



An analysis of phytochemical diversity in *Scutellaria* to identify species with medicinal potential

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Scutellaria dependens

Introduction to the *Scutellaria* genus

- Part of the Lamiaceae family
- Rich in medicinal flavonoids

Baicalein	Antitumor, hepatoprotective, & more
Wogonin	Anti-inflammatory, anxiolytic, & more
Oroxylin A	Neuroprotective, & anti-RSV
Scutellarein	Anti-RSV

- Several species more well-studied because of their medicinal uses



S. baicalensis



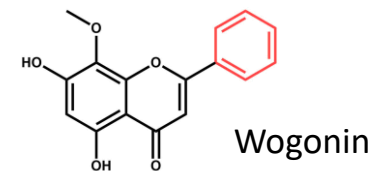
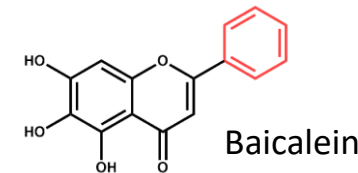
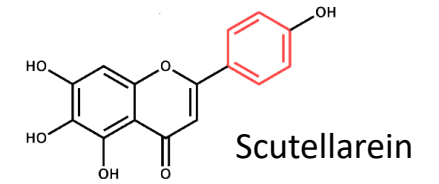
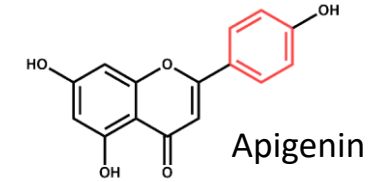
S. barbata



S. lateriflora

Scutellaria baicalensis

- Most famous species
 - Used often in Chinese medicine – Huang Qin
- Unique flavonoid profiles observed
 - Some specific to roots, and some to shoots
- Organ-specific biosynthetic pathway proposed by Zhao et al. (2016)
- Reference genome published by Zhao et al. (2019)

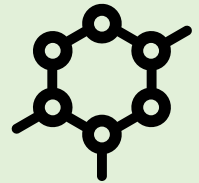


Scutellaria contains >470 species

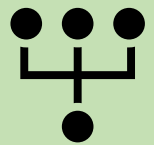
Extent of flavonoid profile similarity is **largely unknown**

An improved understanding of flavonoid diversity in *Scutellaria* can:

1) Reveal interspecific differences in the underlying biosynthetic pathway



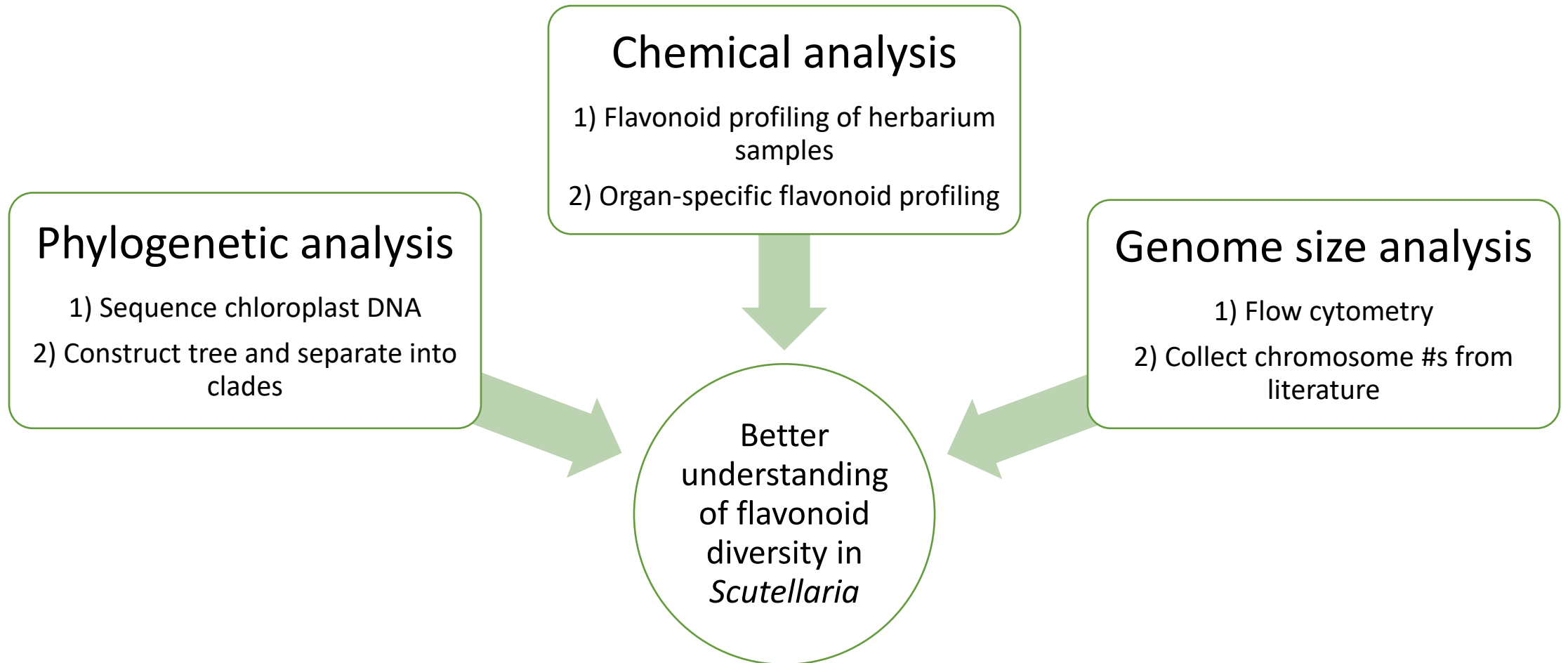
2) Better characterize the evolutionary history of the biosynthetic pathway



