AraCyc and the OMICS Viewer: Making sense of metabolism in your favorite biological process

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Everyone is studying metabolism

Many biological processes connect to metabolism

- Drought tolerance changes in osmolyte concentrations
- Hormone signaling biosynthesis and degradation of hormones
- Photosynthesis chlorophyll production and ROS scavenging
- Translation amino acid biosynthesis and riboswitching
- Plant defense phytoalexin synthesis
- Your favorite process . . .
- AraCyc can help you find these connections!
 - <u>Ara</u>bidopsis Metabolic En<u>Cyc</u>lopedia
 - Database of metabolic pathways found in Arabidopsis
 - www.arabidopsis.org/biocyc/ (TAIR)
 - www.plantcyc.org/ARA (Plant Metabolic Network)



AraCyc 4.5 (released June 2008)

Pathways	288
Compounds	1956
Reactions	1723
Genes (in pathways)	1914
Citations	2279

How can you connect these to your research efforts?

OMICS Viewer to the rescue . . .

- Overlay experimental data on a metabolic map
 - Transcript data (for enzymes)
 - Proteomic data (for enzymes)
 - Metabolomic data
- Use multiple data sources
 - Your data
 - Publicly available data
 - Gene Expression Omnibus
 - NASC Proteomics Database
 - NSF2010 Metabolomics
 - Many more . . .
- Generate new testable hypotheses about your favorite
 - gene
 - metabolite
 - biological process
 - etc.

Addressing common research conundrums . . .

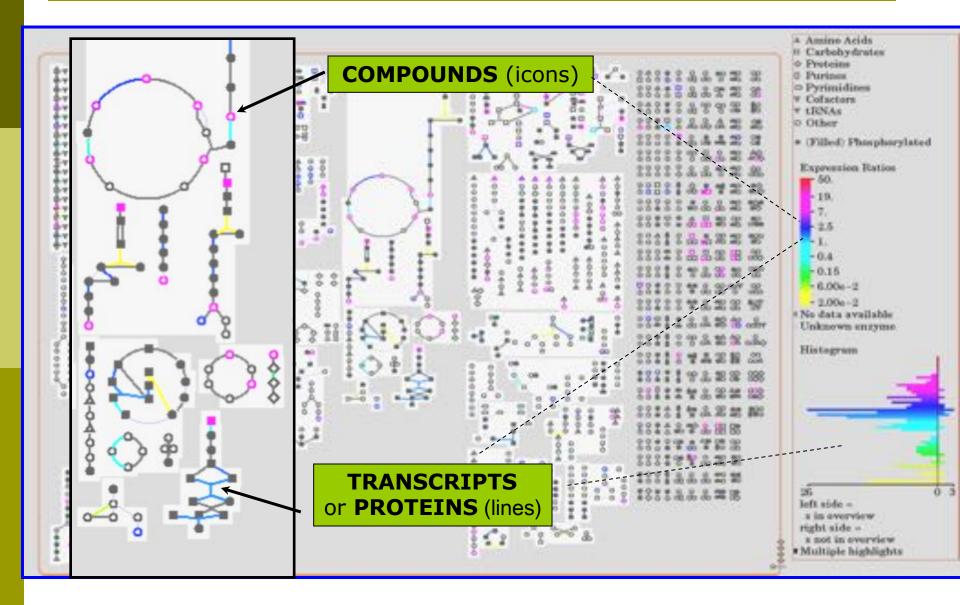
My (single/double/triple/quadruple) mutant has "no phenotype"!!!!

- Compare transcript levels / protein levels / metabolite levels in wild-type and mutant plants using the OMICS viewer
- Look for "hidden" perturbations in metabolism
- I have a mutant with a defect in <u>(biological process)</u>
 . . . but I don't know the mechanism
 - Use the OMICS viewer to compare data from WT and mutant plants
 - Download publicly available data sets related to the biological process
 - Scan for affected areas of metabolism
- I just did a microarray experiment and a bunch of metabolic enzymes popped up . . .
 - Use the OMICS Viewer to quickly identify metabolic <u>pathways</u> that are up- or down-regulated
- And many more . . .

