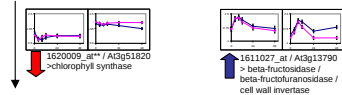
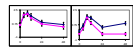


Examples:



Key:

Biochemical pathway



Expression profile (natural log scale) of selected gene of interest in *V. aestivalis* 'Norton' leaf (left panel) and *V. vinifera* 'Cabernet sauvignon' leaf (right panel) against time (h) during PM-inoculation (blue line) and mock-inoculation (red line).



This only apply to *V. vinifera*. Transcript level that is down-regulated (red) or up-regulated (blue) in response to PM infection in *V. vinifera*

1620009_at** / At3g51820
> chlorophyll synthase

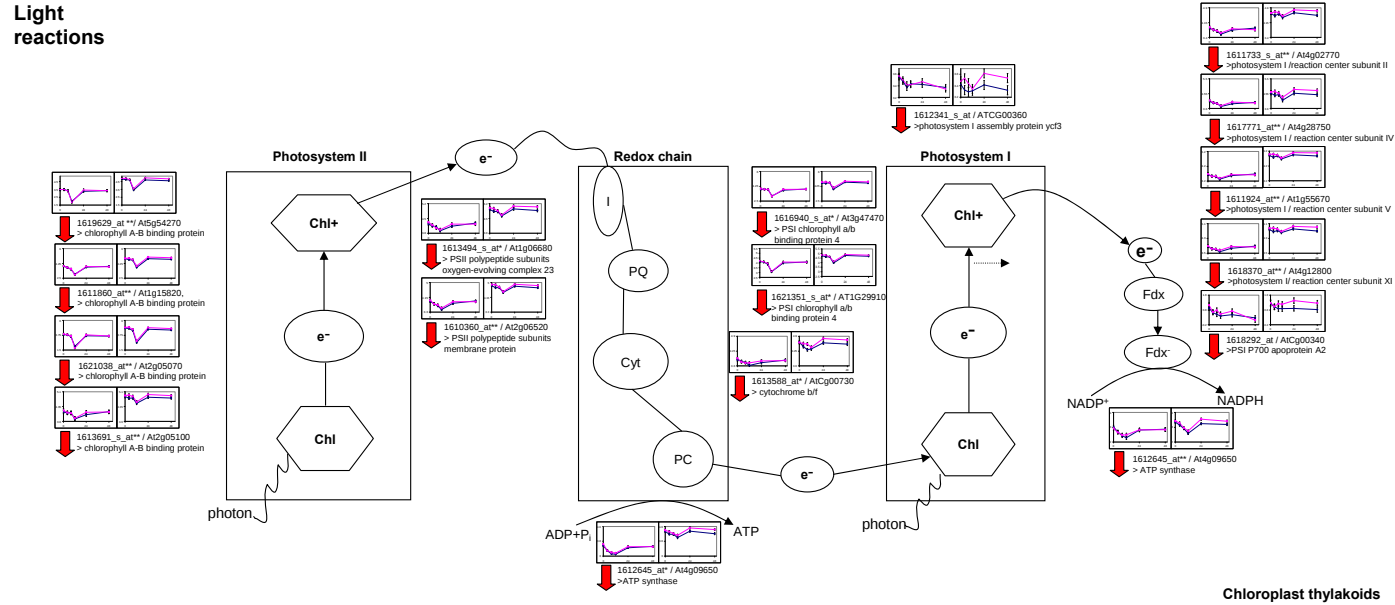
Vitis Affymetrix probeset ID / matching *Arabidopsis* Gene Identifier
> putative functional homologue.

