Preeti Bais, Metabolomics 2014, 4:2
http://dx.doi.org/10.4172/2153-0769.S1.024

OMICS Group Conferences
Accelerating Scientific Discovery

3rd International Conference and Exhibition on
Metabolomics & Systems Biology
March 24-26, 2014 Hilton San Antonio Airport, San Antonio, USA

Biomarker discovery in functional genomics using metabolomics

Preeti Bais
The Jackson Laboratory, USA

A large number of genes in an organism cannot be functionally annotated using sequence genomics techniques alone. We present a metabolomics based biomarker discovery pipeline that uses single gene knock out mutants under strictly controlled environmental conditions to discover gene function. Since no single metabolomics detection platform can cover the whole metabolome of an organism, seven different mass spectrometry based metabolomics platforms are combined together to get a more comprehensive view of the mutation. Many potential biomarkers in a non-targeted analysis are structurally unknown and cannot be used in understanding the biological relevance. Partial correlation networks between the metabolites across multiple mutation lines provide a way to computationally predict and incorporate the structurally unknown metabolic features. A proof-of-concept analysis on the three single gene knock mutants in the glutathione degradation (GSH) pathway of the *Arabidopsis* confirms the known biology that OXP1 is responsible for conversion of 5 oxoproline (5 OP) to glutamic acid like the mammals but GGTs may not be major contributors for the 5OP production in *Arabidopsis* plant as they are in the animals. This project is innovative because it harnesses the stable relationship between two metabolites across multiple mutations for a rapid and inexpensive *in-silico* method to predict the structures of unknown metabolites to form hypothesis about the function of a gene.

Biography

Preeti Bais is associate scientist at the Computational Sciences group at the Jackson Lab's new research institute at University of Connecticut - JAX Genomics Medicine (JGM). It is an independent, nonprofit organization focusing on mammalian genetics research to advance human health. She holds a Ph.D. in bioinformatics and computational biology and has worked in the metabolomics field for many years including her tenure as a principal scientist at Stemina Biomarker Discovery, where she worked on many projects involving metabolomics analysis of Human Embryonic (hES) and Induced Pluripotent Stem (IPS) cells based assays for drug toxicity screening, autism biomarker detection using blood samples and cancer drug efficacy testing using orthotropic mouse models of GBM.

preetibais@hotmail.com