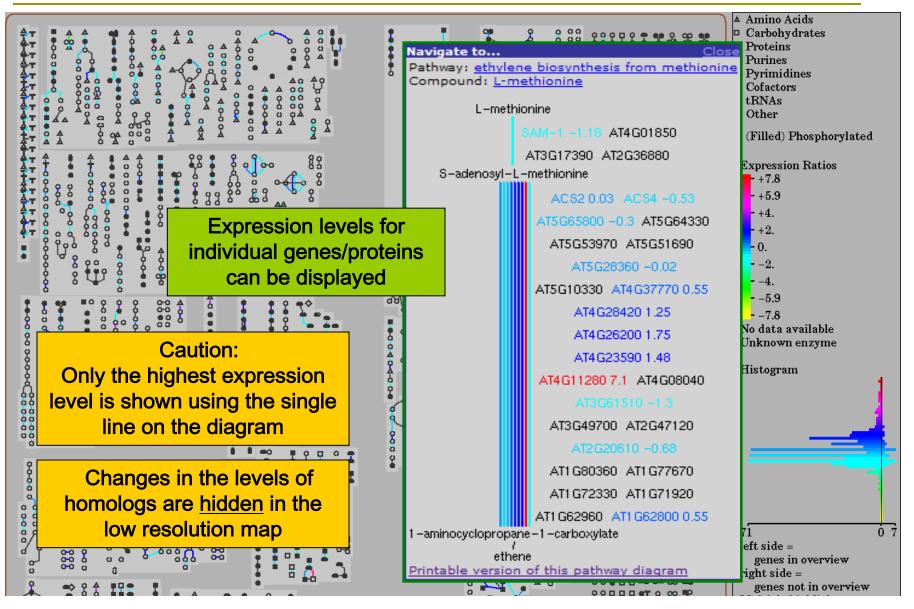
OMICS Viewer Overview



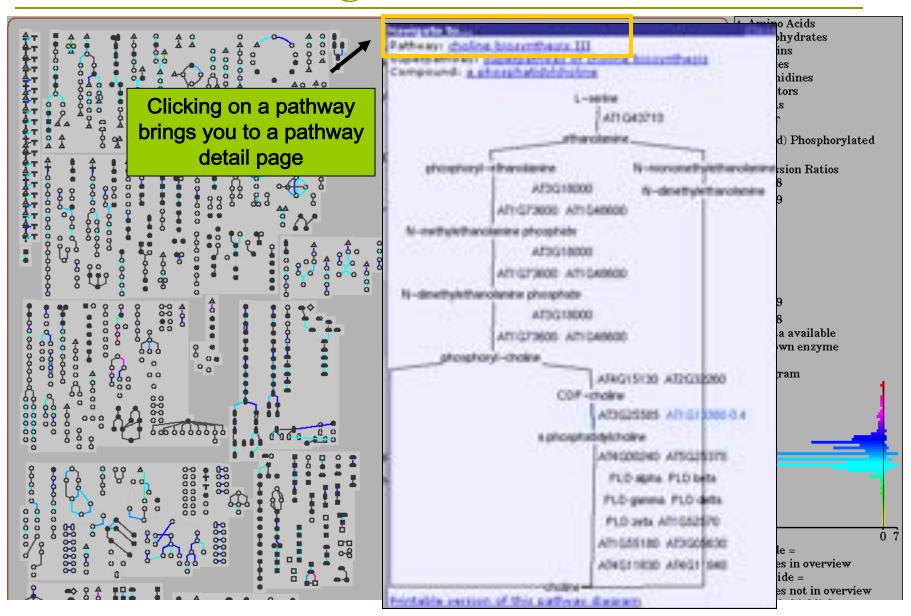
OMICS Viewer Overview



Viewing gene/protein families

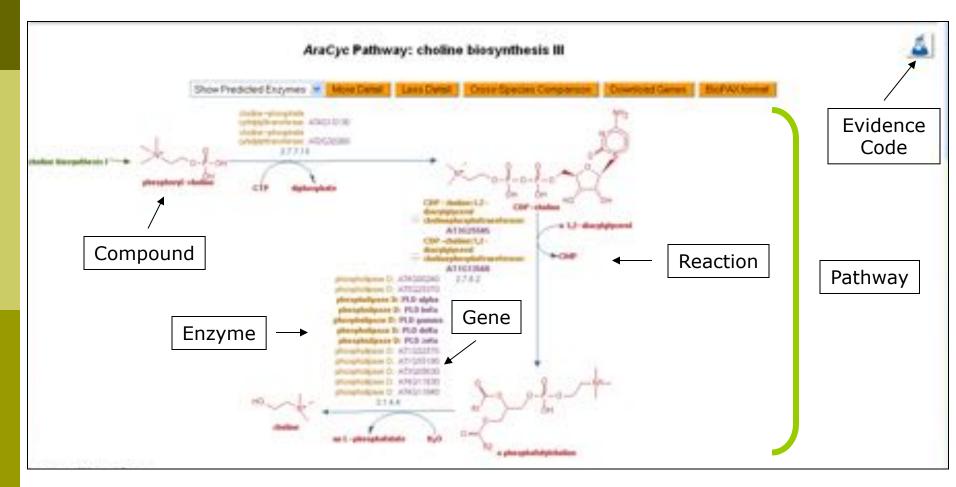


Getting more information



AraCyc Pathway pages

All items can be clicked on to obtain more information

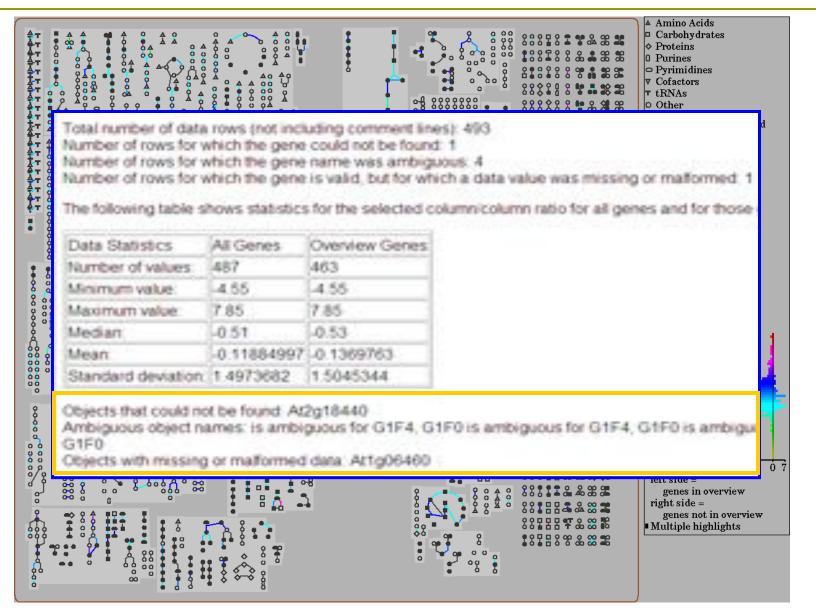


+ Additional curated information

AraCyc Pathway pages

Superclasses Basesthesis, a Eats Acds and Lands, a Chill	te Bezahlern	Classification		
Summary: General Information: Choirs is a fundamental matebolic non-plactic plant membranes [Min(02)] Chailes is also a to accumulated and confers also tolerance to salisity, drou	precursor for the formation of phyci	ne betaine (glycine ketaine)	investigation in the second of the second	tail plants such as spinach, where this correspondentiand
The choice biosynthetic pathway enables plants to decou to environmental conditions where large and variable amou			datafightered Mergenheim.) a	and provides them with the metabolic flexibility to adapt
Pathway information: The first step in choice biosynthe Ethenolamine is widely recognized as the entrance compo		f serine to athendiamine (<u>Bors</u>	mit I, which is catalyzed by a	sente decarborylase unique to plants [<u>RomanD.</u>]
The pathway variant displayed (hocleotide pathway) repres where three consecutive N-methylation steps are carried to [] Hotelt_]				
