#### **PLANT BIOCHEMISTRY**

# A specialized flavone biosynthetic pathway has evolved in the medicinal plant, *Scutellaria baicalensis*

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Qing Zhao,  $^{1,2,3,4}$  Yang Zhang,  $^{2*}$  Gang Wang,  $^{3}$  Lionel Hill,  $^{2}$  Jing-Ke Weng,  $^{5}$  Xiao-Ya Chen,  $^{1,4,6}$  Hongwei Xue,  $^{1,4}$  Cathie Martin  $^{2,4}$ 

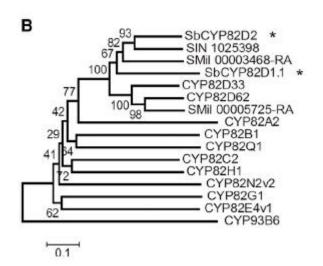


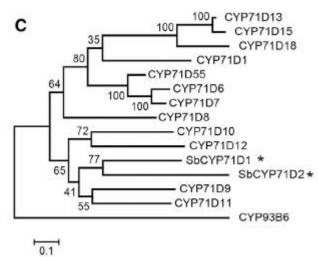
# Two CYP82D Enzymes Function as Flavone Hydroxylases in the Biosynthesis of Root-Specific 4'-Deoxyflavones in *Scutellaria baicalensis*

Qing Zhao<sup>1,2,7</sup>, Meng-Ying Cui<sup>1,7</sup>, Olesya Levsh<sup>3,4</sup>, Dongfeng Yang<sup>1,5</sup>, Jie Liu<sup>1</sup>, Jie Li<sup>2</sup>, Lionel Hill<sup>2</sup>, Lei Yang<sup>1</sup>, Yonghong Hu<sup>1</sup>, Jing-Ke Weng<sup>3,4</sup>, Xiao-Ya Chen<sup>1,6</sup> and Cathie Martin<sup>1,2,\*</sup>

### F6H in basil + mint

# F6H in soybean





### Four candidates:

SbCYP82D2

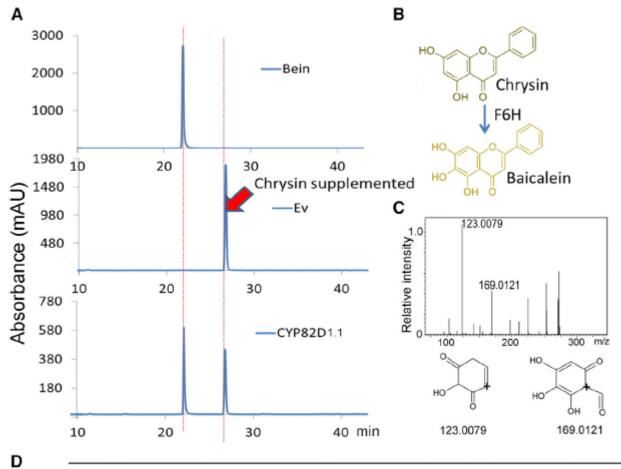
SbCYP82D1.1

SbCYP71D1

SbCYP71D2

Each transformed into yeast and fed with chrysin

Only yeast transformed with SbCYP82D1.1 produces baicalein

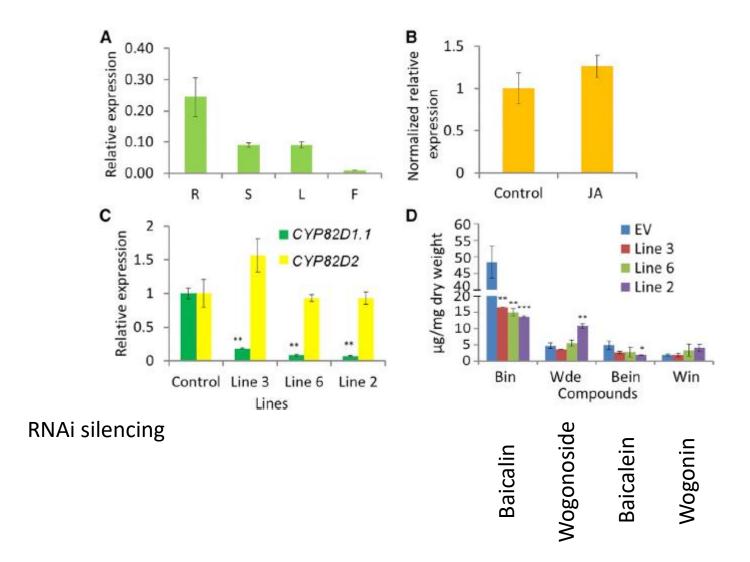


| Enzyme      | Substrate | Km (μM)     | Vmax (pkar mg <sup>-1</sup> protein) | Vmax/Km  |
|-------------|-----------|-------------|--------------------------------------|----------|
| SbCYP82D1.1 | chrysin   | 0.121±0.002 | 733.047±10.014                       | 6013.508 |

