# User's Guide for Plant Reactome Database (Build # 56b, Feb 2018)

**Sushma Naithani and Pankaj Jaiswal**
**Oregon State University**

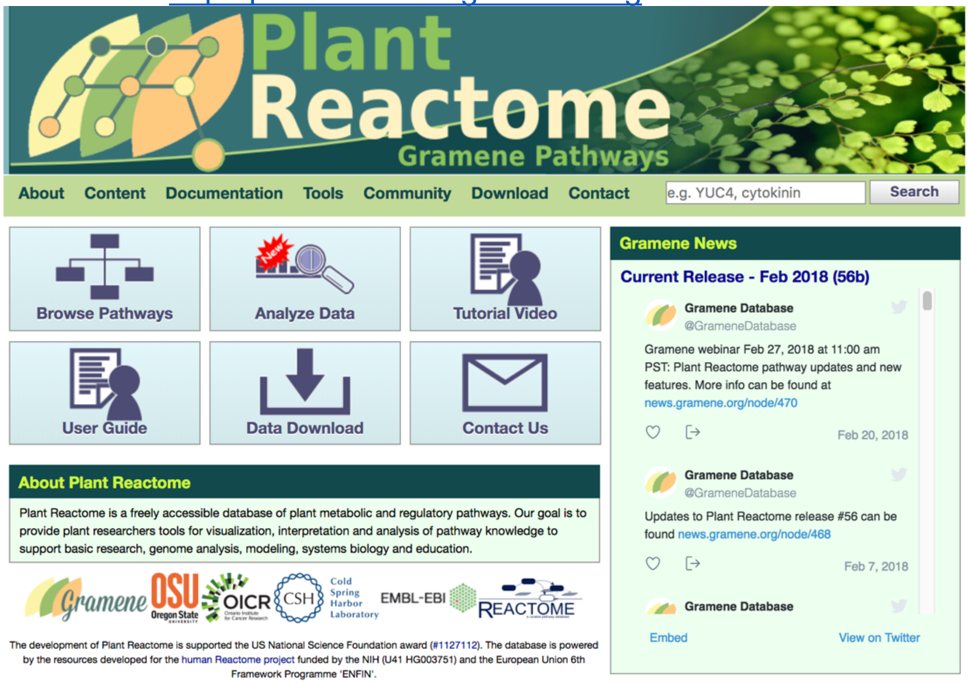
**What is Plant Reactome**: The **Plant Reactome** is a free, open-source, curated and peer reviewed pathway database. Our goal is to provide intuitive bioinformatics tools for the visualization, interpretation and analysis of pathway knowledge to support basic research, genome analysis, modeling, systems biology and education.

## How to access Plant Reactome?

Access is free of cost and you can click on following links to get to the plant pathways

From Gramene: http://www.gramene.org/pathways

Direct Link: http://plantreactome.gramene.org



**About Plant Reactome**

Plant Reactome is a freely accessible database of plant metabolic and regulatory pathways. Our goal is to provide plant researchers tools for visualization, interpretation and analysis of pathway knowledge to support basic research, genome analysis, modeling, systems biology and education.

The development of Plant Reactome is supported the US National Science Foundation award (#1127112). The database is powered by the resources developed for the human Reactome project funded by the NIH (U41 HG003751) and the European Union 6th Framework Programme 'ENFIN'.

**Gramene News**

**Current Release - Feb 2018 (56b)**

Gramene Database
@GrameneDatabase

Gramene webinar Feb 27, 2018 at 11:00 am PST: Plant Reactome pathway updates and new features. More info can be found at news.gramene.org/node/470

Feb 20, 2018

Gramene Database
@GrameneDatabase

Updates to Plant Reactome release #56 can be found news.gramene.org/node/468

Feb 7, 2018

Gramene Database

## What can Plant Reactome do for me?

You can find various **video tutorial in Gramene Database YouTube** channel ( https://www.youtube.com/channel/UCMtmq20XMccsNUaACuqQJ-w). Specific webinars on Plant Reactome are:

Release 56b Feb 2018: https://www.youtube.com/watch?v=LsioX4x5ohk&t=1032s

Expression data analysis: https://www.youtube.com/watch?v=fyAUOBydgwI&t=58s

Plant Reactome basic: https://www.youtube.com/watch?v=d_gVIog56EQ

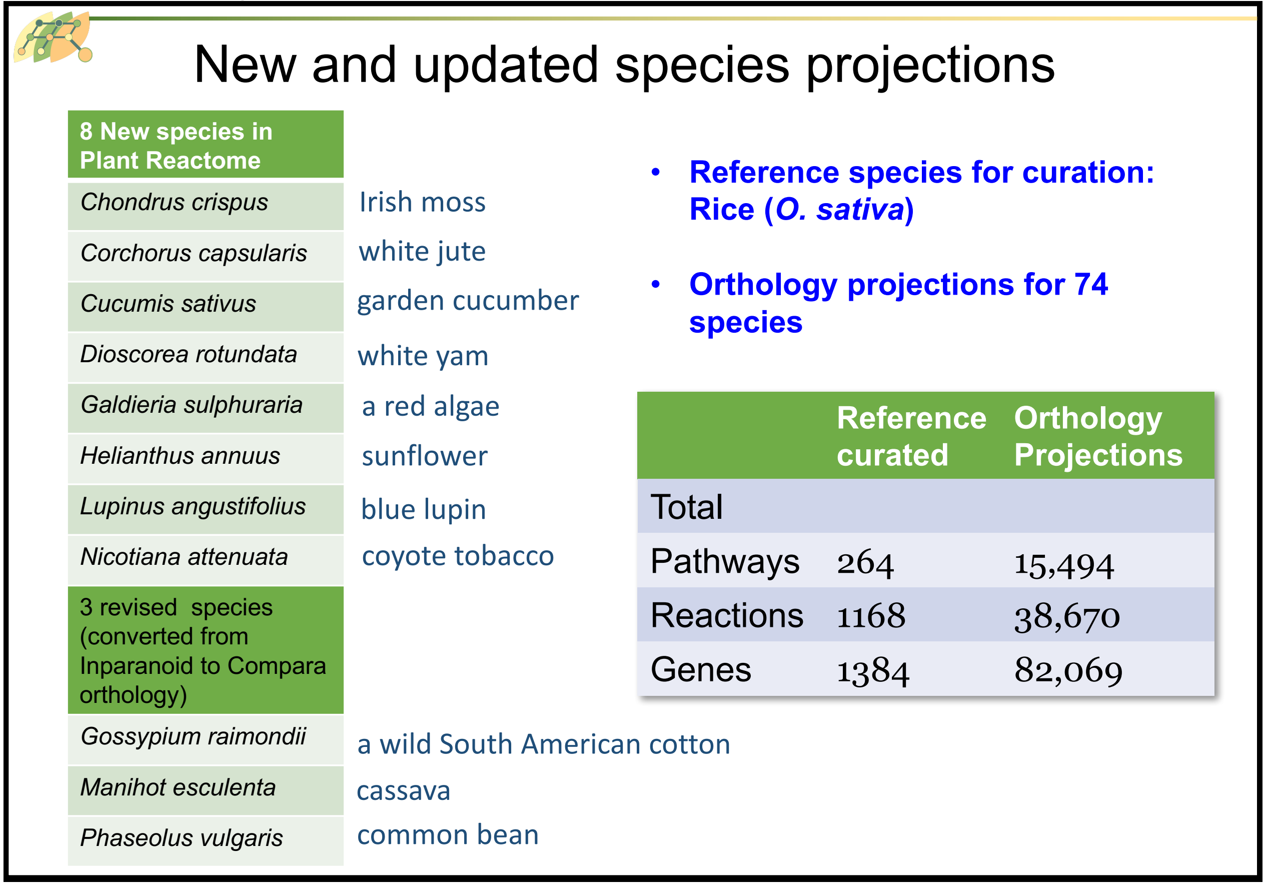
Plant Reactome: https://www.youtube.com/watch?v=4CkVU2Q-THs&t=50s

**How many plant species are covered in Plant Reactome database:** Plant Pathways are available for 75 species. We use rice as a reference species for curation and then use gene-orthology relationships to project pathways on a number of species ranging from unicellular photoautotrophs to higher plants.

As of Release # 56b, the Plant Reactome contains gene homology-based pathway projections for 74 plant species. We regularly update our database for contents and tools. To see current species and associated statistics see http://plantreactome.gramene.org/pages/content/release-summary/

.