The synthesis of internediates on both the phospho-base out that the synthesis of phosphatidylethanolamine and ph assumed that the reactions embedded in the nucleotide at <u>kinewy00.1</u>	tosphatidylcholine is characterized	t by a high dispres of interaction	and furcation an the various lieve	ets of arising intermediates. Consequently, it has been
The release of choline from the different pathway levels is in into phosphatidylcholine with the subsequent release of ch bean [Wanght] Although a well-defined physiological rol distinct cellular functions [<u>Mid-90</u>]. The remaining enzyme substrates. This may be beneficial to process the federoge	toline, as in tobacco (<u>McMailOS</u>) Is of phospholipase D (PLD) still a es involved in this pathway, phospi	The latter reaction has been al wad further research, progress hoaminoaicohol cytidylyttavelk	own to be specifically catalyzed has been made to assign some r race and COP-aminoalcohol pho	(by physpholipase D (<u>physpholipases</u>) in cardor members of the haterogeneous family of PLD's to sighotraneferace, cover a broader spectrum of
Dispersion of the second secon	Superpathwa	ays		Summary
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If an anzyme name is shown in bold, there is experimental evid	lance for this enzymatic activity.			
References				
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OMICS Viewer Statistics



OMICS Viewer in action

Multiple data sets can be entered using the same input file

- An animation can show changes in data sets:
 - wild type /mutant a / mutant b / mutant c / . . .
 - time points 0, 1, 2, 3, . . .
 - compound concentration x, y, z, . . .

