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Nectar metabolomics reveals taxonomic Classification of Brassica Species

Kirthi Narayanaswamy¹, Nick Thoma¹, Akhil Bhargava³, Lucas Showman¹, Preeti Bias², Clay Carter³ and Ann Perera¹¹W.M. Keck Metabolomics Research Laboratory, Iowa State University, Ames IA²The Jackson Laboratory for Genomic Medicine, Farmington, CT³Department of Plant & Microbial Biology, University of Minnesota, St Paul, MN

In this study we have used a novel approach to reveal taxonomic relationships for several species in the Brassica genus. Brassica is a polytypic genus of the family Brassicaceae. We have used flower nectar of six related species of Brassica to conduct metabolite profiling. A novel GC-MS method has been developed with focus on capturing data of low abundance metabolites in the context of a few high abundant metabolites in a complex extract. This new multidimensional GC-MS-MS method using capillary flow technology with fast heating/cooling rates, and “heart-cutting” allows analysis of highly abundant as well as low abundant metabolites in floral nectar metabolite profiling. By applying this strategy to flower nectar samples we have readily detected nearly 50 low abundance metabolites such as amino acids, hydrocarbons, fatty acids and phenolic phytochemicals, whose abundance was previously poorly characterized in nectars. Cluster analysis of nectar metabolites shows Brassica species group into their own clusters revealing connections among species. As a result, this study on metabolite profiles of nectar in six different species revealed their genetic relationship.

Biography

Kirthi Narayanaswamy is a scientist at the W. M. Keck Metabolomics Facility at Iowa State University. She received her Ph.D. in biochemistry at the Indian Institute of Science, performed post-doctoral research work at Iowa State University, and worked as a research scientist at the Ames Lab. The W. M. Keck Metabolomics Research Laboratory houses different analytical platforms for non-targeted complete metabolite profiling, targeted metabolite profiling, and mass spectrometry imaging. Kirthi is involved in training on-campus users to use the analytical platforms to meet their research goals, and in helping meet the needs of off-campus clients through developing methods for processing their samples.

kirthi@iastate.edu

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