3) Help identify candidate species for biotechnology applications



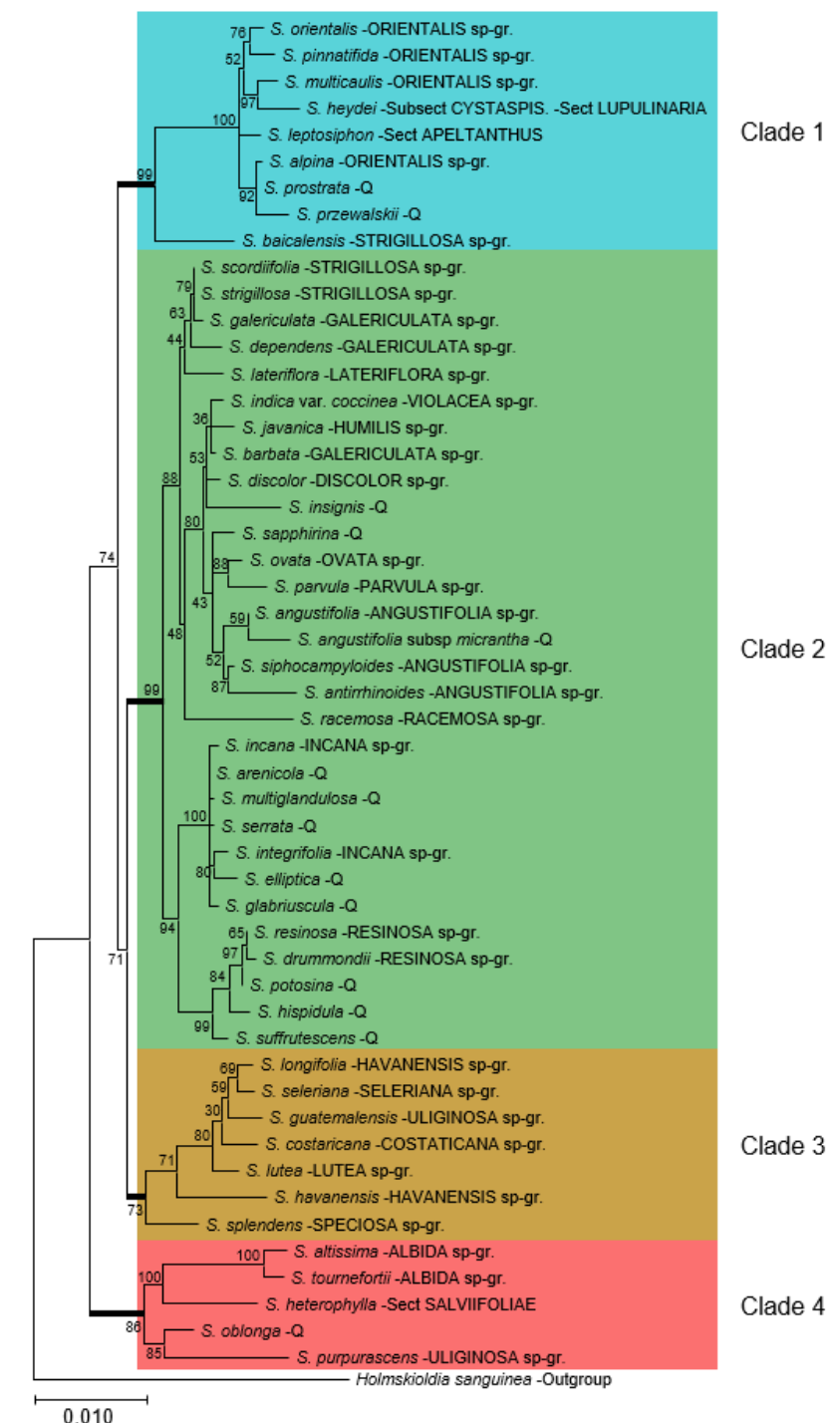
Approach



Phylogenetic analysis

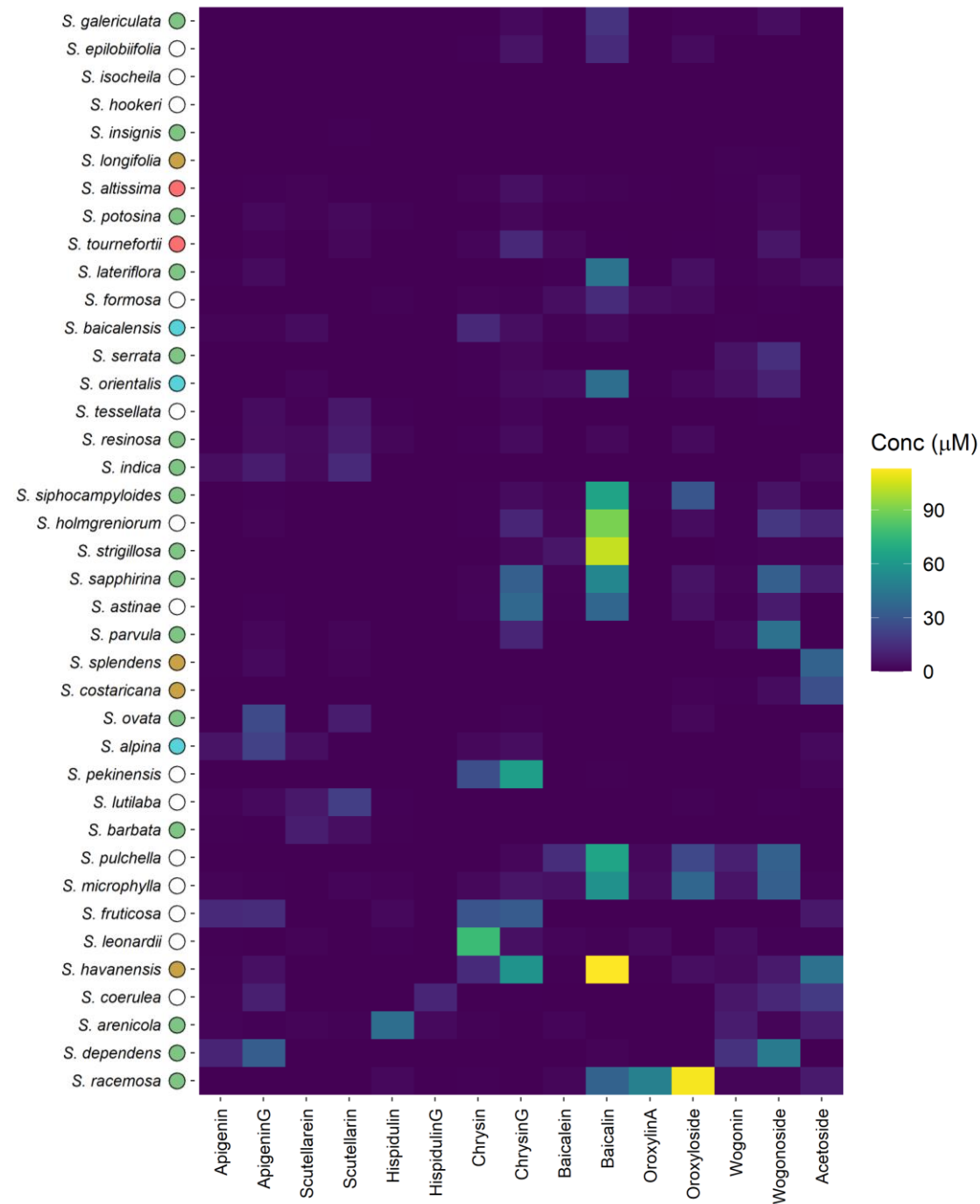
- Tree constructed from chloroplast sequences of 50 species + 1 outgroup
 - Both subgenera represented (*Scutellaria* and *Apelthanthus*)
 - 22 out of 38 species-groups represented
- Separated into 4 clades for downstream comparison

Unpublished phylogenetic data provided by **Yoonkyung Lee** and **Sangtae Kim**

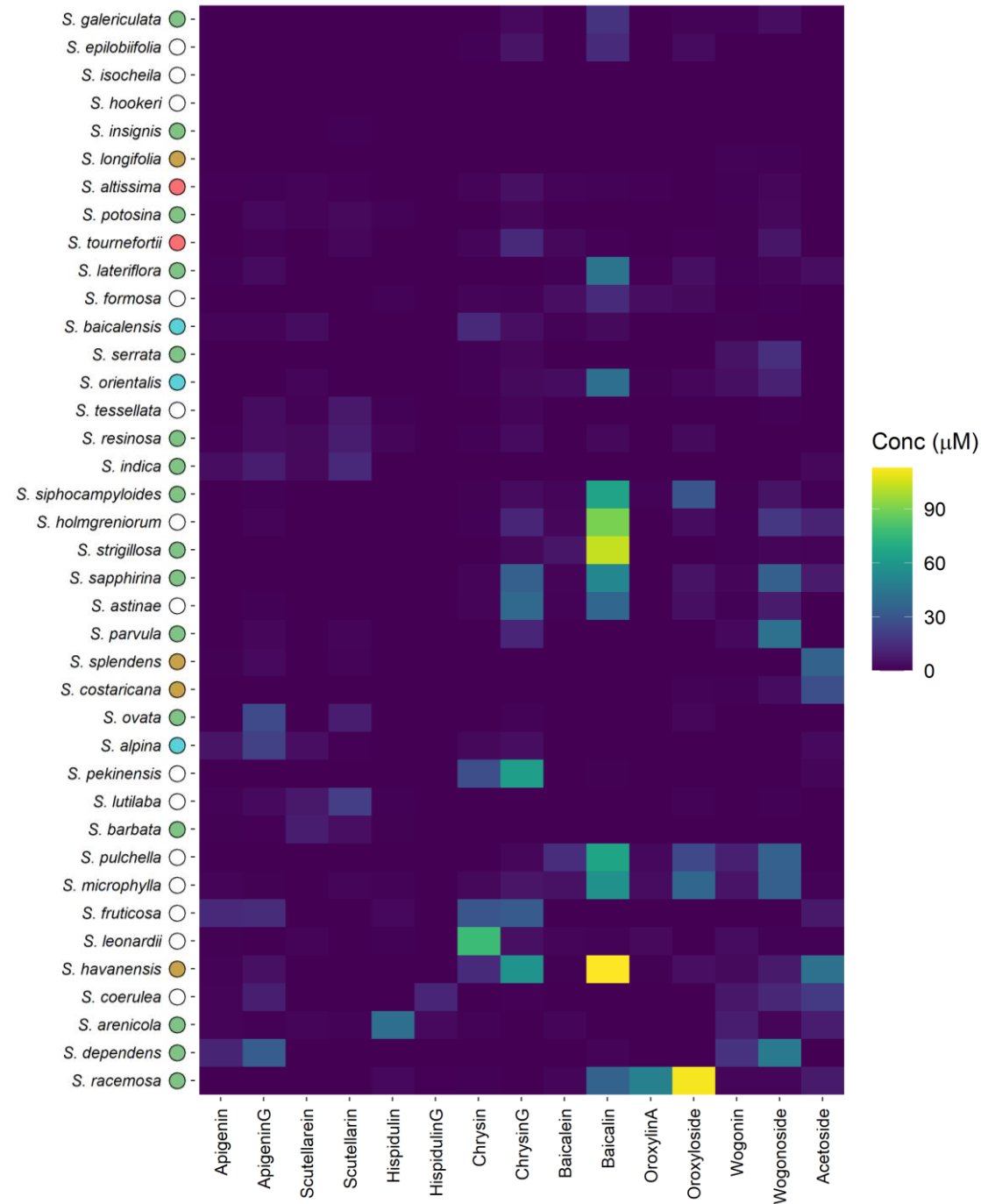
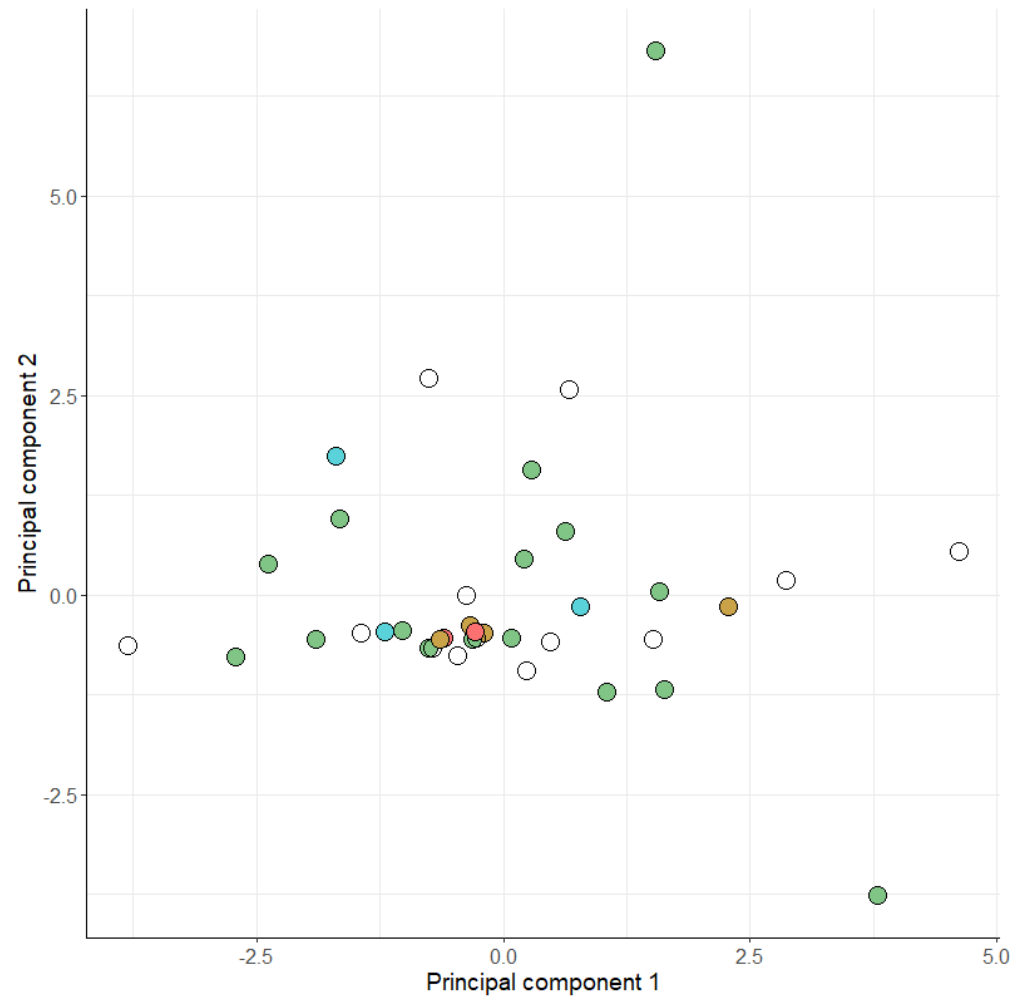


Chemical analysis

- 39 species selected for targeted profiling via HPLC
 - Flavonoids extracted from aerial parts
- Order of species determined by hierarchical clustering
- Weak relationship between flavonoid and phylogenetic data
- Subset of species selected for further profiling