**A brief summary of release 56b updates**



## New and updated species projections

| 8 New species in Plant Reactome | |
|---|---|
| *Chondrus crispus* | Irish moss |
| *Corchorus capsularis* | white jute |
| *Cucumis sativus* | garden cucumber |
| *Dioscorea rotundata* | white yam |
| *Galdieria sulphuraria* | a red algae |
| *Helianthus annuus* | sunflower |
| *Lupinus angustifolius* | blue lupin |
| *Nicotiana attenuata* | coyote tobacco |
| **3 revised species (converted from Inparanoid to Compara orthology)** | |
| *Gossypium raimondii* | a wild South American cotton |
| *Manihot esculenta* | cassava |
| *Phaseolus vulgaris* | common bean |

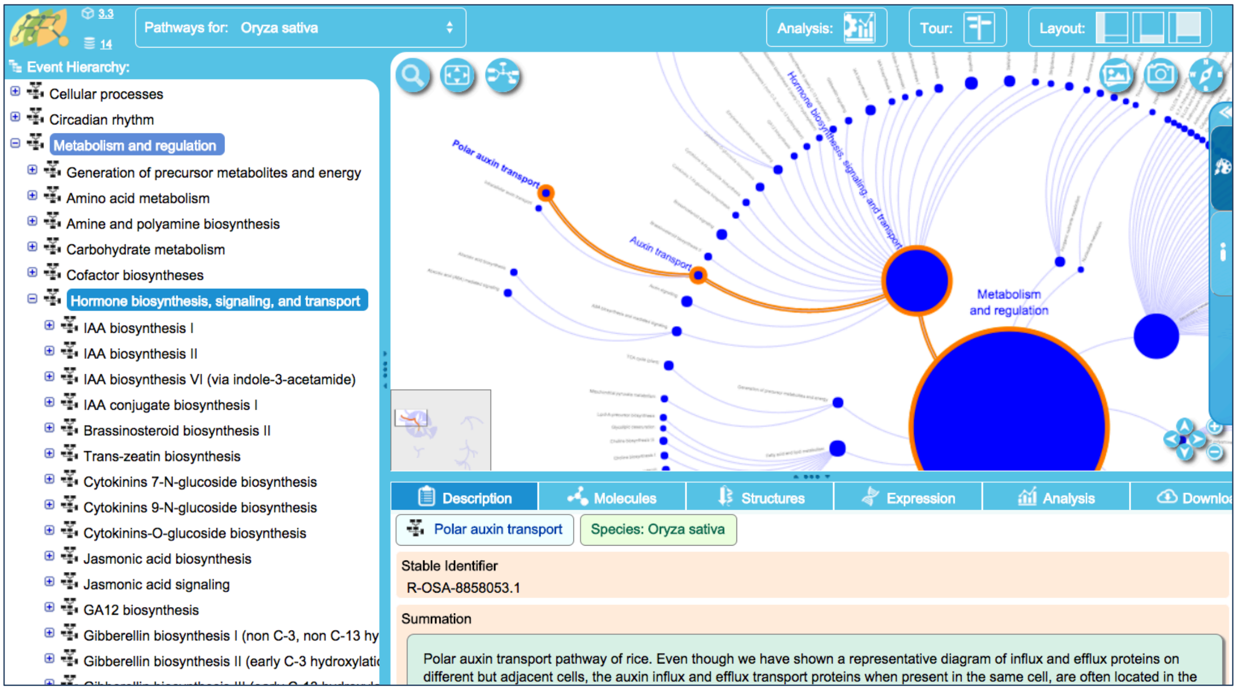
- **Reference species for curation: Rice (*O. sativa*)**
- **Orthology projections for 74 species**

| | Reference curated | Orthology Projections |
|---|---|---|
| Total | | |
| Pathways | 264 | 15,494 |
| Reactions | 1168 | 38,670 |
| Genes | 1384 | 82,069 |

**How can I see list of pathways and select a specific pathway (Browse pathway)?** You can click on the “Browse Pathways” link on the PR homepage and get into Pathway Browser that lists pathways, shows a pathway diagram, and associate data on various pathway entities. Here first you will get the top-level view of pathways using Fireworks display which allows you to further select a pathway by functional category. Below are the examples of Pathway Browser views.

Gramene

# New “Fireworks” pathway hierarchy display



Stable Identifier
R-OSA-8858053.1

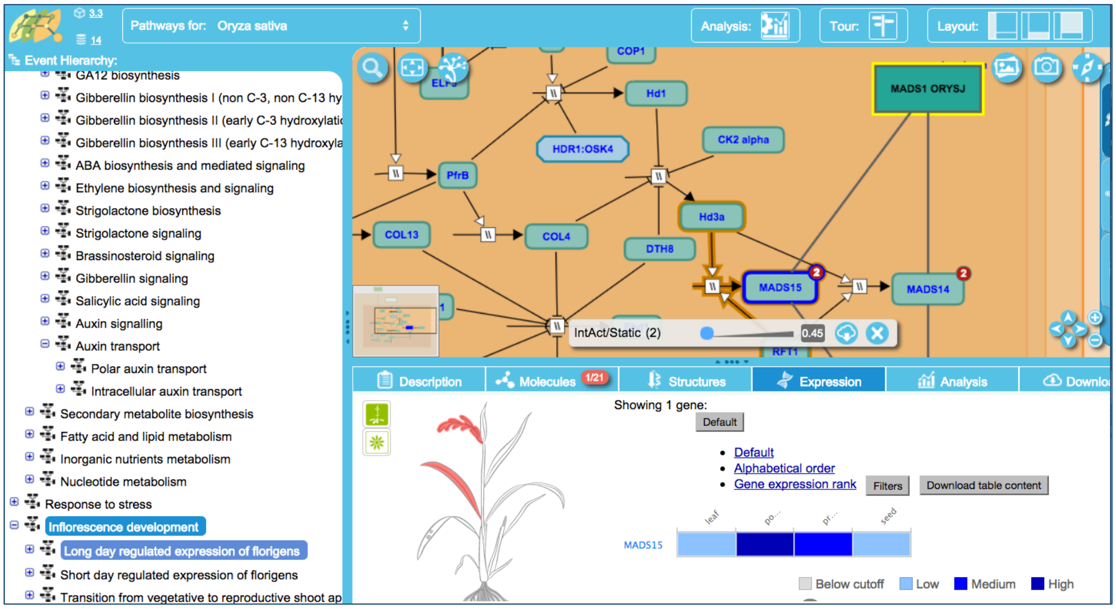
Summation

Polar auxin transport pathway of rice. Even though we have shown a representative diagram of influx and efflux proteins on different but adjacent cells, the auxin influx and efflux transport proteins when present in the same cell, are often located in the

- Explore pathways by functional category

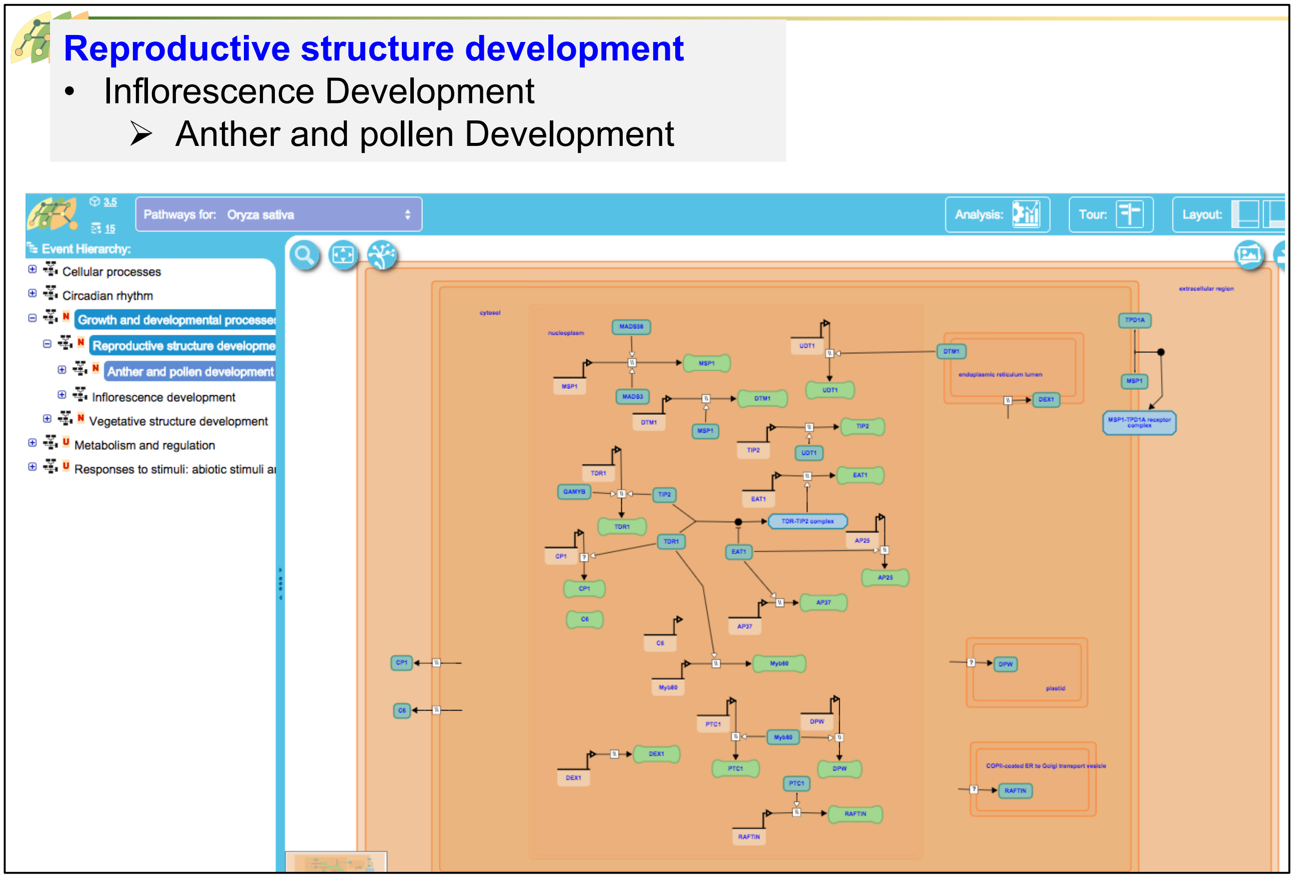
Plant Reactome
Gramene Pathways

Integrates with ATLAS, Ensembl, and links to other collaborators via search (i.e. MaizeGDB, TAIR, Congenie)



## What type of pathways are present in the Plant Reactome?

We have covered ~80% of metabolic pathway space. Now our focus is on curation of plant growth and developmental pathways, genetic regulatory pathways and how plants respond to various stimuli (i.e. biotic and abiotic stress). In previous example, you have seen metabolic and hormone signaling pathway. Here is an example of Anther development.



