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Applications of metabolomics in plant biology

Manoj Kumar Sharma and Surya Kant Mishra
S. V. P. University of Agriculture & Technology, India

Metabolomics is one of the newest 'omics' science. It is the systematic study of the unique chemical fingerprints called metabolites that specifies cellular processes of an organism at different developmental stages and under different environmental conditions. Metabolomics embraces several strategies that aim to increase our understanding of how metabolite levels and their interactions influence phenotypes. Metabolomics has proven to be very rapid and superior to any other post-genomics technology for pattern-recognition analyses of biological samples. One of the key advantages of metabolomics is that a sequenced genome is not required to make sense of the data. Basically, this technique can elucidate differences in genomes without using any DNA. Metabolomics is a growing field that uses several high throughput detection and quantification techniques like- NMR, FT-IR, LC-NMR, LC-MS, LC-EC-MS, LC-UV, GC-MS, CE-MS, HPLC-MS, DIMS, FT-ICR-MS, TOF-MS and Q-TOF for metabolome analysis in an efficient and effective way due to their sensitivity and robustness. AraCyc, MetNet, MetaCyc, ArMet, MeT-RO, MIAMet, CSBDB, MetAlign, MetGeneAlyse, Metlin, CODA, KEGG, Correlation optimized warping (COW), principal components analysis (PCA) and independent component analysis (ICA) are several important bioinformatics and statistical tools for metabolome analysis. Metabolomics studies mainly focuses on the observed changes in metabolite concentration to changes in gene expression and perhaps even in the genes themselves. Metabolomics can be used in analysing diversity, linking genotypic to phenotypic diversity, analysing of plant-pathogen interactions, in determining the nutritional difference between traditional and genetically modified crops, in characterizing specific metabolic networks including those associated with several plant metabolisms including-nitrogen metabolism, lipid metabolism, glucosinolate metabolism, starch metabolism, chloroplast-targeted gene products and flavonol metabolism, in understanding the adaptive response of biotic and abiotic stress tolerance in crop plants, identification of uncommon and valuable phytochemicals, in the integration of transcript and protein profiling and in the identification of regulated key sites in metabolic networks. Metabolomics is considered an efficient tool for addressing future needs in agriculture and human nutrition for assessing food safety. Recent studies on plant biology focused on several applications of metabolomics including the confirmation of the effects of bioengineering of plant metabolic enzymes, studying plant biochemistry including the connectivity of different pathways, in engineering of biodegradation and mineralization processes for the removal of toxic substances from atmosphere, in discovering novel pathways, in uncovering silent phenotypes of mutations and in the nutraceutical breeding of crop plants. Identification and quantification of specific metabolites in complex mixtures and their data analysis and integration remains the major problems of metabolomics studies. As the scientific knowledge of metabolic pathways increases (including the gene, the proteins, and metabolites involved), this can be expected to improve in near future.

Biography

Manoj Kumar Sharma is a Ph.D. scholar and working on sugar cane & rice crops to investigate the effects of drought stress on both crop's proteome and metabolome.

m.manojkumarsharma@yahoo.com

Influence of malathion in total lipid in liver of *Clarias batrachus*

Iram Shamim, R K Gautam, Sanjeevni Shakya and Vishal Khajuria
Dr B R Ambedkar University, India

The aquatic ecosystem is facing the threat of shrinking genetic base and biodiversity due to indiscriminate use of pesticides. The purpose of this research topic was to evaluate total lipid after 4 day treatment of Malathion in liver tissue. Firstly, experimental fishes were kept under normal condition in lab of School of Life Sciences, Khandari Campus, Agra. After one week, fishes were divided into four groups A, B, C and D (5 fishes to each group). After each 24 hours interval, fishes were taken out for biochemical investigation after malathion intoxication. The result of this experiment shows a significant decrease in lipid in *Clarias batrachus*. The lipid depleted significantly due to the inhibition of lipid synthesis and increased utilization of stored lipids as a source of energy to conduct regular metabolic functions.

iramshamim5@gmail.com