable. In this regard, we have initiated two studies designed to evaluate: 1) the utility of general metabolomic profiles for the identification of chemical fingerprints linked to pathogen resistance in American × Chinese chestnut hybrids, and 2) specific metabolic pathway components in the phenylpropanoid pathway as biomarkers for developmental progression (i.e. fruit tree flowering) linked to annual climatic cycling. Our results indicate that evaluation of metabolite composition can be used to develop chemical fingerprint-based models to predict pathogen resistance in chestnut although further evaluation is needed to confirm these results and test the applicability of this approach on a larger scale. In addition, we found that evaluation of metabolite composition can be used to identify phenylpropanoid intermediates associated with developmental progression and adaptive trait variation in the perennial tree species peach and apricot. These studies highlight the potential utility and applicability of metabolite-based assay methods for breeding trees resistant to biotic and abiotic stresses imposed by invasive pathogens and a rapidly changing climate.

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