F test (FDR $P < 0.05$) confirmed gene with significantly higher / lower transcript level in all 6 timepoints in *V. aestivalis* in comparison with *V. vinifera* during mock treatment is indicated with '*' and during both mock and PM treatment is indicated with '**'

Selected gene of interest used here were PM-responsive genes identified from *V. vinifera* (see Table S1 for details). The expression profile of selected genes in the PM-susceptible *Vitis vinifera* as well as PM-resistant *V. aestivalis* were included to contrast the changes over time. Mapping of genes to biochemical pathways were performed by using The Kyoto Encyclopedia of Genes and Genomes (KEGG) pathways [<http://www.genome.ad.jp/kegg/pathway.html>], The Mapman [<http://gabi.rzpd.de/projects/MapMan>], The Arabidopsis Lipid Gene Database [<http://www.plantbiology.msu.edu/lipids/genesurvey/index.htm>] and in some case manually.

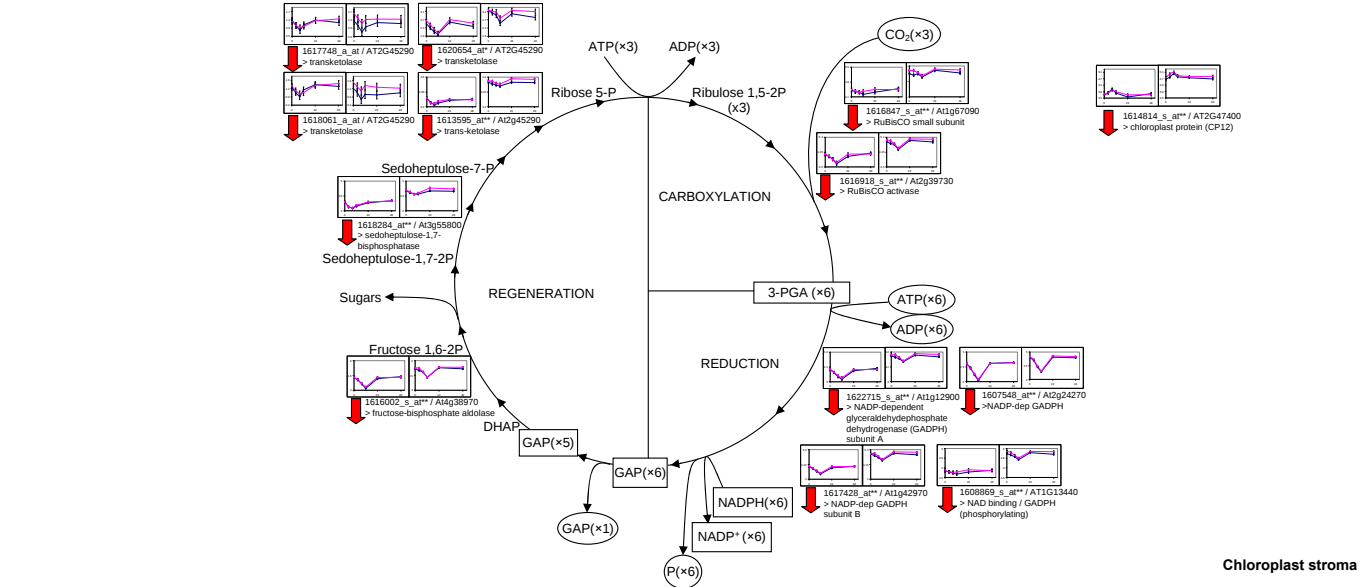
FS3A Regulation of photosynthesis and tetrapyrrole biosynthesis in the two *Vitis* species, *V. aestivalis* and *V. vinifera*

Light reactions

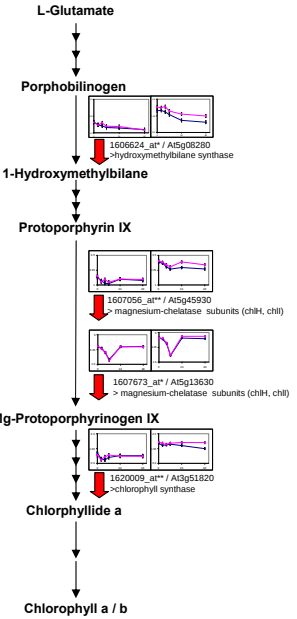


This shows, in response to PM infection, the down-regulation of *V. vinifera* genes involved in light reaction and Calvin cycle of photosynthetic pathways and in the tetrapyrrole biosynthesis. Most of these down-regulated *V. vinifera* genes are expressed at significantly lower level in *V. aestivalis* during mock (marked in “*”) and during both mock and PM treatments (marked in “**”)

