Ming Chen et al., J Comput Sci Syst Biol 2013, 6:4
http://dx.doi.org/10.4172/0974-7230.S1.004

OMICS Group Conferences
Accelerating Scientific Discovery

International Conference on
Integrative Biology Summit
August 05-07, 2013 Embassy Suites Las Vegas, NV, USA

Ricenet: Genome-scale multi-level network reconstruction of rice

Ming Chen, Lili Liu, Qian Mei and Zijun Zhang
Zhejiang University, China

As one of the world's most important food plants, rice has important syntenic relationships with the other cereal species and is a model plant for the grasses. Genome-scale multi-level network reconstruction is a key step in systemic understanding of the molecule regulatory mechanism in organisms. We integrated protein-protein interactions (PPIs), gene regulations and microRNA-Target interactions into metabolic network and developed the genome-scale multi-level network model of rice, which could provide an available framework for plant genome-scale multi-level network model reconstruction. Firstly, we reconstructed a genome-scale metabolic model (OsaGEM) covering primary metabolism for a compartmentalized plant cell based on the Rice genome. OsaEM is a literature-based, genome-wide metabolic model, which at the moment contains 4,462 function genes, 3,031metabolits involved in 3,316 reactions and the 3,316 reactions compartmentalized into the cytoplasm, mitochondrion, plastid, peroxisome, and vacuole. Gap analysis, flux balance analysis, gene deletion simulate were performed as well. Furthermore, the Protein-Protein interactions (PRIN), gene regulations and microRNA-Target interactions were integrated into the metabolic model. Finally, RiceNet, a database of storing and visualizing the genome-scale multi-level network was constructed. This system-based framework enables the exploration of global phenotypic effects of gene knockouts, gene insertion, and up-/ down-regulation of gene expression.

Biography

Ming Chen received his Ph.D. in Bioinformatics from Bielefeld University, Germany, in 2004. Currently he is working as a Professor in Bioinformatics at College of Life Sciences, Zhejiang University. He is serving as an academic leader in Bioinformatics at Zhejiang University. He is a committee member of Chinese societies for “Modeling and Simulation of Biological Systems”, “Computational Systems Biology” and “Functional Genomics & Systems Biology”.

mchen@zju.edu.cn