| Substrates   | Chr      | Api        | 7-O-Mechr  | Pin |  |
|--------------|----------|------------|------------|-----|--|
| SbCYP82D1.1a | 100±0.54 | 90.43±1.95 | 85.85±1.52 | ND  |  |
| SbCYP82D1.1b | 100±0.56 | 92.32±1.42 | 87.94±1.44 | ND  |  |

 $^a$  Substrates supplied at 5  $\mu\text{M};\,^b$  Substrates supplied at 2.5  $\mu\text{M};\,\text{ND, not detectable}.$ 

Ε



# the plant journal



Unexpected roles for ancient proteins: flavone 8-hydroxylase in sweet basil trichomes is a Rieske-type, PAO-family oxygenase

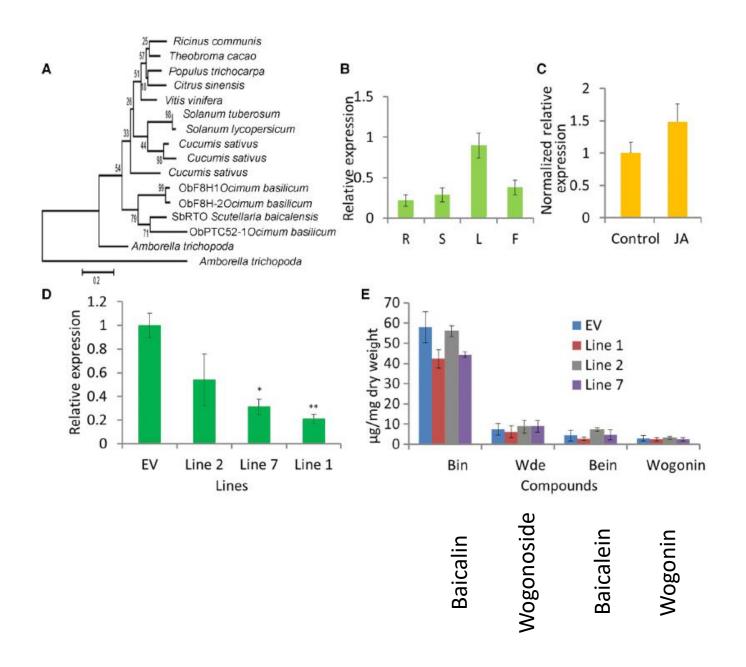
Anna Berim 🔀, Jeong-Jin Park, David R. Gang 🔀

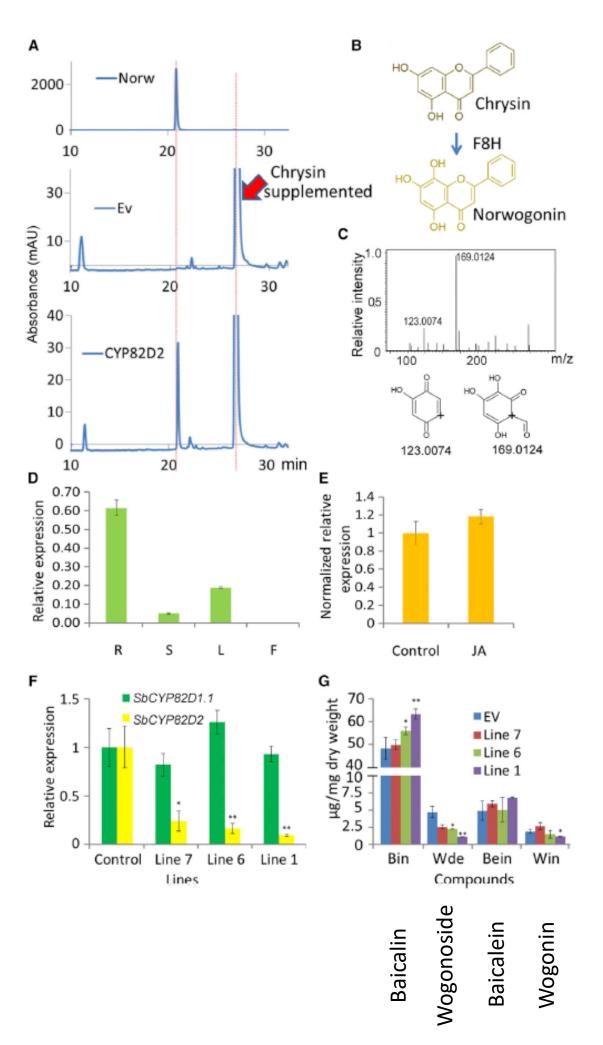
First published: 19 August 2014 | https://doi.org/10.1111/tpj.12642 | Citations: 16



