Integration of mutant phenotypes with metabolic pathways in **SoyBase**

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PAG 2014

**SoyBase**

- USDA-ARS soybean genetics and genomics database
- Soybean genetic data
- Develop tools and maps to present soybean genetic, genomic, expression and phenotype data
- Collect mutant stock and phenotype data

**Fast Neutron Mutagenesis**

- Seeds exposed to neutron radiation
- Produces point and deletion mutations
- Lines may have one or more deletions and also point mutations

**SoyBase mutant search tool**
Mutant search tool – Browse by trait value

Integration of SoyCyc display into the mutant search tool – why?
• Highlighting genes from knock-out or deletion mutagenesis experiments provides a quick visual way to browse phenotype data in the context of metabolic pathways
• Can quickly identify lesions in the same pathway even though they have no gene names or functions seemingly in common yet have similar phenotypes

Mutant search tool – Integration of SoyCyc data
• Comparative Genomic Hybridization (CGH) identifies approximate deleted genomic region
• Sequence coordinates are used to identify potentially deleted genes
• Gene list compared to genes identified in SoyCyc as potentially being metabolic enzymes

SoyBase: integrating soybean genetics and genomics
http://www.soybase.org
Integration of SoyCyc data – SoyCyc “Oomics viewer” API

- URL based API to the Omics Viewer
- Allows the automated submission of jobs to the omics viewer for Cellular Overview annotation
- Cellular Overview page is generated in HTML allowing the page to be modified by programmatic control (Page Hijacking)

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User Interface Interactions with SoyCyc – Phenotype selector

An image can be removed from the list by clicking on the [-] button.

The Compare button will show a grid of medium size views of all of the images in the cart.

Multiple mutant comparisons can be useful in instances where mutants have similar phenotypes but no deleted genes in common. In this case the underlying biochemical basis for the phenotype might become evident if the mutants all affect the same pathway although at different steps.

Return to Fast Neutron Mutants Search Page
Phenotypic similarity of independent deletions to identify potential metabolic origins of the phenotype

Questions?