

Development of a Metabolomic Method to Define the Phenylalanome in Arabidopsis thaliana

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In the study of metabolomics, one of the greatest challenges can be accurately identifying compounds detected in biological extracts, especially when standards are not readily available. Current metabolomic methods are also limited in that they provide little to no information about a compound's metabolic origin. In this study, we sought to address these issues by developing a novel metabolomic method that employs stable isotope feeding, LC-MS, Xcms, and an analytical software algorithm to study the 'phenylalanome' of *Arabidopsis thaliana*. Using this approach we were able to develop a method that, based on current results, is capable of detecting over 30 distinct compounds derived from phenylalanine. These results are promising, and indicate that with further refinement the method should be capable of detecting a significantly greater number of compounds. If implemented, the greater understanding of metabolism provided by this new approach should prove invaluable in harnessing plant genetics to produce desired outcomes. Additionally, the techniques developed in this study have the potential, when applied more broadly, to map a multitude of secondary metabolic networks in a variety of biological systems.