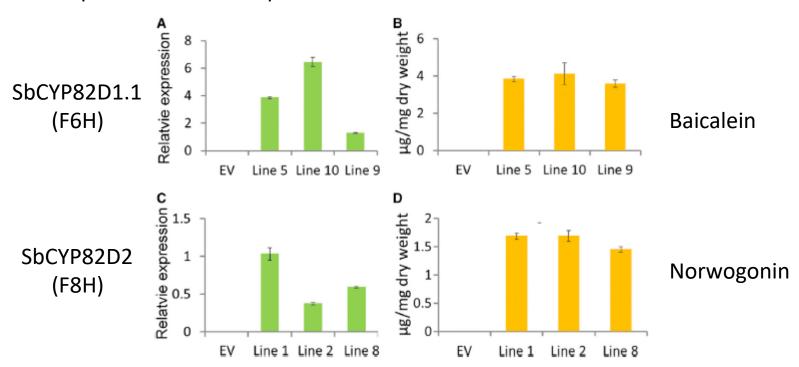
# Two CYP82D Enzymes Function as Flavone Hydroxylases in the Biosynthesis of Root-Specific 4'-Deoxyflavones in *Scutellaria baicalensis*

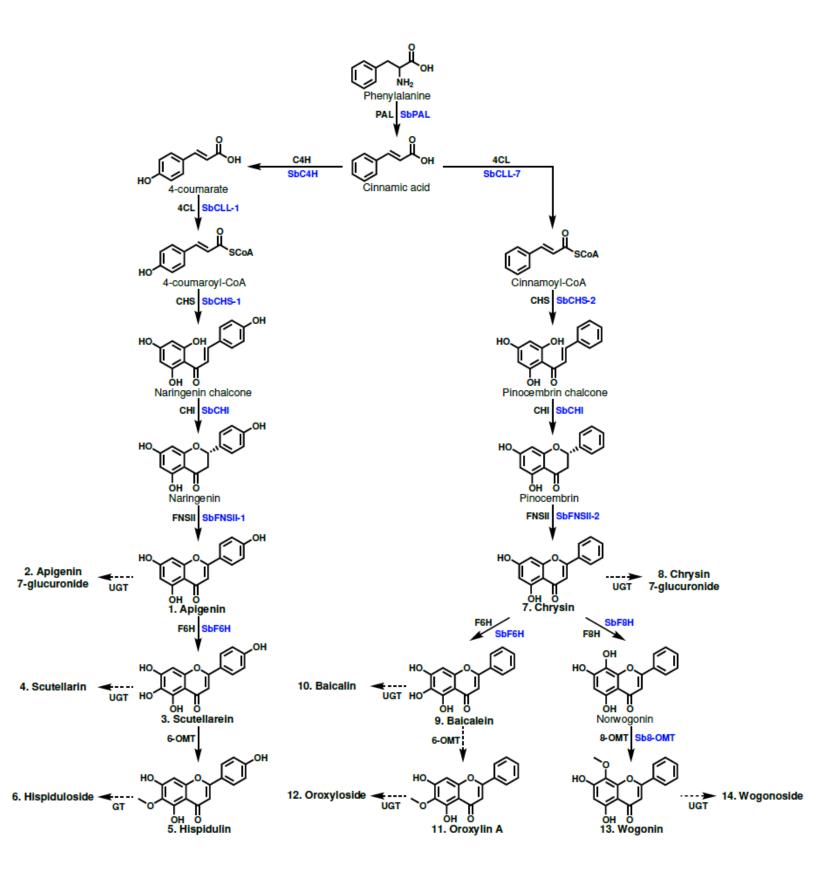
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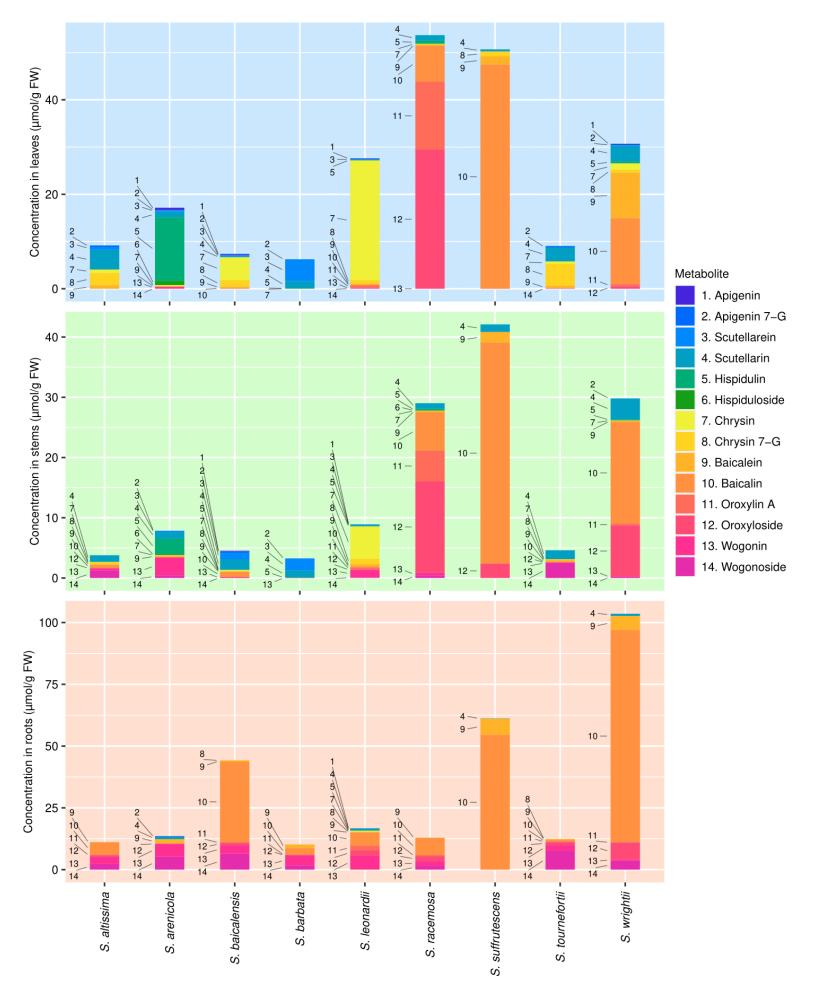


