NUS National University of Singapore | Department of Biological Sciences, Faculty of Science

SEMINAR

Thurs, 12 Nov 2015 | 4pm | DBS Conference Room 1

Hosted by Professor Prakash Kumar

Plant systems biology

application to rice for understanding metabolic and regulatory characteristics under environmental stresses toward crop improvement



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Rice plants are exposed to a wide range of environmental stresses during their cultivation, that seriously affects the annual global rice production. Thus, a comprehensive understanding on how rice plants respond to these changing environments both at metabolic and gene regulation levels will provide a significant insight towards improved rice varieties. To do so, we employed systems biology approach, and initially developed a core mathematical model of rice [1] which allows us to characterize cellular behavior and metabolic states under various abiotic stress conditions, such as i) photorespiratory pathway in rice leaves and identification of essential and lethal genes of the pathway [2], and ii) metabolically and transcriptionally regulated reactions and potential transcription factors involved in the regulation of germination and coleoptile elongation of rice seeds under anoxia [3]. The core model was later expanded to reconstruct a fully compartmentalized genome scale metabolic model. Transcriptomics and metabolomics data were then systematically integrated with the model to identify the potential transcription factors, i) in leaf, root and panicle tissues at three different developmental stages in response to drought stress [4], and ii) the control of light-mediated signaling mechanisms [5]. The information derived from the current in silico analysis in conjunction with multi-omics profiling can potentially guide for developing new breeding and/or engineering targets as crop productivity strategies.

Artwork by Ann Nee, DBS, NUS