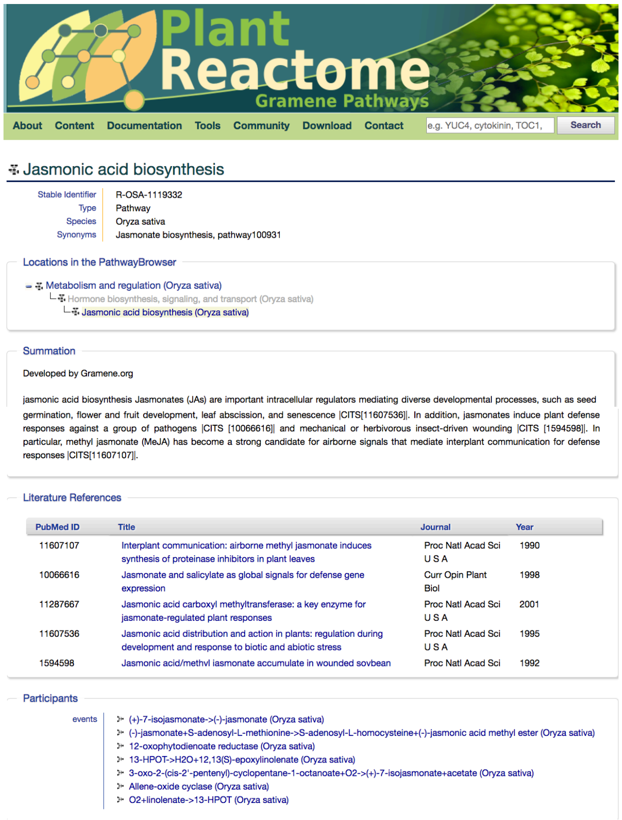
**Reproductive structure development**

- Inflorescence Development
  - ➢ Anther and pollen Development

## Can I identify pathways associated with gene or protein of my interest?

Yes. you can search gene or your interest in Gramene or Plant Reactome home page. Here is the summary of how you can search in the Gramene and Plant Reactome.

# Extensive search and data integration features



Jasmonic acid biosynthesis

| | |
|---|---|
| Stable Identifier | R-OSA-1119332 |
| Type | Pathway |
| Species | Oryza sativa |
| Synonyms | Jasmonate biosynthesis, pathway100931 |

Locations in the PathwayBrowser

- Metabolism and regulation (Oryza sativa)
  - Hormone biosynthesis, signaling, and transport (Oryza sativa)
    - Jasmonic acid biosynthesis (Oryza sativa)

Summation

Developed by Gramene.org

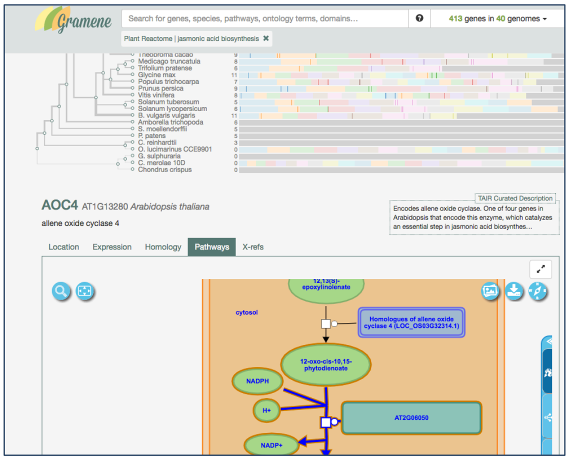
jasmonic acid biosynthesis Jasmonates (JAs) are important intracellular regulators mediating diverse developmental processes, such as seed germination, flower and fruit development, leaf abscission, and senescence |CITS[11607536]|. In addition, jasmonates induce plant defense responses against a group of pathogens |CITS [10066616]| and mechanical or herbivorous insect-driven wounding |CITS [1594598]|. In particular, methyl jasmonate (MeJA) has become a strong candidate for airborne signals that mediate interplant communication for defense responses |CITS[11607107]|.

Literature References

| PubMed ID | Title | Journal | Year |
|---|---|---|---|
| 11607107 | Interplant communication: airborne methyl jasmonate induces synthesis of proteinase inhibitors in plant leaves | Proc Natl Acad Sci U S A | 1990 |
| 10066616 | Jasmonate and salicylate as global signals for defense gene expression | Curr Opin Plant Biol | 1998 |
| 11287667 | Jasmonic acid carboxyl methyltransferase: a key enzyme for jasmonate-regulated plant responses | Proc Natl Acad Sci U S A | 2001 |
| 11607536 | Jasmonic acid distribution and action in plants: regulation during development and response to biotic and abiotic stress | Proc Natl Acad Sci U S A | 1995 |
| 1594598 | Jasmonic acid/methvl iasmonate accumulate in wounded sovbean | Proc Natl Acad Sci | 1992 |

Participants

events
- (+)-7-isojasmonate->(-)-jasmonate (Oryza sativa)
- (-)-jasmonate+S-adenosyl-L-methionine->S-adenosyl-L-homocysteine+(-)-jasmonic acid methyl ester (Oryza sativa)
- 12-oxophytodienoate reductase (Oryza sativa)
- 13-HPOT->H2O+12,13(S)-epoxylinolenate (Oryza sativa)
- 3-oxo-2-(cis-2'-pentenyl)-cyclopentane-1-octanoate+O2->(+)-7-isojasmonate+acetate (Oryza sativa)
- Allene-oxide cyclase (Oryza sativa)
- O2+linolenate->13-HPOT (Oryza sativa)

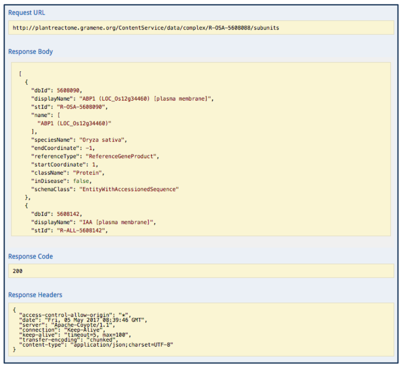


**AOC4** AT1G13280 *Arabidopsis thaliana*

allene oxide cyclase 4

TAIR Curated Description

Encodes allene oxide cyclase. One of four genes in Arabidopsis that encode this enzyme, which catalyzes an essential step in jasmonic acid biosynthes...



Request URL

```
http://plantreactome.gramene.org/ContentService/data/complex/R-OSA-5608088/subunits
```

Response Body

```
[
  {
    "dbId": 5608090,
    "displayName": "ABP1 (LOC_Os12g34460) [plasma membrane]",
    "stId": "R-OSA-5608090",
    "name": [
      "ABP1 (LOC_Os12g34460)"
    ],
    "speciesName": "Oryza sativa",
    "endCoordinate": -1,
    "referenceType": "ReferenceGeneProduct",
    "startCoordinate": 1,
    "className": "Protein",
    "inDisease": false,
    "schemaClass": "EntityWithAccessionedSequence"
  },
  {
    "dbId": 5608142,
    "displayName": "IAA [plasma membrane]",
    "stId": "R-ALL-5608142",
```

Response Code

```
200
```

Response Headers

```
{
  "access-control-allow-origin": "*",
  "date": "Fri, 05 May 2017 08:39:46 GMT",
  "server": "Apache-Coyote/1.1",
  "connection": "Keep-Alive",
  "keep-alive": "timeout=5, max=100",
  "transfer-encoding": "chunked",
  "content-type": "application/json;charset=UTF-8"
}
```

**Search for a gene or protein in Plant Reactome and find associated pathways:**

**<u>Here is a specific example Use case study using Tomato COI1 gene:</u>**

As a researcher, you are working on fruit ripening in tomato, and interested in learning about regulation of ripening associated pathways during fruit development. You also have a few related hypotheses that you would like to test, for which you quickly need to extract relevant genes and pathways.

> Example: ‘CORONATINE-INSENSITIVE1’ (or COI1), a gene required for the maternal control of seed maturation, jasmonate-signaled defense response and glandular trichome development (reference: Li et al (2004): Plant Cell, **16**:126, PMID:).

Plant Cell. 2004 Jan; 16(1): 126–143. PMCID: PMC301400
doi: 10.1105/tpc.017954

**The Tomato Homolog of CORONATINE-INSENSITIVE1 Is Required for the Maternal Control of Seed Maturation, Jasmonate-Signaled Defense Responses, and Glandular Trichome Development**W

Lei Li,[a] Youfu Zhao,[a] Bonnie C. McCaig,[a] Byron A. Wingerd,[b] Jihong Wang,[c] Mark E. Whalon,[b] Eran Pichersky,[c] and Gregg A. Howe[1,a,d]

Author information ► Article notes ► Copyright and License information ►

**This article has been corrected.** See Plant Cell. 2004 March; 16(3): 783.

This article has been cited by other articles in PMC.

**ABSTRACT**

Jasmonic acid (JA) is a fatty acid–derived signaling molecule that regulates a broad range of plant defense responses against herbivores and some microbial pathogens. Molecular genetic studies in Arabidopsis have established that JA also performs a critical role in anther and pollen development but is not essential for other developmental aspects of the plant's life cycle. Here, we describe the phenotypic and molecular characterization of a sterile mutant of tomato (*jasmonic acid–insensitive1* [*jai1*]) that is defective in JA signaling. Although the mutant exhibited reduced pollen viability, sterility was caused by a defect in the maternal control of seed maturation, which was associated with the loss of accumulation of JA-regulated proteinase inhibitor proteins in reproductive tissues. *jai1* plants exhibited several defense-related phenotypes, including the inability to express JA-responsive genes, severely compromised resistance to two-spotted spider mites, and abnormal development of glandular trichomes. We demonstrate that these defects are caused by the loss of function of the tomato homolog of CORONATINE-INSENSITIVE1 (COI1), an F-box protein that is required for JA-signaled processes in Arabidopsis. These findings indicate that the JA/COI1 signaling pathway regulates distinct developmental processes in different plants and suggest a role for JA in the promotion of glandular trichome–based defenses.