# Overexpression in Arabidopsis

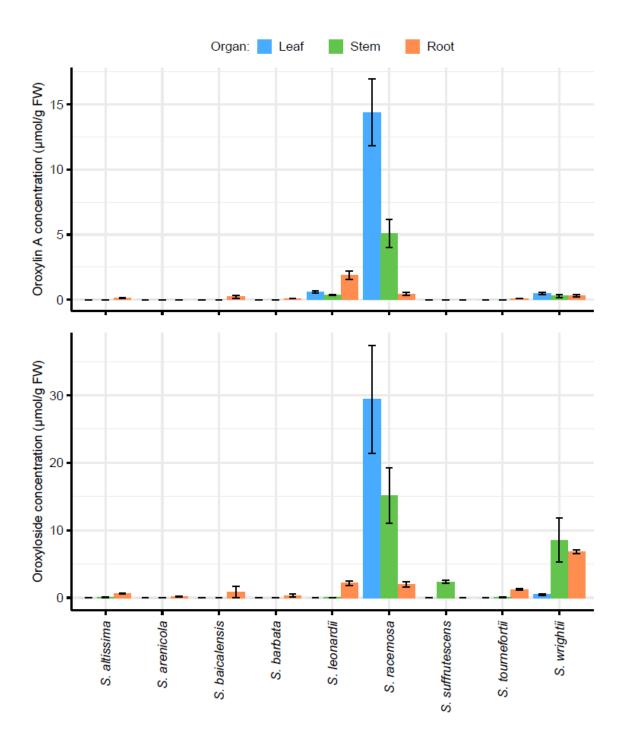




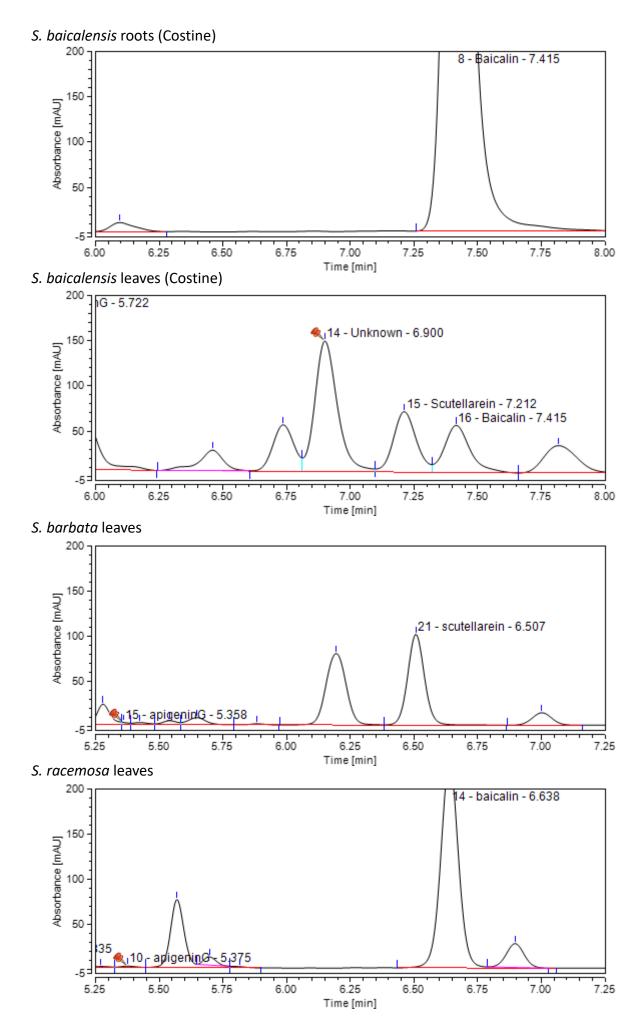
**Figure 1.** Proposed 4´-hydroxyflavone and 4´-deoxyflavone pathway. Structures of glycosylated metabolites are not shown to save space but are included in Appendix S1. Enzyme names in blue are specific isoforms that have been identified in *S. baicalensis*, and enzyme names in black are general names. Metabolites that were quantified have names in bold and are numbered to match the labeling of Figure 2.



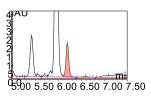
**Figure 2.** Organ-specific metabolite data collected from 9 *Scutellaria* species via High Performance Liquid Chromatography (HPLC). Samples were taken in biological triplicate, and the average concentration of each metabolite calculated. Metabolites are numbered to match their order of occurrence in the flavone pathway, shown in Figure 1.

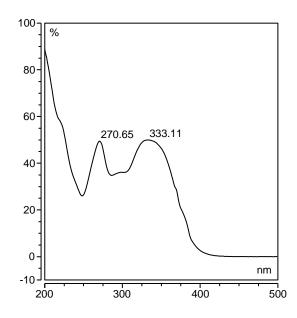


**Figure 3.** Organ-specific oroxylin A (top) and oroxyloside (bottom) concentrations in 9 *Scutellaria* species, as determined via High Performance Liquid Chromatography (HPLC). Concentrations were averaged from tissue samples taken from 3 biological replicates, and error bars represent standard error.



**Figure 4.** Comparison of chromatograms collected via HPLC from (A) *S. baicalensis* roots, (B) *S. baicalensis* leaves, (C) *S. barbata* leaves, and (D) *S. racemosa* leaves. Time interval displayed was selected to center the unknown peak in the chromatograms.





