



# COMPUTATIONAL BIOLOGY WEBINAR @ IMSc

## UNRAVELLING RICE CELLULAR PHYSIOLOGY

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More than 20% caloric intake of the whole world population comes from rice; however, this rice production is under several biotic and abiotic stresses. Thus, society needs efficient stress tolerant high yield rice cultivars. A deep understanding of the rice cellular and plant physiology, and how its outcome depends on the interactions of several levels of different cellular networks will help the rice biotechnologist to achieve this goal. Towards this aim, the focus of this presentation would be use of analytical techniques to understand the rice cellular physiology.

Firstly, I will discuss how integration of different omics data and network theory can not only unravel various regulatory interactions connecting phenotypic changes with cellular and/or molecular events triggered by stress, but also provides a framework to deepen our understanding of stress cellular physiology. However, this technique will not be very useful to understand the cellular metabolism and thus, we use two different metabolic modelling tools, namely flux balance analysis (FBA) and elementary flux mode (EFM) analysis techniques.

Secondly, I will describe how we create a structural metabolic model that contains the reactions that participate in photorespiration in the plastid, peroxisome, mitochondrion and cytosol, and the metabolite exchanges between them, and analyse this model (i) to understand biochemical basis of leaf ammonium accumulation and chlorosis in GS2 mutant type and (ii) to address the impact of photorespiration on metabolism. We also provide a formal demonstration that photorespiration itself does not impact on the CO<sub>2</sub>:O<sub>2</sub> ratio (assimilation quotient), except in those modes associated with concomitant nitrate reduction.

GOOGLE MEET LINK:

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