

Category	: International Rice Research Conference
Select Theme	: Systems physiology
Keyword 1	: Drought tolerance
Endorsement email	:
Keyword 2	: Submergence and flood tolerance
Keyword 3	: Photosynthesis
Title of Entry	: Modeling rice metabolism for elucidating stress responses and guiding crop improvement
Presenting author	: Bijayalaxmi Mohanty
Presenting author email	: bijayalaxmi.mohanty@gmail.com
Co author 1	: Meiyappan Lakshmanan
Co author 2	: Dong-Yup Lee
Co author 3	:
Co author 4	:
Co author 5	:
Co author 6	:
Co author 7	:
Co author 8	:
Co author 9	:
Co author 10	:
Co author 11	:
Co author 12	:
Co author 13	:
Co author 14	:
Affiliation presenting author	: Temasek Life Sciences Laboratory, 1 Research Link, National University of Singapore, Singapore 117604/Department of Chemical and Biomolecular Engineering, National University of Singapore, 4 Engineering Drive 4, Singapore 117585, Singapore
Affiliation 1	

Affiliation 2 : School of Chemical Engineering, Sungkyunkwan University, Seobu-ro 2066, 16419 Suwon- si, Gyeonggi-do, Republic of Korea/Department of Chemical and Biomolecular Engineering, National University of Singapore, Singapore 117585, Singapore

Affiliation 3 :

Affiliation 4 :

Affiliation 5 :

Affiliation 6 :

Affiliation 7 :

Affiliation 8 :

Affiliation 9 :

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Abstract : Rice is one of the major food crops of the world. Although the overall yield of rice has been increasing since the Green Revolution in 1960s, the growing population and adverse climatic changes pose huge challenges for their sustained production in the future. Moreover, several abiotic and biotic stresses such as high light, drought, flooding and salinity affect the crop productivity significantly. Therefore, systematic approaches are highly required to explore their effects on rice crops' phenotypic and cellular responses. It could be achieved by combining the available multiple high throughput data such as genomics, metabolomics, proteomics and transcriptomics, thereby analyzing the possible biochemical adaptations to several abiotic stresses. Concurrently, the advent of constraint-based metabolic reconstruction and analysis paves way to characterize the cereals cellular physiology under various stresses via the mathematical network models, which is relatively new. Since early 2000s, the plant metabolic modeling studies have started to appear in the literature on Arabidopsis (~40%) possibly because it is the first plant to have its genome sequenced. In this study, we have employed similar systems biology approach, and initially developed a core mathematical model of rice which allows us to characterize cellular behaviour 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, and ii) metabolically and transcriptionally regulated reactions and potential transcription factors involved in the regulation of coleoptile germination and elongation of rice seeds under anoxia. The core model was then further expanded to reconstruct a fully compartmentalized genome scale metabolic model. Subsequently, transcriptomics and metabolomics data were 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, and ii) the control of light-mediated signaling mechanisms. The information derived from the current in silico analysis in conjunction with multiomics profiling can potentially guide for developing new breeding and/or engineering targets as crop productivity strategies. Besides, such studies can also be applied to other food crops to identify agronomic traits for crop improvement.

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