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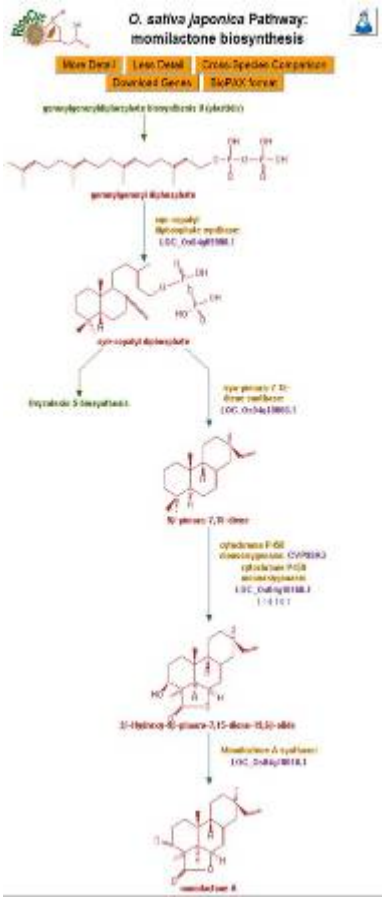
Research Area

Comparative Plant Genomics, Functional genomics, Systems Biology, Bioinformatics, Genome Annotation, Biochemical and Regulatory Pathway Databases, Genome Databases, Ontology Development.



Description of Research

Databases and bioinformatics projects

Gramene database: It is a comparative plant genomics platform and a Systems Biology database. This is the first such database that allows researchers to carryout in-silico investigation using either or both the forward and reverse genetics approaches to find the genes, proteins, phenotypes, function, expression, gene-gene interaction, metabolic pathways and polymorphic markers in the region of interest. It also allows researchers to make comparisons across genetic maps, genomes and gene orthologs.

RiceCyc: A database of metabolic pathways in Rice. This is a first of its kind pathway database dedicated to rice pathways. It allows researchers to find the rice genes and their role in given biochemical pathways. We are also looking at

extending thsi model to include regulatory gene networks and pathways. The databse website also mirrors pathways from 8-9 plant species for comparative analysis.

Rice Genome Annotations and functional characterization of the genes using in-silico and manual curation driven by homology (orthologs and paralogs), and assignment of functional domains and Gene Ontology annotations

Plant Ontology Consortium: Is a project on development of structured common set of plant anatomy and growth stage vocabularies for use in Genomics data sets, gene and phenotype annotations. The project also provides standard protocols and the database for ontology based annotations.

Biomedical Ontologies: Ontologies are structured controlled vocabularies that are used in annotation of gene function, expression and phenotypes in a standardized way by various plant and model organism databases. These vocabularies are organized using a mathematical model Directed Acyclic Graph (DAG) and are key to any successful query to find similarities in function, spatial and temporal expression and phenotypes across databases. Some of the ontologies amy group works on are:

- Gene Ontology (GO) (an ontology of molecular functions, biological process and cellular components)
- Plant Ontology (PO; plant structure, growth & development stages of Angiosperms)
- Plant Trait Ontology (TO) for scoring phenotypes and traits
- Cereal Plant Ontology (GRO; cereal plant structure and growth & development ontology)
- Plant Growth Environment/treatment Ontology (EO)
- Phenotype and Trait Attribute Ontology (PATO)

Research Group Members

Justin Elser (Postdoc)
Palitha Dharmawardhana (Postdoc)

Teaching

BOT331 Plant Physiology

Related Links

Lab Projects
Gramene Database
The Plant Ontology

Publications

Azevedo, J., F. Courtois, et al. (2008). "Intraplastidial trafficking of a phage-type RNA polymerase is mediated by a thylakoid RING-H2 protein." Proc Natl Acad Sci USA 105(26):

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Anuradha Pujar*, Pankaj Jaiswal*, et al. Whole Plant Growth Stage Ontology for Angiosperms and its Application in Plant Biology. Plant Physiology 2006, 142(2):414-28

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chloroplasts. Plant J. 2002; 31(2): 199-209

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Bruskiewich R, Coe E H, Jaiswal P, McCouch S, Polacco M, Stein L, Vincent L, Ware D; The Plant Ontology (TM) Consortium and plant ontologies; Comparative and Functional Genomics, 2002, vol.3(2), pp137-142

Doreen Ware, Pankaj Jaiswal, Junjian Ni, Xiaokang Pan, Kuan Chang, Kenneth Clark, Leonid Teytelman, Steve Schmidt, Wei Zhao, Samuel Cartinhour, Susan McCouch and Lincoln Stein; Gramene: a resource for comparative grass genomics. Nucleic Acids Research, 2002, Vol. 30, No. 1 103-105.

Jaiswal P, Sane AP, Ranade SA, Nath P and Sane PV, Mitochondrial and total DNA RAPD patterns can distinguish restorers of CMS lines in sorghum. Theor Appl Genet, 1998, 96: 791-796.

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