**INTRODUCTION**

**Share**
Facebook Twitter Google+

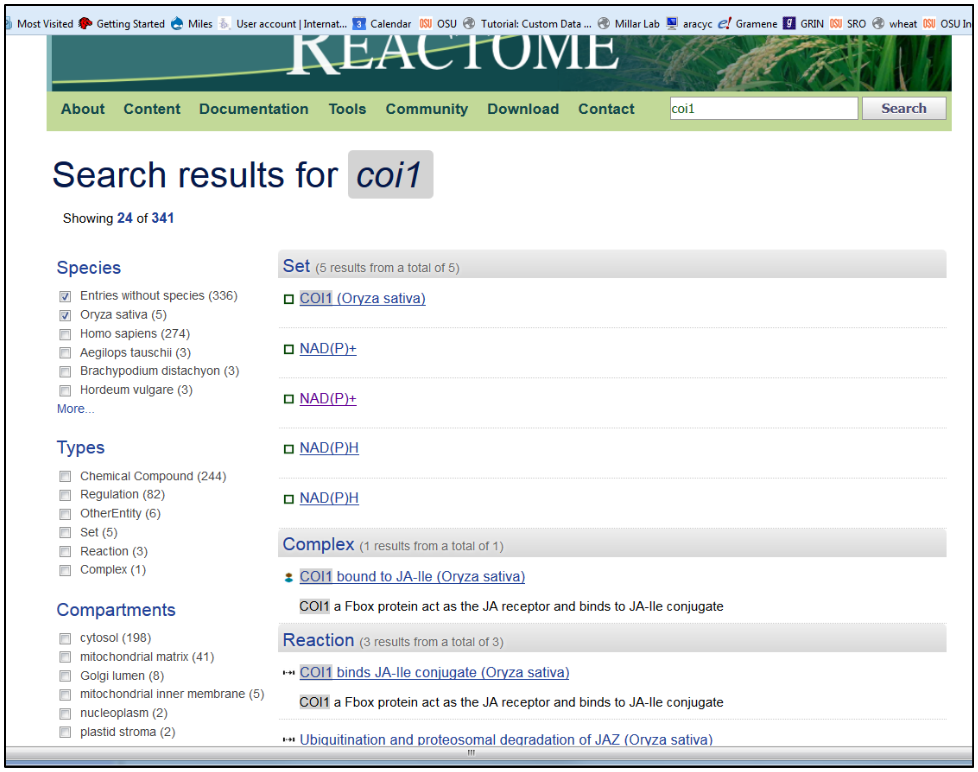
**Save items**
Add to Favorites

**Similar articles in PubMed**
The wound response mutant suppressor of prosystemin-mediated responses6 (spr6) is a weak allele of the [Plant Cell Physiol. 2006]
Virulence systems of Pseudomonas syringae pv. tomato promote bacterial speck disease in tomato by targeting the ja [Plant J. 2003]
The tomato suppressor of prosystemin-mediated responses2 gene encodes a fatty acid desaturase required fc [Plant Cell. 2003]
Jasmonate: an oxylipin signal with many roles in plants. [Vitam Horm. 2005]
Jasmonates in flower and seed development. [Biochimie. 2013]
See reviews...
See all...

**Cited by other articles in PMC**
Jasmonate Signalling and Defence Responses in the Model Legume Medicago truncatula—A Focus on Respons [Plants. 1/01]
Control of Carbon Assimilation and Partitioning by Jasmonate: An Accounting of Growth–Defense Tradeoffs [Plants. 1/01]
Dynamics of Jasmonate Metabolism upon Flowering and across Leaf Stress Responses in Arabidopsis thaliana [Plants. 1/01]
Beyond the Canon: Within-Plant and Population-Level Heterogeneity in Jasmonate Signaling Engaged by F [Plants. 1/01]
Overexpression of SlUPA-like induces cell enlargement, aberrant

Users can type name of a gene in the search box in the Plant Reactome home page. Searching for COI1 will give the following result:

(http://plantreactome.gramene.org/content/query?q=coi1&species=Oryza+sativa&species=Entries+without+species&cluster=true



Search results for *coi1*

Showing 24 of 341

**Species**
- ☑ Entries without species (336)
- ☑ Oryza sativa (5)
- ☐ Homo sapiens (274)
- ☐ Aegilops tauschii (3)
- ☐ Brachypodium distachyon (3)
- ☐ Hordeum vulgare (3)

More...

**Types**
- ☐ Chemical Compound (244)
- ☐ Regulation (82)
- ☐ OtherEntity (6)
- ☐ Set (5)
- ☐ Reaction (3)
- ☐ Complex (1)

**Compartments**
- ☐ cytosol (198)
- ☐ mitochondrial matrix (41)
- ☐ Golgi lumen (8)
- ☐ mitochondrial inner membrane (5)
- ☐ nucleoplasm (2)
- ☐ plastid stroma (2)

**Set** (5 results from a total of 5)
- COI1 (Oryza sativa)
- NAD(P)+
- NAD(P)+
- NAD(P)H
- NAD(P)H

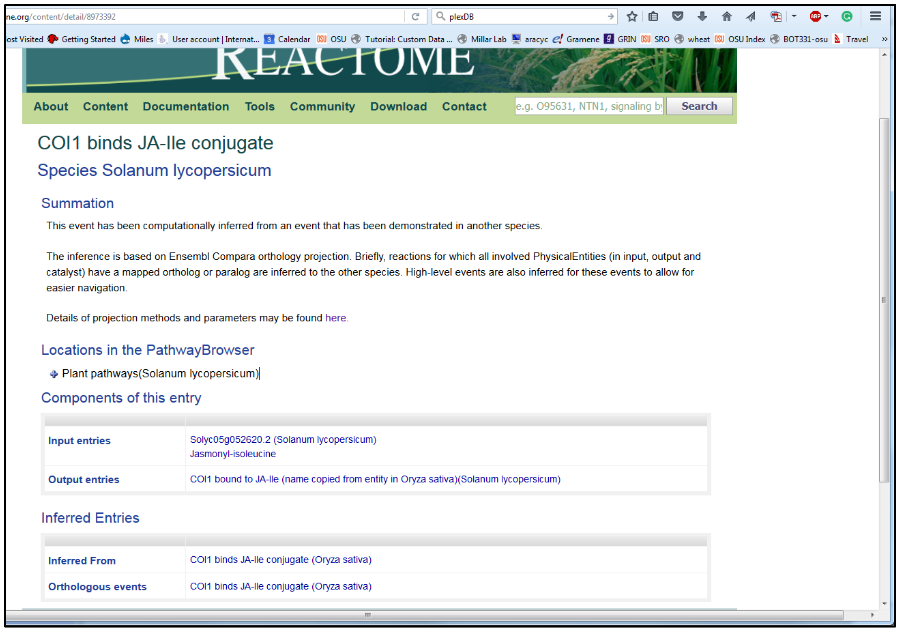
**Complex** (1 results from a total of 1)
- COI1 bound to JA-Ile (Oryza sativa)
  COI1 a Fbox protein act as the JA receptor and binds to JA-Ile conjugate

**Reaction** (3 results from a total of 3)
- COI1 binds JA-Ile conjugate (Oryza sativa)
  COI1 a Fbox protein act as the JA receptor and binds to JA-Ile conjugate
- Ubiquitination and proteosomal degradation of JAZ (Oryza sativa)

)

By default, the database searches are on ‘*Oryza sativa*’. However, from the Species section, uncheck the *O. sativa* and entries without species and click on the ‘more’ option to find tomato (*Solanum lycopersicum*). After the selection, you will see http://plantreactome.gramene.org/content/query?q=coi1&species=Solanum+lycopersicum&cluster=true

The results also suggest that the COI1 gene product participates in a reaction where it binds Jasmonate-Ile and forms a complex. Now click on the Reaction Link for ‘COI1 binds JA-Ile conjugate (Solanum lycopersicum)’.



COI1 binds JA-Ile conjugate

Species Solanum lycopersicum

Summation

This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on Ensembl Compara orthology projection. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped ortholog or paralog are inferred to the other species. High-level events are also inferred for these events to allow for easier navigation.

Details of projection methods and parameters may be found here.

Locations in the PathwayBrowser

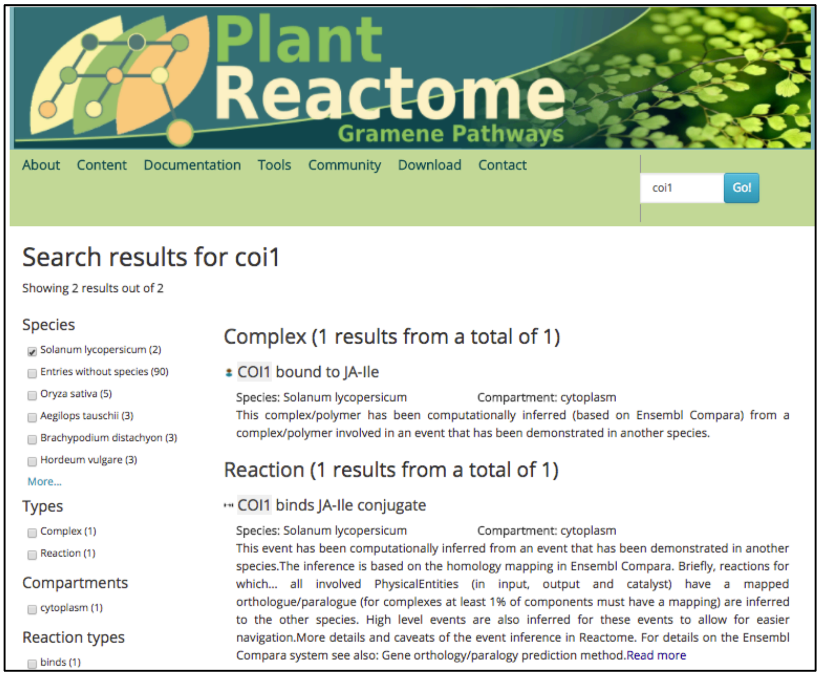
Plant pathways(Solanum lycopersicum)

Components of this entry

| | |
|---|---|
| **Input entries** | Solyc05g052620.2 (Solanum lycopersicum)<br>Jasmonyl-isoleucine |
| **Output entries** | COI1 bound to JA-Ile (name copied from entity in Oryza sativa)(Solanum lycopersicum) |

Inferred Entries

| | |
|---|---|
| **Inferred From** | COI1 binds JA-Ile conjugate (Oryza sativa) |
| **Orthologous events** | COI1 binds JA-Ile conjugate (Oryza sativa) |



Search results for coi1

Showing 2 results out of 2

Species

☑ Solanum lycopersicum (2)
☐ Entries without species (90)
☐ Oryza sativa (5)
☐ Aegilops tauschii (3)
☐ Brachypodium distachyon (3)
☐ Hordeum vulgare (3)
More...

