Curation of Metabolic Pathways

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Non-climacteric Fruit Ripening Of Strawberry

Strawberry Fruit Development

Berry Formation | TS | Ripening

Anthesis → small green → Large Green → White → Turning Stage → Red ripe

Grape berry Development

Berry Formation | Lag Phase | Véraison | Berry Ripening

Mid-véraison | Harvest
FragariaCyc Web interface
Vitis vinifera Metabolic Pathways: VitisCyc

Developed and curated by the Jaiswal Lab, VitisCyc is a catalog of curated biochemical pathways from Vitis.

If you notice any problems or errors on the pathways, please send a message to VitisCyc curators or by clicking the ‘Feedback’ button at the top right corner of this page or on the bottom of the respective pathway display page.
Overview of the *Vitis vinifera* Metabolic Map

**Biosynthesis**
- Generation of Precursor Metabolites

**Degradation**
Degradation reactions and compounds not associated with pathways

Super-pathways (54): Biosynthesis

Degradation/Utilization/Assimilation (154), Detoxification (8), Energy related (37), Transport (7)

VitisCyc
Vitis vinifera Pathway: Gibberellin Biosynthesis I (non C-3, non C-13 hydroxylation)

Manual curation - identification of genes/ Evidence

Manual Curation Evidence/support

If an enzyme name is shown in bold, there is experimental evidence for this enzymatic activity.
Genome Annotation and Curation of Metabolic Pathways

- **Arabidopsis**
  - 27,025 genes
  - 10,384 clusters
  - 23,163 genes in clusters

- **Grape**
  - 30,434 genes
  - 9,477 clusters
  - 23,030 genes in clusters

- **Rice**
  - 56,797 genes
  - 11,719 clusters
  - 39,207 genes in clusters

- **Strawberry**
  - 33,264 genes
  - 9,895 clusters
  - 18,170 genes in clusters

- **Total unique clusters comprising 21 species**
  - 28,149 clusters

- **15,969 clusters had at least one of these 4 species**

Vitis vinifera Pathway: Gibberellin Biosynthesis I (non C-3, non C-13 hydroxylation)

Manual curation - identification of genes/ Evidence

Manual Curation Evidence/support
Zenoni et al RNA-seq expression data. RPKM values analyzed by looking for genes preferentially expressed in 10 and 15 weeks compared to the 5 week sample. Maximum cutoff used = 2

About 9,000 genes are differentially expressed. Of these ~3400 in 5-week sample, ~1200 in 10-week and ~900 in 15-week sample mapped to the VitisCyc metabolic network.
Leucodelphinidin Flavonoid Biosynthesis

Vitis vinifera Pathway: leucodelphinidin biosynthesis

leucodelphinidin

anthocyanin biosynthesis (delphinidin 3-O-glucoside)

dihydromyricetin

dihydrokaempferol

leucopelargonidin and leucocyanidin biosynthesis

3',4',5'-penta-hydroxyflavanone

transe dihydroquercetin

eriodictyol

leucodelphinidin biosynthesis

leucopelargonidin and leucocyanidin biosynthesis

enzyme name is shown in bold; there is experimental evidence for this enzymatic activity

ins of Mapped Genes:

Oregon State University
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