Calvin cycle



Tetrapyrrole / Chlorophyll biosynthesis



[illegible][illegible][illegible]

Metabolic Pathway Diagram: Fatty Acid Metabolism in Arabidopsis thaliana

Legend:

- Red:** Down-regulation of fatty acid synthesis.
- Blue:** Up-regulation of beta-oxidation and isoprenoid biosynthesis.
- Red Circle:** Peroxisome / Mitochondria.
- Green Circle:** Plastid.
- Blue Background:** Cytosol.
- Green Background:** Plastid.

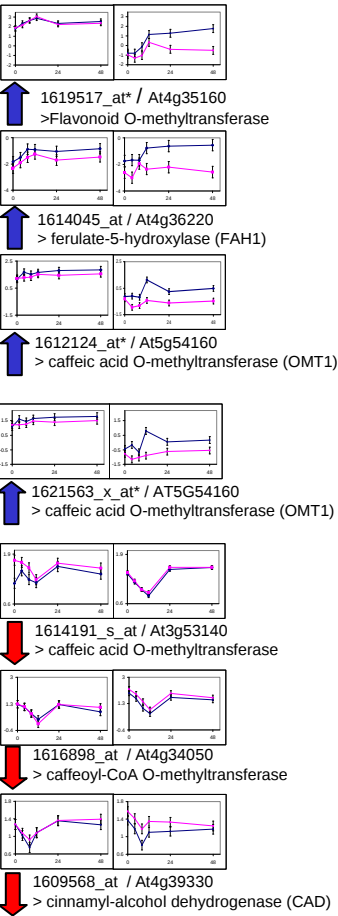
Key Pathways and Enzymes:

- FS3B Glycolysis:** Pyruvate → Acetyl-CoA (via 1620802_at / At1g01090, pyruvate dehydrogenase E1 component alpha subunit).
- FS3E Isoprenoid biosynthesis:** Acetyl-CoA → Malonyl-CoA (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
- Fatty Acid Synthase (FAS) Pathway:**
 - Malonyl-CoA + ACP → Malonyl-ACP (via 1614903_at** / AT5G47630, acyl carrier protein).
 - Malonyl-ACP + 3-Ketobutyryl-ACP → 3-Hydroxybutyryl-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 3-Hydroxybutyryl-ACP → Trans-2Δ-Butenoyl-ACP → Butyryl-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - Butyryl-ACP + Malonyl-ACP → Octanoyl-ACP (via 1621627_at** / AT2G20860, Lipoic acid synthase).
 - Octanoyl-ACP → Lipoyl-ACP (via 1621627_at** / AT2G20860, Lipoic acid synthase).
 - Lipoyl-ACP → 16:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 16:0-ACP → 18:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 18:0-ACP → 18:1-ACP (via 1615908_at / AT4g13050, Acyl-ACP thioesterases / Oleoyl-ACP hydrolase (FadA)).
- Beta-oxidation Pathway:**
 - 18:1-ACP → 18:0-ACP (via 1615908_at / AT4g13050, Acyl-ACP thioesterases / Oleoyl-ACP hydrolase (FadA)).
 - 18:0-ACP → 16:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 16:0-ACP → 14:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 14:0-ACP → 12:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 12:0-ACP → 10:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 10:0-ACP → 8:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 8:0-ACP → 6:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 6:0-ACP → 4:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 4:0-ACP → 2:0-ACP (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).
 - 2:0-ACP → Acetyl-CoA (via 1610577_at / At1g74960, 3-ketoacyl-ACP synthase).