Types

☐ Complex (1)
☐ Reaction (1)

Compartments

☐ cytoplasm (1)

Reaction types

☐ binds (1)

Complex (1 results from a total of 1)

COI1 bound to JA-Ile

Species: Solanum lycopersicum Compartment: cytoplasm
This complex/polymer has been computationally inferred (based on Ensembl Compara) from a complex/polymer involved in an event that has been demonstrated in another species.

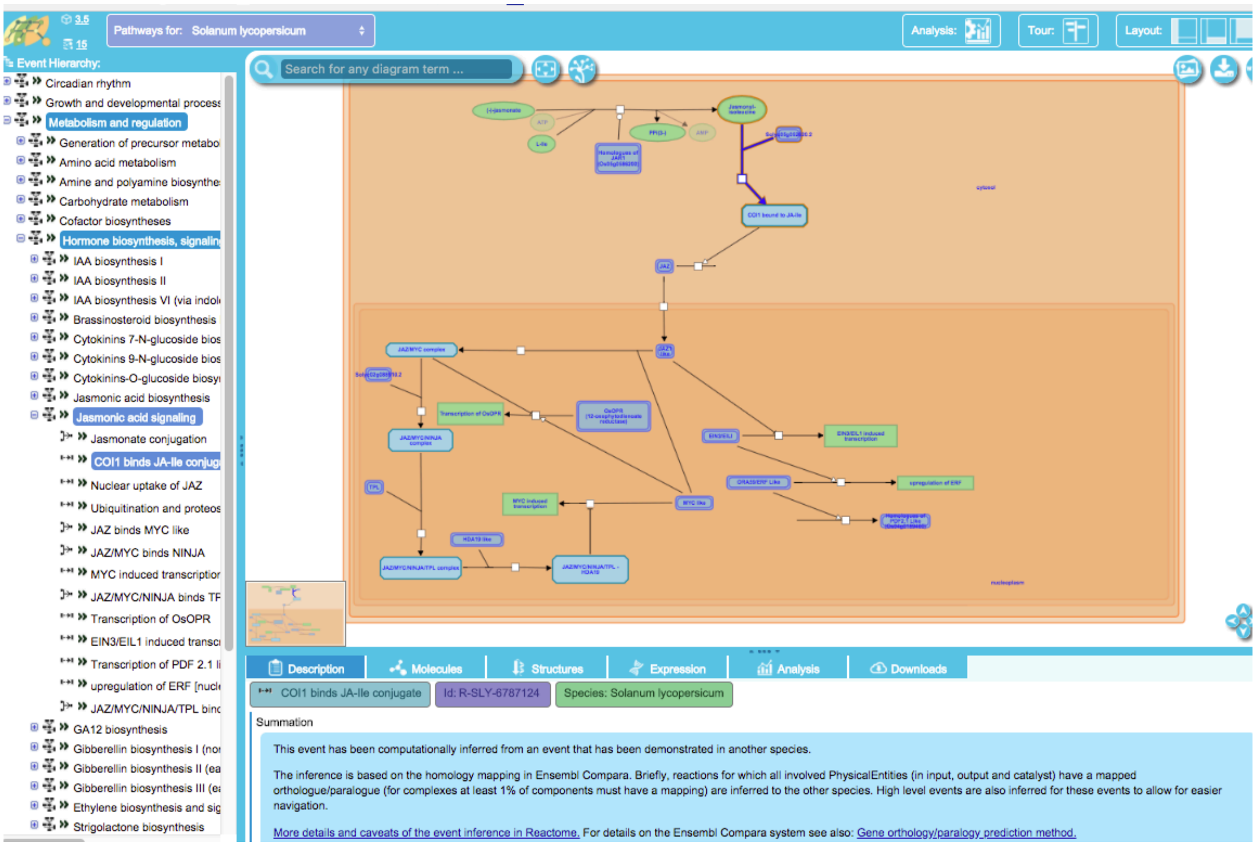
Reaction (1 results from a total of 1)

COI1 binds JA-Ile conjugate

Species: Solanum lycopersicum Compartment: cytoplasm
This event has been computationally inferred from an event that has been demonstrated in another species.The inference is based on the homology mapping in Ensembl Compara. Briefly, reactions for which... all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 1% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.More details and caveats of the event inference in Reactome. For details on the Ensembl Compara system see also: Gene orthology/paralogy prediction method.Read more

It will take you to the Reaction detail page which tells you about how the reaction was curated/projected, inputs and outputs of the reactions and the pathway this reaction is associated with. Click on the ‘+’ sign next to the ‘Plant Pathways (Solanum lycopersicum). The hierarchy chart opens up telling about the pathways this reaction is associated with. In this case, the Jasmonic acid biosynthesis and signaling.

[http://plantreactome.gramene.org/PathwayBrowser/#/R-SLY-6787011&SEL=R-SLY-6787124&PATH=R-SLY-2744345,R-SLY-2744341](http://plantreactome.gramene.org/PathwayBrowser/#/R-SLY-6787011&SEL=R-SLY-6787124&PATH=R-SLY-2744345,R-SLY-2744341)



This event has been computationally inferred from an event that has been demonstrated in another species.

The inference is based on the homology mapping in Ensembl Compara. Briefly, reactions for which all involved PhysicalEntities (in input, output and catalyst) have a mapped orthologue/paralogue (for complexes at least 1% of components must have a mapping) are inferred to the other species. High level events are also inferred for these events to allow for easier navigation.

More details and caveats of the event inference in Reactome. For details on the Ensembl Compara system see also: Gene orthology/paralogy prediction method.

In the browser, you see the reaction and pathways highlighted to suggest its placement in the data structure.

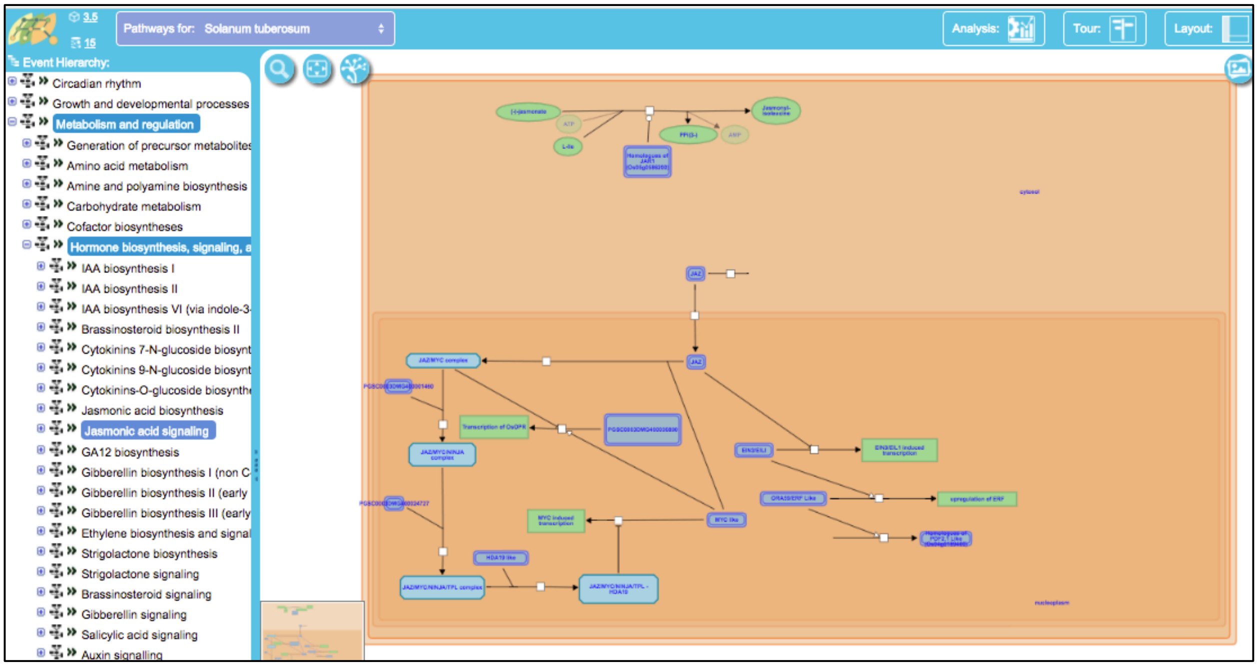
See list of molecules participating in the reaction (click the molecules button in cyan box). You will see the highlighted genes products and inputs/outputs
Click on the + sign next to chemical compounds of genes based on your interest to see a full list. Depending on your selection in the left-hand tree, if it is for pathway you will see a larger list. Also, there is a download data option in this tab.
We chose to use gene products section to look for the tomato gene that was mapped to this reaction. **It turns out that tomato gene Solyc05g052620.2 was mapped to COI1 function in this pathway**.

## How can I navigate to projected pathways in another plant species (or my species of interest)?

Can I find a similar event in Potato? And find COI1 gene homologs.

