

Category	: International Rice Research Conference
Select Theme	: Systems physiology
Keyword 1	: Phenomics
Endorsement email	:
Keyword 2	: Nutrients (such as mineral uptake, translocation, and regulation)
Keyword 3	:
Title of Entry	: Using multivariate analyses to compare rice metabolic profiles
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Select only one type of presentation	: 15 minute oral presentation
Abstract	<p>: Rice varieties are often grouped based on quality parameters and their ability to adapt to certain stress and stimuli. Metabolites, which are products or by-products of various biochemical pathways, have been associated with differences in quality of the grain and/or the plant's response to stress. In this study, we identified 117 metabolites from 320 rice varieties using GC-TOF-MS. These included a large number of sugars, some amino acids, secondary metabolites, tricarboxylic acid cycle intermediates and a few unknowns. Through multivariate analysis approaches, we determined the metabolites that can distinguish the different rice quality groups across two grain developmental stages. Results provided insights into the differences of grain quality parameters for each grouping. Use of non-traditional approaches in extracting information from large dataset generated may contribute to the identification of proxy traits that can be eventually used in breeding programs.</p> <p style="text-align: right;">Read more»</p>

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