

## Mapping cellular metabolism with fluxomics

Shyam K. Masakapalli, PhD Department of Biology and Biochemistry, University of Bath, UK

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## Abstract

The study of metabolism over many decades has produced the detailed metabolic maps routinely seen in our biochemistry text books. Although these are well defined with several metabolites and connecting enzymatic reactions, our ability to accurately predict metabolic responses to perturbations such as stress and genetic manipulation is still very limited. The major gap is the lack of direct measurements of *in vivo* metabolic activities i.e. flux or flow of carbon across all the reactions that precisely govern cellular function and physiology. The gap is being met by the emergence of 'Fluxomics'– system-wide quantification of fluxes using metabolic flux analysis and mathematical modelling.

This talk will focus on introducing fluxomics of plant and microbial systems in defining metabolic phenotypes in response to perturbations. I will highlight the i) complex metabolic responses of *Arabidopsis thaliana* cell suspension to different nitrogen sources ii) metabolic phenotypes of transgenic tobacco hairy root cultures engineered to enhance flux towards terpenoid indole alkaloid pathway intermediates such as geraniol and iii) metabolic systems biology methods currently being implemented to engineer *Geobacillus thermoglucosidasius*, an industrial thermophile, for production of targeted chemicals from renewable lignocellulose-derived feedstocks. Future perspectives on this rapidly evolving field will also be discussed.