Suberin Biosynthesis

Wild type



mutant A

mutant B





OMICS Viewer data inputs

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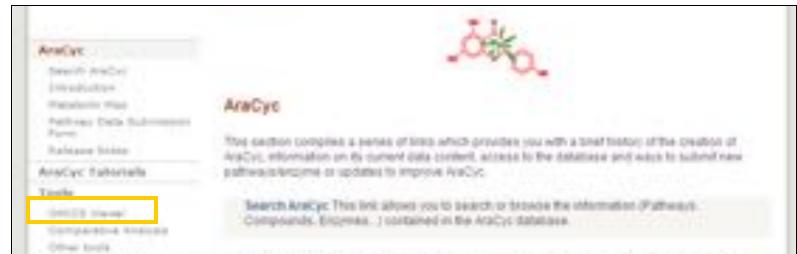
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OMICS Viewer data upload

TAIR - www.arabidopsis.org



AraCyc - www.arabidopsis.org/biocyc



OMICS Viewer data upload

PMN – www.plantcyc.org

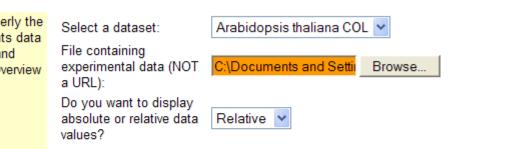
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Introdu	Introduction		Taola Overview Metabolic Mage + OBDCS Viewer +		Analys (Antoinington)		
The Plant Metabolic Network (PMN) is a cultable and biochemists with a common goal to build a pathway databases. A central feature of the PM plant biochemical pathway database, containing literature and computational analyses about the		Pathway Toole Biorye Bundle		Tutwiel		1.0	
		p curated internation train the genes, enzymes, compounds,		On June 17, 2008, PlantCyc made its web debut, containing blochemical pathways with information from over			

OMICS Viewer data upload

Pathway Tools Omics Viewer

The Pathway Tools Omics Viewer (formerly the Pathway Tools Expression Viewer) paints data values from the user's high-throughput and other experiments onto the Metabolic Overview diagram for an organism.

The Omics Viewer can be used for:

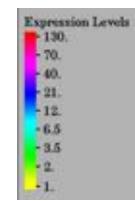


- Select species
- Upload data file
- Enter appropriate parameters
- □ GO!

New ideas to pursue . . .

Wild type



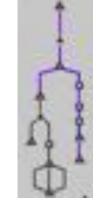


The transcript levels of several enzymes in the **Iysine biosynthesis pathway**

are reduced ~4-fold!

Mutant with "no phenotype"

Mutant with a metabolic phenotype



New hypotheses and experiments

Acknowledgements

AraCyc, the PMN, and TAIR

Sue Rhee (*PI and Co-PI*) Eva Huala (*Director and Co-PI*)

Current Curators:

- Peifen Zhang (Director and lead curator- metabolism)
- Tanya Berardini (lead curator functional annotation)
- David Swarbreck (lead curator structural annotation)
- Debbie Alexander (curator)
- A. S. Karthikeyan (curator)
- Donghui Li (curator)

Recent Past Contributors:

- Christophe Tissier (curator)
- Hartmut Foerster (curator)



Tech Team Members:

- Bob Muller (Manager)
- Larry Ploetz (Sys. Administrator)
- Raymond Chetty
- Anjo Chi
- Vanessa Kirkup
- Cynthia Lee
- Tom Meyer
- Shanker Singh

National Science Foundation

- Chris Wilks

Metabolic Pathway Software:

- Peter Karp and SRI group (NIH)



If you have any questions or want a live demo . . .

Come to the Curation Booth – Booth #1 Open throughout the conference!



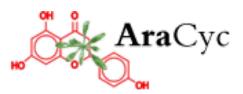
Please stop by during a poster session

Thank you . . .



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curator@arabidopsis.org



www.arabidopsis.org/biocyc

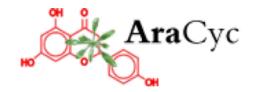
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