Key: G3P: glycerol-3-phosphate; ACP acyl carrier protein; Fatty acids are denoted by number of carbon atoms and double bonds e.g. 18:1

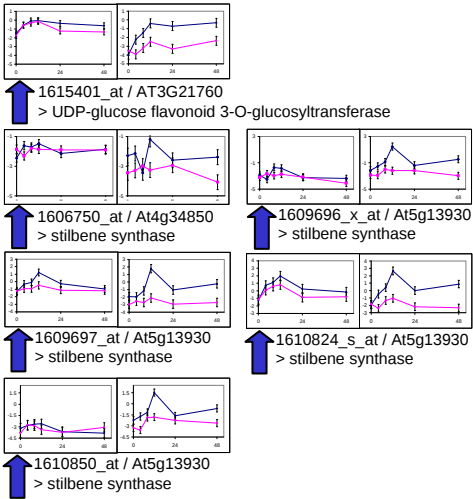
FS3D Secondary metabolism: phenylpropanoid and lignin biosynthesis

Phenolpropanoids

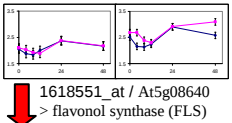


Flavonoids

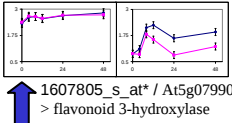
Stilbene



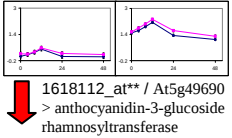
Flavonols



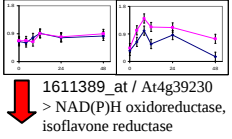
Dihydroflavonols



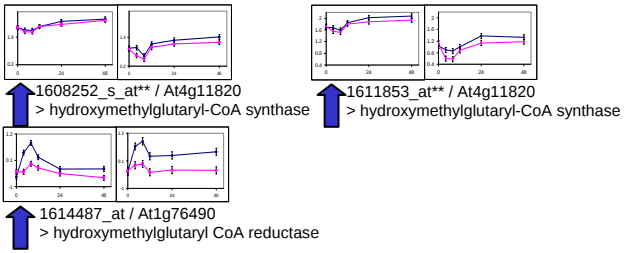
Anthocyanins



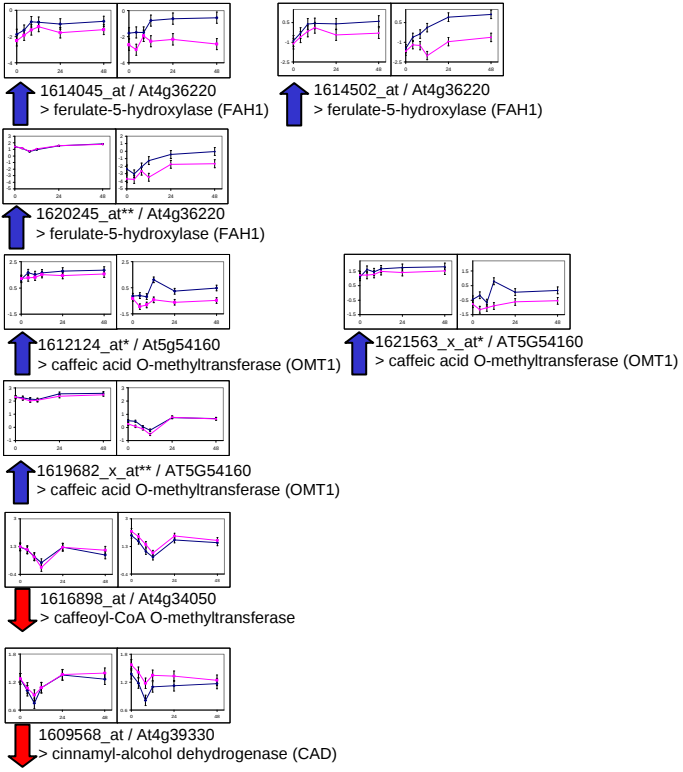
Isoflavonoids



MVA Pathway



Lignin and Lignans



FS3E Isoprenoid biosynthesis