A. Fill in your answer…………….

On the Pathway Browse page, select '*Solanum tuberosum*' from the species drop down list. As soon as you select the potato species, the browser view will refresh. [http://plantreactome.gramene.org/PathwayBrowser/#/R-STU-6787011&PATH=R-STU-2744345,R-STU-2744341](http://plantreactome.gramene.org/PathwayBrowser/#/R-STU-6787011&PATH=R-STU-2744345,R-STU-2744341)



**Result: You will see that this reaction was not projected for potato, as JA-Ile to JAZ connection is missing in potato.**

There are following possible reasons for this difference.

The potato gene homolog was not identified that's why we do not see the mapped gene and the missing reaction from potato.

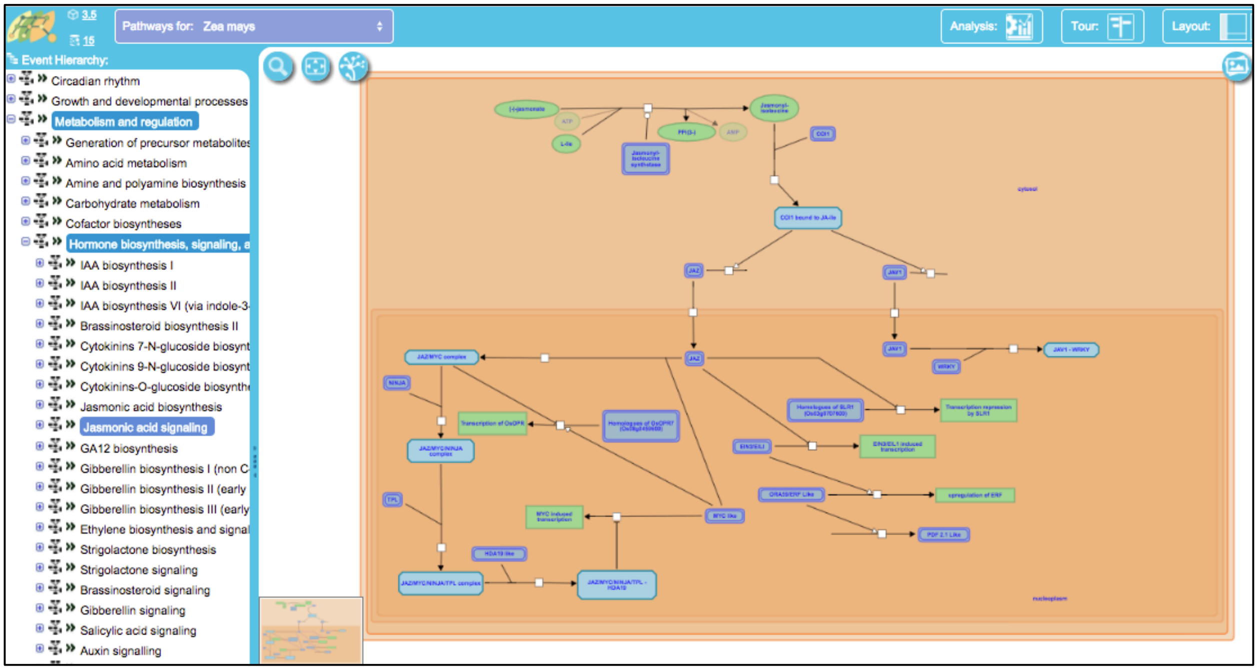
Absence of potato gene could be due to

- Annotated gene was not identified by the potato genome project. Therefore missing
- The gene was there but it didn't meet the homolog calling criteria, thus missing from the gene family cluster
- This may be case of either true biology or evolutionary effects or the genotype that was sequenced to produce reference potato genome.
- These are all good observations, that become research questions that can be discussed in the Genome exercise.

**Projections in other species**:

Let's try another species '*Zea mays'*, we see the reaction being projected in maize as well.

Select *Zea mays*
http://plantreactome.gramene.org/PathwayBrowser/#/R-ZMA-6787011&PATH=R-ZMA-2744345,R-ZMA-2744341


Pathways for: Zea mays

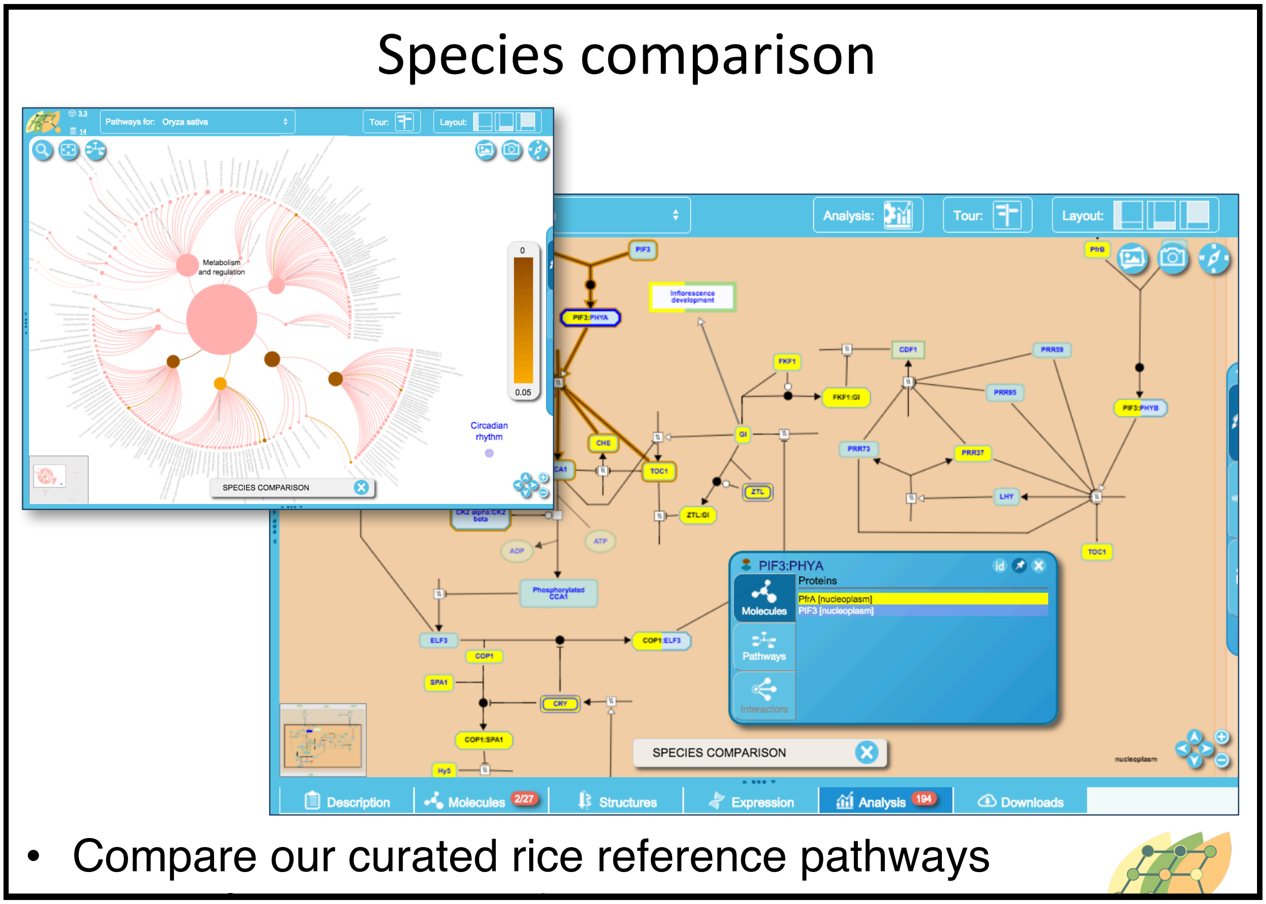
**Can I compare a pathway between reference species rice and anyone of the 74-plant species for which pathway projection are available?**

Step 1: Open browser and navigate to a pathway page e.g. Jasmonic acid signaling pathways in reference species rice (*Oryza Sativa*).

Step2: Click on the Analsis (icon on the top; above the pathway diagram). A new window with Analysis Tools menu

Step 3: From the species comparison drop down option select your favorite species and then hit 'Go'.

**As a result, a new pathway browsing window, showing the projection of Tomato pathway over the reference pathway from rice will open as shown here.**