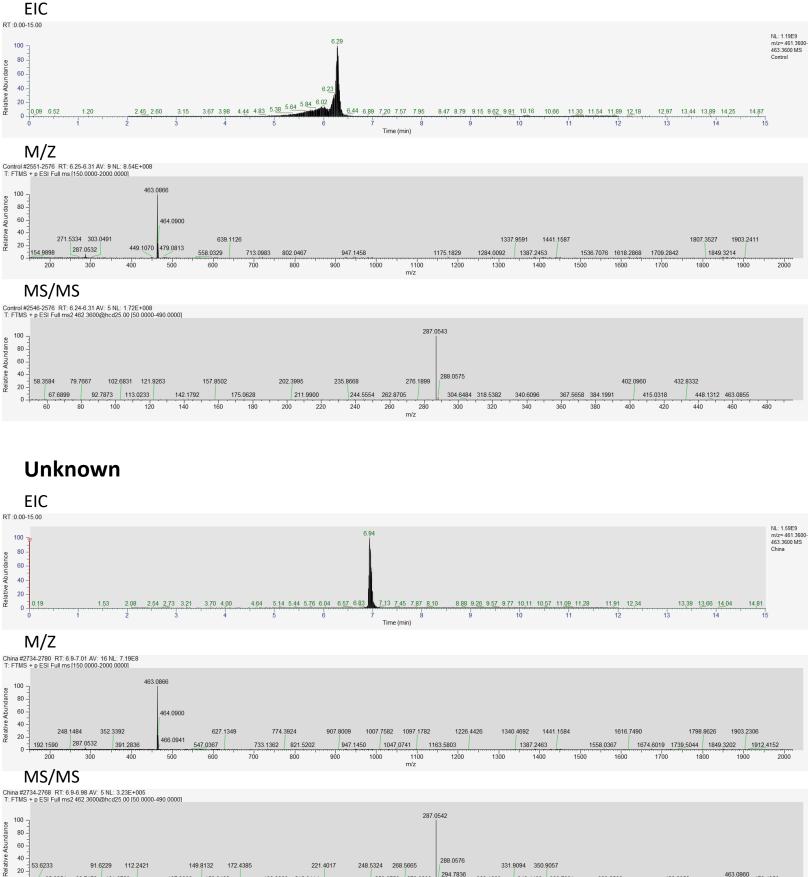
# **Scutellarin**



40 -

53.6233

65.8251 88.7<u>176</u> 101.8729



288.0576

294.7836

248.5324 268.5665

259.0750 279.9239

Figure 5. LC-MS + NMR data used to elucidate identity of unknown metabolite.

137.9368 159.9462

### Predicted structure from NMR data:

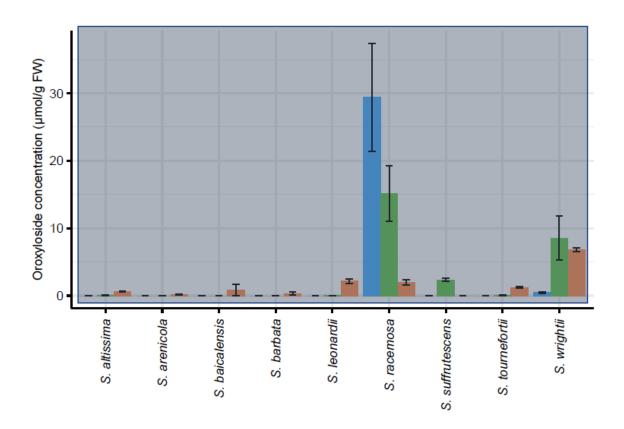
# Structure from PubChem: Isoscutellarein

# Identity of unknown: Isoscutellarein 8-glucuronide

## TODO:

Quantify isoscutellarein 8-glucuronide in all extractions Apigenin feeding

Yeast activity test with Rieske-type oxygenase from *S. baicalensis* Tobacco infiltration with RTO



**Figure 6.** Organ-specific isoscutellarein 8-glucuronide concentrations in 9 *Scutellaria* species, as determined via High Performance Liquid Chromatography (HPLC). Concentrations were averaged from tissue samples taken from 3 biological replicates, and error bars represent standard error.

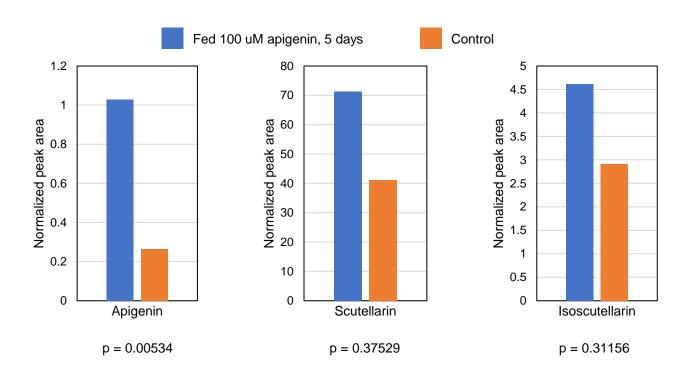


Figure 7. S. barbata apigenin feeding results / Yeast activity test / N. benthamiana infiltration

# Proposed pathway: