



Plant Metabolic Network, data and tools for learning and studying plant metabolism

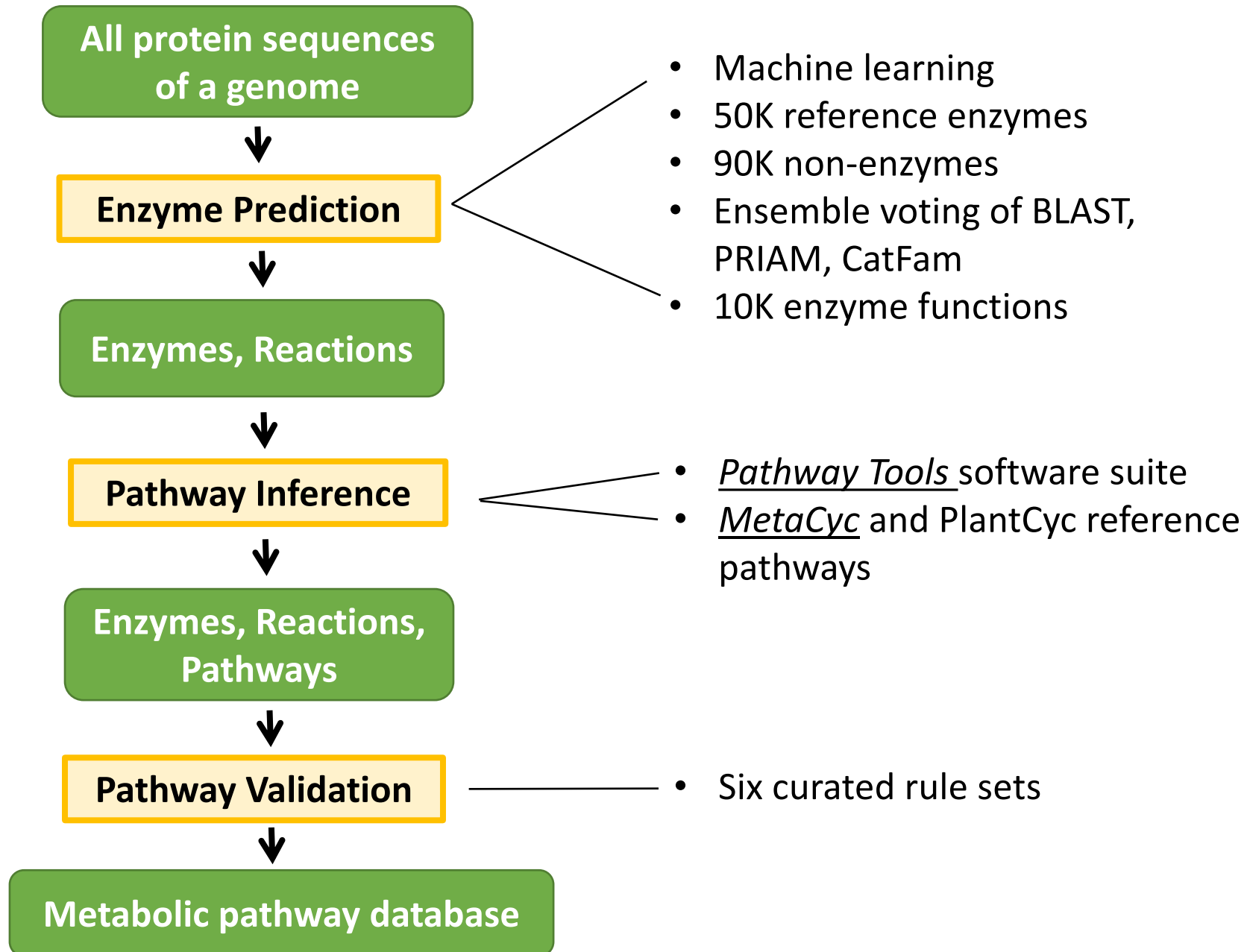
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PMN develops and provides

- Pipeline for high quality enzyme function prediction and metabolic pathway inference from sequenced plant genomes
- Metabolic pathway databases for 22 plant genomes
- Experimental information of enzymes and pathways for over 400 plant species
- Free online access and free download

The PMN pipeline



22 species-specific databases

PlantCyc

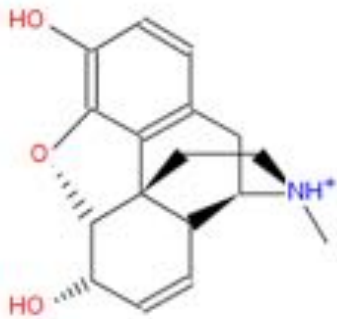
Green

Each database:

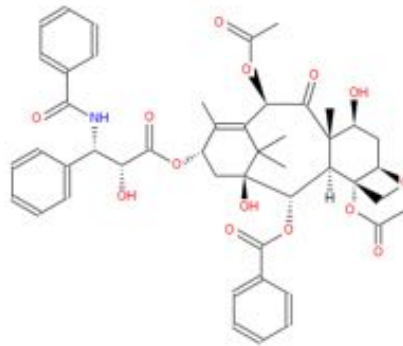
- 2,768 ~ 14,006 Enzymes
- 373 ~ 619 Pathways

Lower level

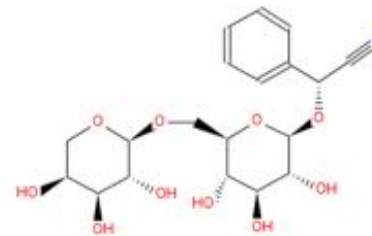
- 400+ species
- 140,581 Enzymes
3,376 with EV-EXP
- 1,213 Pathways
886 with EV-EXP



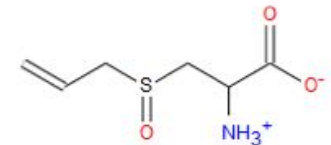
Morphine
(*Papaver somniferum*)



Taxol
(*Taxus brevifolia*)



Vicianin
(*Vicia sativa*)



Alliin
(*Allium sativum*)

Lookup your gene

PMN

Home Databases Search Metabolism Analysis SmartTables Help

gene **Pavir.J10036.1.p** enzyme **Pavir.J10036.1.p**

Panicum vfrgatum

Accession IDs	G3E-16257 (SwitchgrassCyc) PAVIR.J10036.1
Reactions	mugineate + 2-oxoglutarate + oxygen → 3-epihydroxymugineate + succinate 2'-deoxymugineate + 2-oxoglutarate + oxygen → 3-epihydroxy-2'-deoxymugi
Pathway	hydroxylated mugineic acid phytosiderophore biosynthesis
Evidence	Inferred computationally without human oversight [EPPMN15]

Summary Reactions (2) References Show All

Gene-Reaction Schematic

The diagram illustrates a gene-reaction network. A central gene node, Pavir.J10036.1.p, is connected to four other gene nodes: Pavir.J00852.1.p, Pavir.Ca00416.1.p, Pavir.Cb01901.1.p, and an unlabeled gene node. Additionally, it is connected to two reaction nodes, both labeled 1.14.11.25.



Enzyme View: All Organisms

Show Predicted Enzymes

More Detail

Less Detail

2'-deoxymugineic acid phytosiderophore biosynthesis

2'-deoxymugineate

oxygen
2-oxoglutarate

2'-deoxymugineic acid, 2-oxoglutarate: oxygen oxidoreductase (3-hydroxylating) (Hv): hv-ids2
 mugineic acid 3-dioxygenase (At): At-EMT32960
 mugineic acid 3-dioxygenase (Pv):

oxygen
2-oxoglutarate

mugineic acid synthase (Hv): Hv-ids3

2'-deoxymugineic acid 2'-dioxygenase (At): At-EMT06140
 2'-deoxymugineic acid 2'-dioxygenase (Tt): Tt-TRUR3_32928-P1
 2'-deoxymugineic acid 2'-dioxygenase (Pv): Pv-Pvnt_A401854.1 p
 2'-deoxymugineic acid 2'-dioxygenase (Sb): Sb-Sobe_008G109600.1 p

Summary:

Graminaceous plants use the chelating method for iron absorption also referred to as Fe(III)-phytosiderophore transport or strategy II Fe-uptake. Fe-chelating compounds are secreted into the rhizosphere, these compounds have six coordination sites (3 -COOH, 2 -NH and 1 -OH) that bind to Fe. These compounds are called mugineate family siderophores and seven compounds have been identified. Extensive biochemical and physiological studies have resulted in the entire pathway being worked out along with the corresponding genes being cloned [Okumura94]. Variations in the amounts of phytosiderophore secreted leading to increased tolerance in some species allows the possibility of engineering the critical enzymes into non-resistant species [Kobayashi01]. *Hordeum vulgare* secretes very high amounts of mugineate's including the hydroxylated ones 3-epihydroxy-2'-deoxymugineate and 3-epihydroxymugineate and is also the most resistant to Fe-deficiency [Higuchi99].