## Species comparison

- Compare our curated rice reference pathways

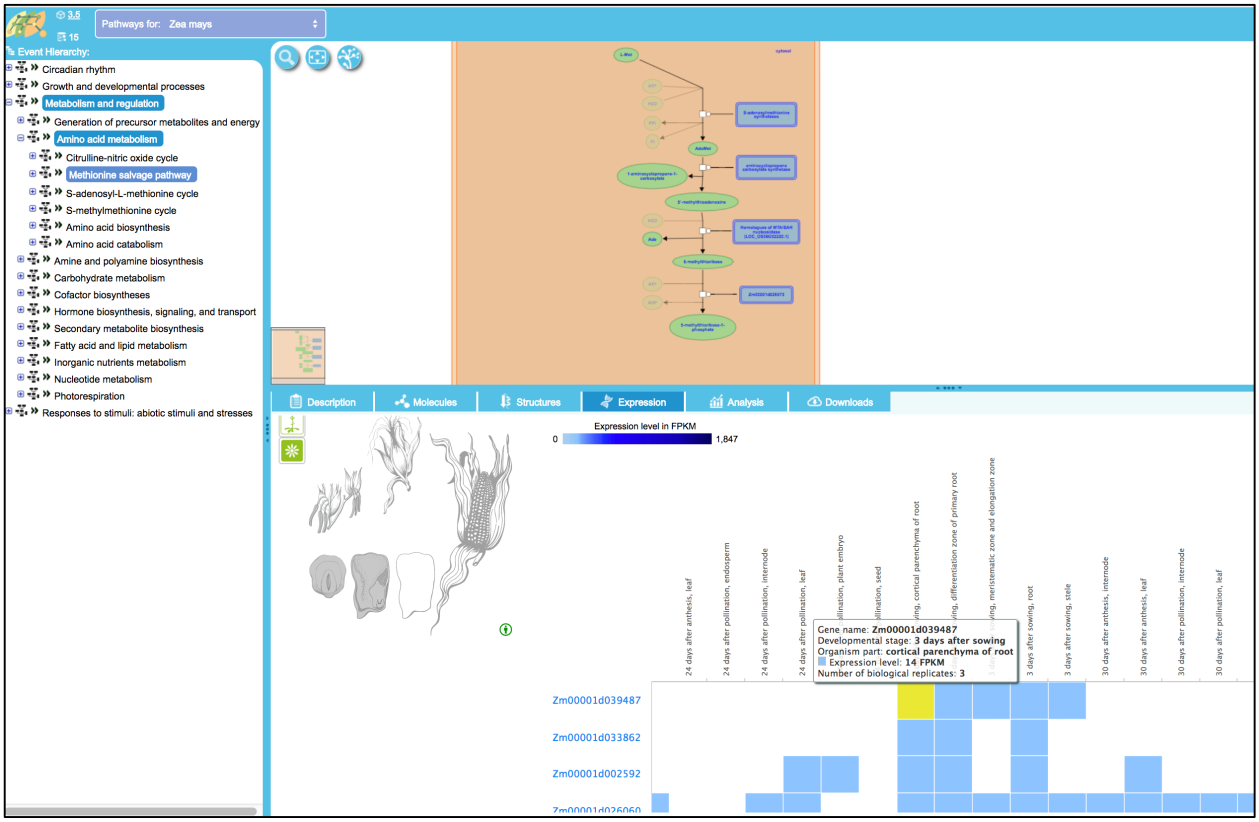
In this pathway diagram, complete blue boxes represent rice enzyme and genes for which no corresponding orthologs were found in tomato. The filled yellow box represents the enzyme for which tomato orthologs have been found. The box filled with yellow and blue represent the difference in the number of genes mapped to this particular enzyme in reference species rice and the projected species tomato. <u>Users can click on a given enzyme to see for which rice genes homologs have been identified in the tomato (rice gene highlighted in yellow color) and for which gene orthologs were not found in tomato (genes highlighted with blue color.</u>

Users can further download results to view gene-to-gene mappings between the two species and detailed pathway and reaction info.

**How to link to other external DBLinks for accessing Genome Browser, gene expression, etc. from Plant Reactome**

Users can click on the “molecules” icon below the pathway diagram window and then click on the Proteins to list the name of the protein coding genes. By clicking on an individual gene, will take them to Gramene gene and genome browser window, where they can access all the functionalities of genome browser and the genomic diversity data from tomato an example is shown below: (Please refer to the genomic exercise to find out how you can find information related to gene, genome, genomic data).

If, user click on chemical compound and then select a particular compound the external page for compound ChEBI (example: [http://www.ebi.ac.uk/chebi/searchId.do?chebiId=CHEBI:37569)](http://www.ebi.ac.uk/chebi/searchId.do?chebiId=CHEBI:37569) will open up. Similarly, clicking on the Expression tab (located below the pathway diagram) will show a baseline transcription profile of the genes associated with a given pathway. Here we show an example for maize: showing basal expression profile of genes.



- Circadian rhythm
- Growth and developmental processes
- Metabolism and regulation
  - Generation of precursor metabolites and energy
  - Amino acid metabolism
    - Citrulline-nitric oxide cycle
    - Methionine salvage pathway
    - S-adenosyl-L-methionine cycle
    - S-methylmethionine cycle
    - Amino acid biosynthesis
    - Amino acid catabolism
  - Amine and polyamine biosynthesis
  - Carbohydrate metabolism
  - Cofactor biosyntheses
  - Hormone biosynthesis, signaling, and transport
  - Secondary metabolite biosynthesis
  - Fatty acid and lipid metabolism
  - Inorganic nutrients metabolism
  - Nucleotide metabolism
  - Photorespiration
- Responses to stimuli: abiotic stimuli and stresses

Gene name: **Zm00001d039487**
Developmental stage: **3 days after sowing**
Organism part: **cortical parenchyma of root**
Expression level: **14 FPKM**
Number of biological replicates: **3**

**Currently, expression data feature is not available for all species. This data is fetched remotely from EMBL-EBI's Plant Gene Expression Atlas.**

### Q5. How one can we analyze transcriptomic data using Plant Reactome?

A note about web browsers: At present the Firefox, Netscape and Safari are having problems with projection of expression data on plant pathways. Although Safari, allows the display of the expression data mapped to pathways in tabulated format. We suggest users currently use Chrome.

Here is the case study for analysis of transcriptomic data analysis of a publicly available data from published study.

Study: Transcriptome analysis of various tissues in tomato cultivar Heinz

Reference: PMID: 22660326 (Nature. 2012 May 30;485(7400):635-41. doi: 10.1038/nature11119). **The tomato genome sequence provides insights into fleshy fruit evolution.**

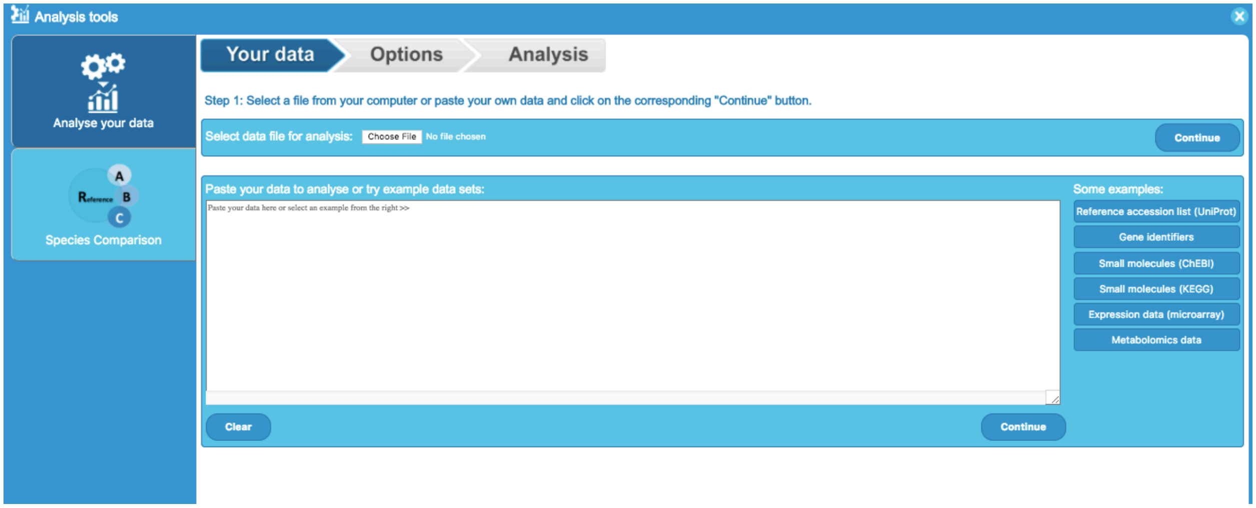
Data: http://ted.bti.cornell.edu/cgi-bin/TFGD/digital/experiment.cgi?ID=D004

File: https://www.dropbox.com/s/0i3b1jqoroxb9gz/tomato-baseline-ted-bti-D004-3-log2fold.txt?dl=0

**Experiment description:** Illumina RNA-Seq analysis of leaves, roots, flower buds, fully opened flowers, and 1 cm, 2 cm, 3 cm, mature green, breaker, and breaker+10 fruits of tomato cultivar Heinz, and leaves, immature green, breaker, and breaker+5 fruits of *Solanum pimpinellifolium*

1. Go to the pathway browser page of your favorite species, for example, tomato

2. Click on Tools-→ Choose a data file to upload (under Analysis Tools) window or enter your data into the text box (as shown in the following figure) http://plantreactome.gramene.org/PathwayBrowser/#/R-SLY-6787011&PATH=R-SLY-2744345,R-SLY-2744341&DTAB=AN&TOOL=AT

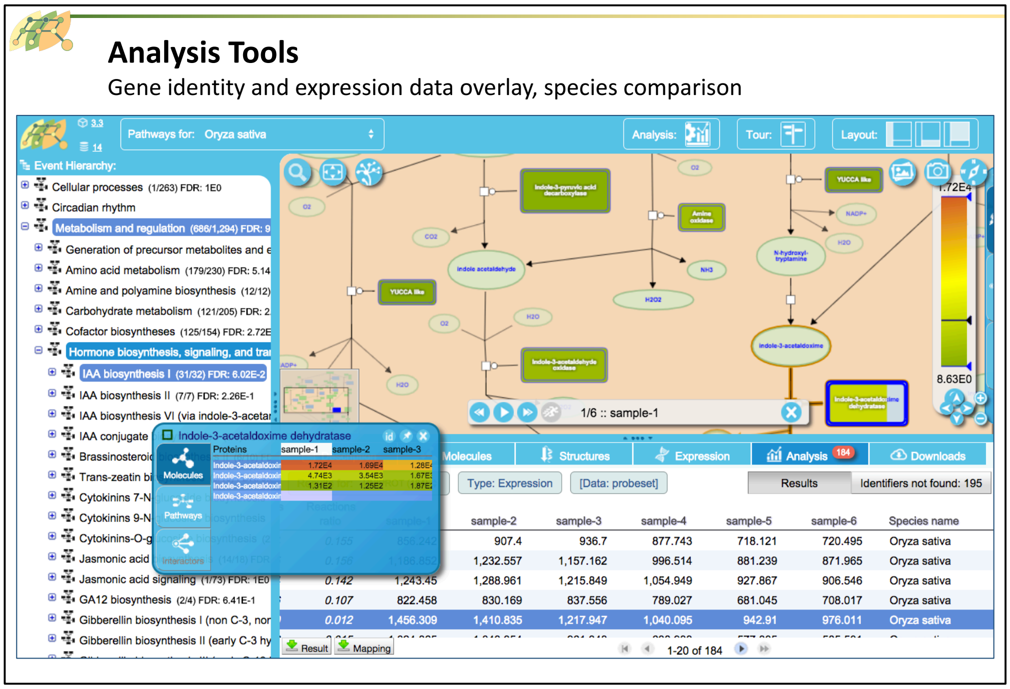


Step 1: Select a file from your computer or paste your own data and click on the corresponding "Continue" button.

Paste your data here or select an example from the right >>

3. After uploading/ pasting the data, click on analyze to map gene expression data on Tomato.

You may get a similar view.



**Analysis Tools**

Gene identity and expression data overlay, species comparison

| Reactions ratio | sample-1 | sample-2 | sample-3 | sample-4 | sample-5 | sample-6 | Species name |
|---|---|---|---|---|---|---|---|
| 0.155 | 856.242 | 907.4 | 936.7 | 877.743 | 718.121 | 720.495 | Oryza sativa |
| 0.156 | 1,186.852 | 1,232.557 | 1,157.162 | 996.514 | 881.239 | 871.965 | Oryza sativa |
| 0.142 | 1,243.45 | 1,288.961 | 1,215.849 | 1,054.949 | 927.867 | 906.546 | Oryza sativa |
| 0.107 | 822.458 | 830.169 | 837.556 | 789.027 | 681.045 | 708.017 | Oryza sativa |
| 0.012 | 1,456.309 | 1,410.835 | 1,217.947 | 1,040.095 | 942.91 | 976.011 | Oryza sativa |

You can see coloring of the proteins according to the expression values. And if you click on a given enzyme or protein a pop-up window would show the difference in the homologous genes mapped to the same reaction. Considering the presence of gene duplications in plant genomes, this features helps to identify candidate genes responsible for a certain activity in a given tissue or in response to a stress condition.

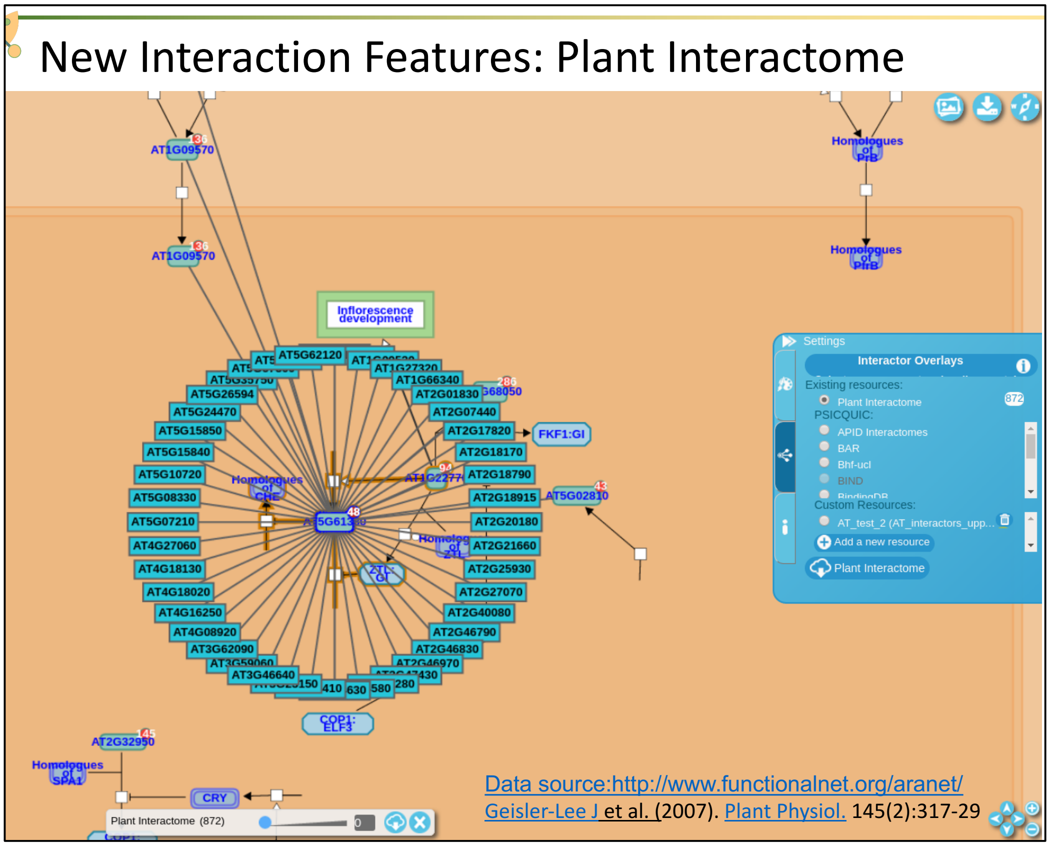
4. Users can browse the left-hand side panel to select an individual pathway, such as Chorismate biosynthesis pathway to see the expression of genes mapped to a pathway.

5. The expression data mapped to the various pathways in plant Reactome can also be downloaded.

## Interaction overlays: New functionality to extend pathway gene-networks

We have built this new functionality that can bring new interaction data on the fly and can be overlaid on the pathways. Additional genes projected on pathways can help you to formulate a better hypothesis for your research.

Here is an example of ATH interaction data, brought from Aranet gene-gene interaction data. We look forward to provide similar data for other plant species, and would like to seek your help from the community to identify high-quality gene-gene interaction data for their species of interest.



New Interaction Features: Plant Interactome

Data source:http://www.functionalnet.org/aranet/
Geisler-Lee J et al. (2007). Plant Physiol. 145(2):317-29

If we don't currently have data for your species available in the Plant Reactome, you can always upload your own data and conduct analysis in the context of Plant Reactome.

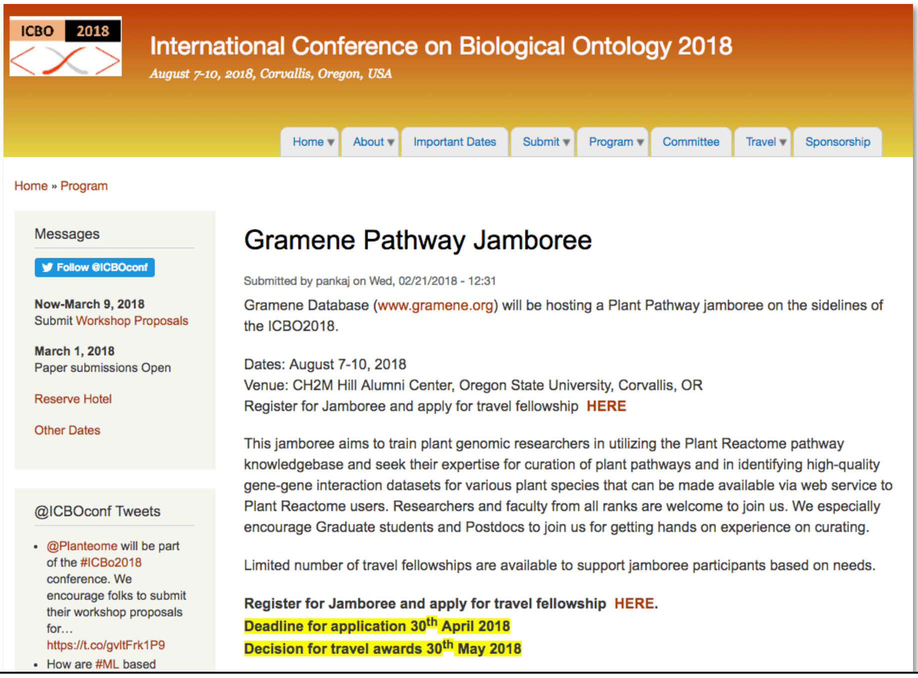
**Can I download Plant Reactome database for conducting analysis in my local desktop?**
Plant Reactome is a complex platform and currently we do not provide this option. However, you can download the pathway diagram, list of genes/ proteins / pathways and the results of your analysis by clicking on the 'Download' icon located in the bottom right-hand side panel.

**How can I send my feedback to Plant Reactome group?**
If you have questions or comments about Plant Reactome data, our website, or the downloads that we provide, we would be pleased to hear from you. You can email us at **reactome-curator@gramene.org**

**Can I learn curation and seek one-to-one help from Gramene curators?**
Yes, we have regular webinars, and onsite booth in PAG and ASPB conference.
You can also participate in our upcoming pathway Jamboree.

# Pathway Jamboree: ICBO 2018

http://icbo2018.cgrb.oregonstate.edu/pathway-workshop



International Conference on Biological Ontology 2018

*August 7-10, 2018, Corvallis, Oregon, USA*

Home » Program

Messages

**Now-March 9, 2018**
Submit Workshop Proposals

**March 1, 2018**
Paper submissions Open

Reserve Hotel

Other Dates

@ICBOconf Tweets

- @Planteome will be part of the #ICBo2018 conference. We encourage folks to submit their workshop proposals for… https://t.co/gvltFrk1P9
- How are #ML based

## Gramene Pathway Jamboree

Submitted by pankaj on Wed, 02/21/2018 - 12:31

Gramene Database (www.gramene.org) will be hosting a Plant Pathway jamboree on the sidelines of the ICBO2018.

Dates: August 7-10, 2018
Venue: CH2M Hill Alumni Center, Oregon State University, Corvallis, OR
Register for Jamboree and apply for travel fellowship **HERE**

This jamboree aims to train plant genomic researchers in utilizing the Plant Reactome pathway knowledgebase and seek their expertise for curation of plant pathways and in identifying high-quality gene-gene interaction datasets for various plant species that can be made available via web service to Plant Reactome users. Researchers and faculty from all ranks are welcome to join us. We especially encourage Graduate students and Postdocs to join us for getting hands on experience on curating.

Limited number of travel fellowships are available to support jamboree participants based on needs.

**Register for Jamboree and apply for travel fellowship HERE.**
**Deadline for application 30th April 2018**
**Decision for travel awards 30th May 2018**