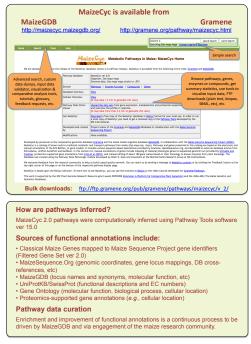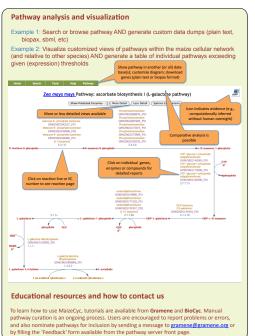# MaizeCyc: Metabolic Networks in Corn

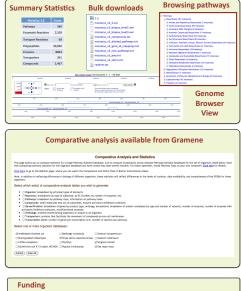Marcela K Monaco[1], Taner Z. Sen[2,3], Palitha D Dharmawardhana[4], Liya Ren[1], Mary Schaeffer[5,6], Vindhya Amarasinghe[4], Jim Thomason[1], Lisa Harper[2,7,8], Jack Gardiner[3,9], Carolyn J. Lawrence[2,3], Doreen Ware[1,10], Pankaj Jaiswal[4]

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MaizeCyc is a genome-wide catalog of known and/or predicted metabolic and transport pathways that enables plant researchers to graphically represent the metabolome of maize, thereby supporting integrated systems biology analyses.

MaizeCyc is available from

MaizeGDB
http://maizecyc.maizegdb.org/

Gramene
http://gramene.org/pathway/maizecyc.html

Advanced search, custom data dumps, input data validator, visualization & comparative analysis tools, tutorials, glossary, feedback requests, etc.

Browse pathways, genes, enzymes or compounds, get summary statistics, use tools to visualize input data, FTP downloads (plain text, biopax, SBML, etc), etc.

Bulk downloads: ftp://ftp.gramene.org/pub/gramene/pathways/maizecyc/v_2/

How are pathways inferred?

MaizeCyc 2.0 pathways were computationally inferred using Pathway Tools software ver 15.0

Sources of functional annotations include:

- Classical Maize Genes mapped to Maize Sequence Project gene identifiers (Filtered Gene Set ver 2.0)
- MaizeSequence.Org (genomic coordinates, gene locus mappings, DB cross-references, etc)
- MaizeGDB (locus names and synonyms, molecular function, etc)
- UniProtKB/SwissProt (functional descriptions and EC numbers)
- Gene Ontology (molecular function, biological process, cellular location)
- Proteomics-supported gene annotations (e.g., cellular location)

Pathway data curation

Enrichment and improvement of functional annotations is a continuous process to be driven by MaizeGDB and via engagement of the maize research community.

Pathway analysis and visualization

Example 1: Search or browse pathway AND generate custom data dumps (plain text, biopax, sbml, etc)

Example 2: Visualize customized views of pathways within the maize cellular network (and relative to other species) AND generate a table of individual pathways exceeding given (expression) thresholds

Show pathway in another (or all) database(s); customize diagram; download genes (plain text or biopax format)

Zea mays mays Pathway: ascorbate biosynthesis I (L-galactose pathway)

More or less detailed views available

Icon indicates evidence (e.g., computationally inferred without human oversight)

Comparative analysis is possible

Click on individual genes, enzymes or compounds for detailed reports

Click on reaction line or EC number to see reaction page

Educational resources and how to contact us

To learn how to use MaizeCyc, tutorials are available from **Gramene** and **BioCyc**. Manual pathway curation is an ongoing process. Users are encouraged to report problems or errors, and also nominate pathways for inclusion by sending a message to gramene@gramene.org or by filling the 'Feedback' form available from the pathway server front page.

Summary Statistics

MaizeCyc 2.0	Count
Pathways	390
Enzymatic Reactions	2,109
Transport Reactions	68
Polypeptides	39,656
Enzymes	8894
Transporters	291
Compounds	1,467

Bulk downloads

- maizecyc_v2.0.zip
- maizecyc_v2_biopax_level2.owl
- maizecyc_v2_biopax_level3.owl
- maizecyc_v2_compounds.txt
- maizecyc_v2_deleted_pathways.txt
- maizecyc_v2_gene_id_mappings.txt
- maizecyc_v2_new_pathways.txt
- maizecyc_v2_pwy.txt
- readme.txt

Browsing pathways

Genome Browser View

Comparative analysis available from Gramene

This page allows you to compute statistics for a single Pathway/Genome Database, and to compare comparisons across multiple Pathway/Genome Databases for the set of organisms listed below. Some of these computations involve comparing summary statistics for the organism database you have chosen may take several minutes. For faster operation, install Pathway Tools on your own computer! Click here for details.

Note: in addition to reflecting differences in biology of different organisms, these statistics will reflect differences in the levels of curation, data availability, and completeness of the PGDBs for these organisms.

Funding

Application example: Organ-specific genes/pathways in maize

Hierarchical clustering of 19.3K highly regulated genes in the specified tissues, 2.2K genes map to MaizeCyc metabolic pathways

Expression values of organ-specific gene clusters mapped to maize pathways

The Omics Viewer allows researchers to upload high-throughput datasets to visualize them in the context of a cellular network of pathways.

Cellular Overview

* Chlorophyllide a biosynthesis

** Phenylpropanoid (lignin) biosynthesis

Number of pathways having genes with organ-specific upregulation

A = anther (159)
E = embryo (122)
D = endosperm (106)
L = leaf (199)
R = root (145)

Data source: Sekhon *et al* (2011) Genome-wide atlas of transcription during maize development. The Plant Journal 66, 553–563