Unification Links: MetaCyc: PWY-5925

Credits:

Created 12-May-2008 by Pujar A, Cornell University

References

- Higuchi99** Higuchi K, Suzuki K, Nakanishi H, Yamaguchi H, Nishizawa NK, Mori S (1999). "Cloning of nicotianamine synthase genes, novel genes involved in the biosynthesis of phytosiderophores." *Plant Physiol* 119(2):471-80. PMID: 9952442
- Kobayashi01** Kobayashi T, Nakanishi H, Takahashi M, Kawasaki S, Nishizawa NK, Mori S (2001). "In vivo evidence that *ids3* from *Hordeum vulgare* encodes a dioxygenase that converts 2'-deoxymugineic acid to mugineic acid in transgenic rice." *Planta* 212(5-6):864-71. PMID: 11348963
- Nakanishi00** Nakanishi H, Yamaguchi H, Sasakuma T, Nishizawa NK, Mori S (2000). "Two dioxygenase genes, *ids3* and *ids2*, from *Hordeum vulgare* are involved in the biosynthesis of mugineic acid family phytosiderophores." *Plant Mol Biol* 44(2):199-207. PMID: 11117263
- Okumura94** Okumura N, Nishizawa NK, Umehara Y, Ohata T, Nakanishi H, Yamaguchi T, Chino M, Mori S (1994). "A dioxygenase gene (*ids2*) expressed under iron deficiency conditions in the roots of *Hordeum vulgare*." *Plant Mol Biol* 25(4):705-19. PMID: 8061321




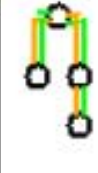
Compare pathway to other species




Arabidopsis

Soybean

Barley

Switchgrass

Organism	Evidence Glyph
AraCyc col	
G. max	
H. vulgare	
P. virgatum	

-  Unique reaction
-  Enzyme present
-  Enzyme absent

Overlay and analyze omics data sets

The screenshot displays a bioinformatics software interface. At the top, a red box highlights the title "SmartTable: Enriched from Expression Ratios". Below the title, there is a description: "211 rows of pathways from AraCyc col", "Owner: Peifen Zhang, Created: 08-Jul-2016 15:31:42, Last Modified: 08-Jul-2016 15:31:44, Source: ENRICHED Genes enriched for pathways from Expression Ratios".

Below the description are two dropdown menus: "ADD TRANSFORM COLUMN" with the text "choose a transform..." and "ADD PROPERTY COLUMN" with the text "choose a property".

A table of pathways is shown, with columns for "Pathways" and "p-values". The table lists the following pathways and their corresponding p-values:

Pathways	p-values
1 Proteinogenic Amino Acids Biosynthesis	1.7923744e-14
2 Amino Acids Biosynthesis	7.283686e-13
3 L-cysteine Biosynthesis	3.5492891e-7
4 Autotrophic CO ₂ Fixation	1.0414992e-6
5 Calvin-Benson-Bassham cycle	1.0414992e-6
6 Sugars Biosynthesis	1.8024729e-6
7 CO ₂ Fixation	1.8949237e-6
8 sucrose biosynthesis I (from photosynthesis)	1.8949237e-6
9 C1 Compounds Utilization and Assimilation	5.3437448e-6
10 Sucrose Biosynthesis	5.505550e-6

To the right of the table, a bar chart is visible, showing a single red bar for the pathway "ATIG17745.2".

Many ways to use the PMN resource

- Search genes, enzymes, compounds, pathways
- Blast PMN enzymes
- Ontology-based browse
- Comparative analysis across species
- Omics data overlay and analysis
- Collage your own pathway

<http://plantcyc.org>

Future development

- Further enhancing accuracy of enzyme function predictions
- Annotating transporters and subcellular location of reactions
- Creating many more pathway databases for sequenced genomes
- Providing online database creation service
- Developing genome-scale metabolic models
- Providing web app for integrated view of metabolism with other information such as gene expression

Thank you!

- The PMN Crew
 - Sue Rhee (PI)
 - Pascal Schlapfer
 - Michael Banf
 - Bo Xue
 - Arvind Chavali
 - Garret Huntress
- Major Collaborators
 - MetaCyc and Pathway Tools
 - MaizeGDB
- Editorial board members
- Users for data submission and correction
- Many PMN Alumni



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