Chemical analysis





● *S. insignis*



● *S. altissima*



● *S. tournefortii*



● *S. baicalensis*



● *S. indica* var. *coccinea*



● *S. strigillosa*



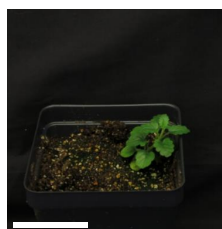
○ *S. pekinensis* var. *alpina*



● *S. barbata*



○ *S. leonardii*



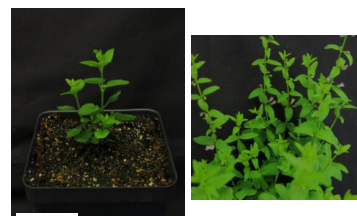
● *S. havanensis*



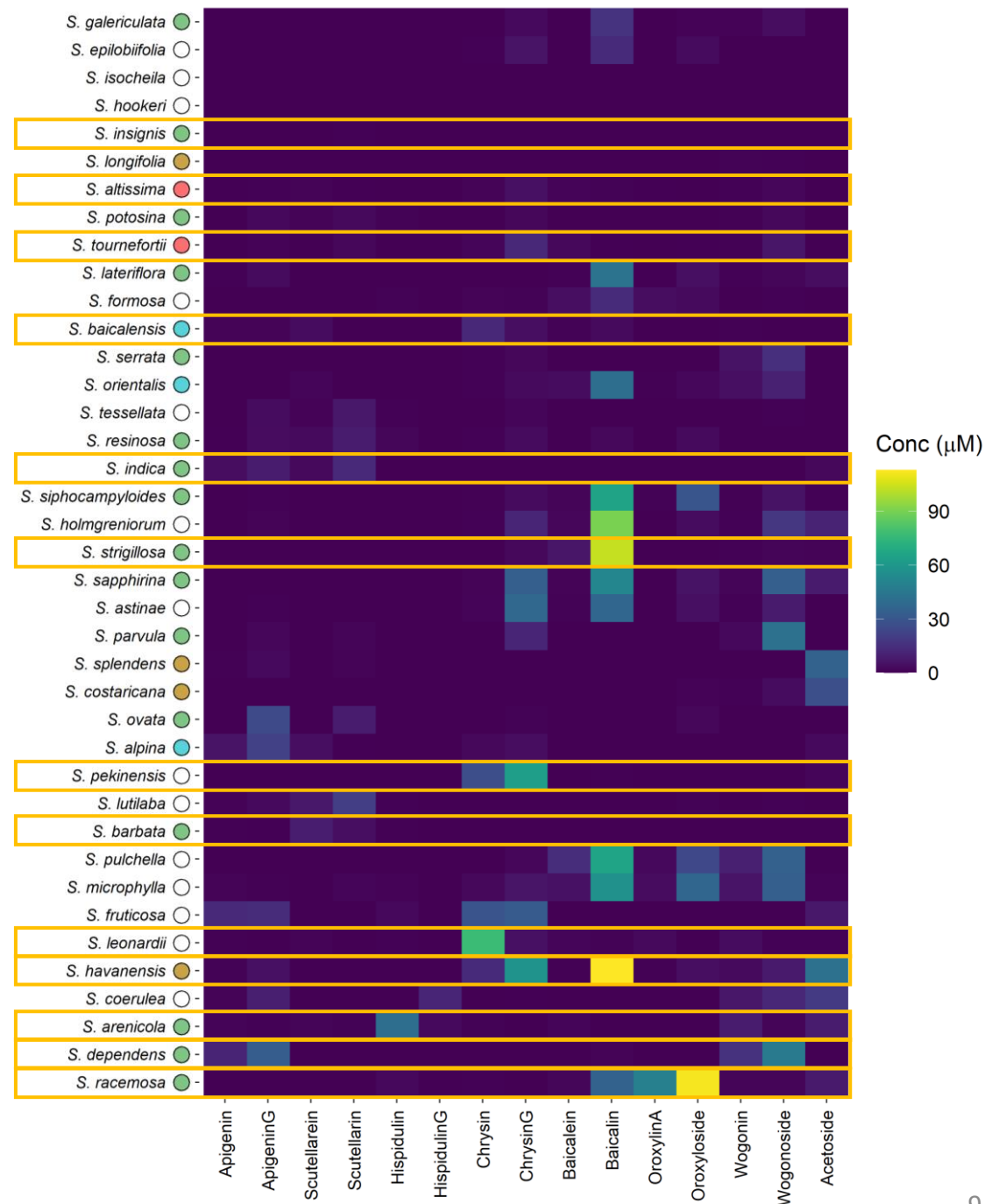
● *S. arenicola*



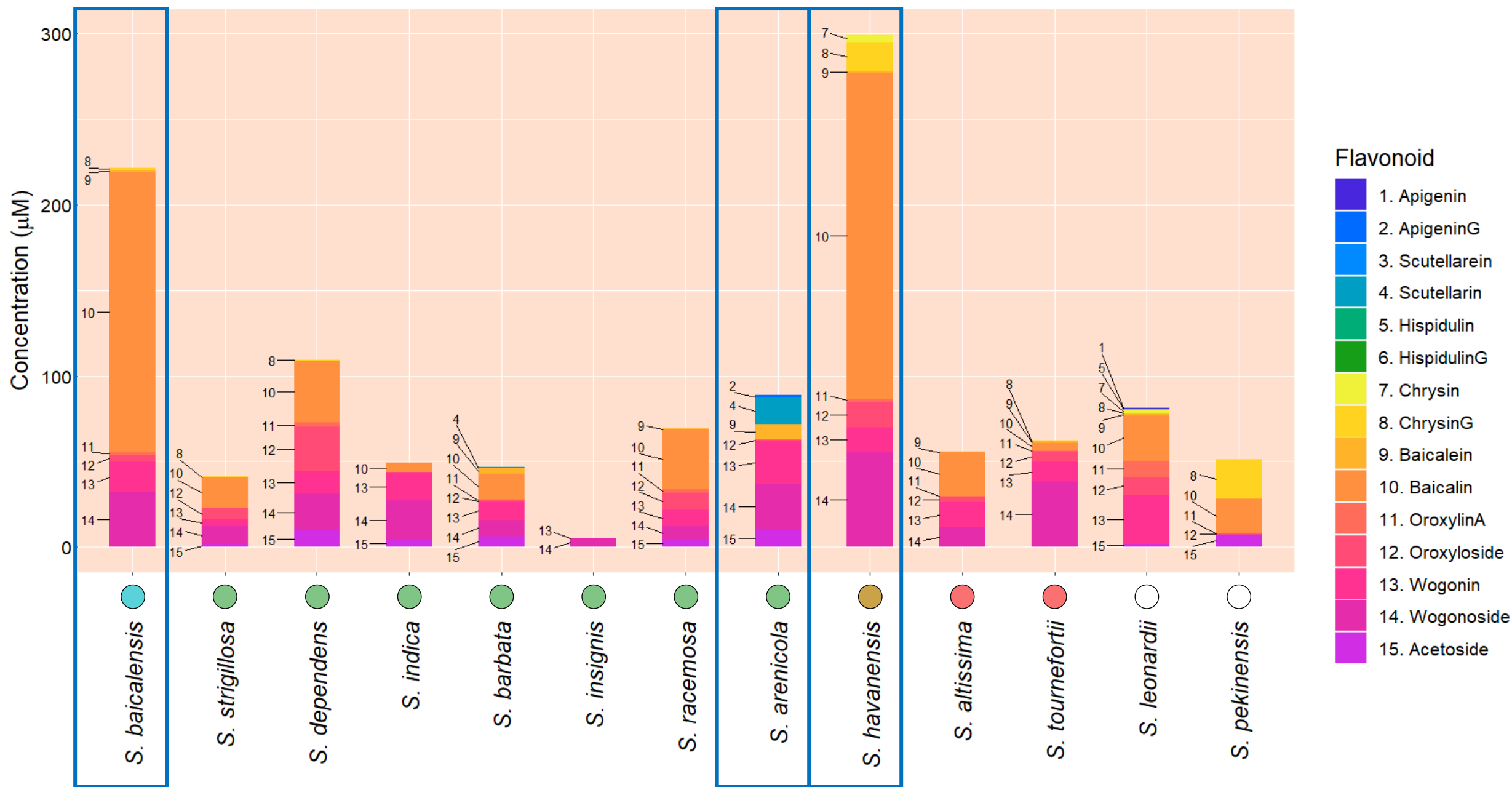
● *S. dependens*



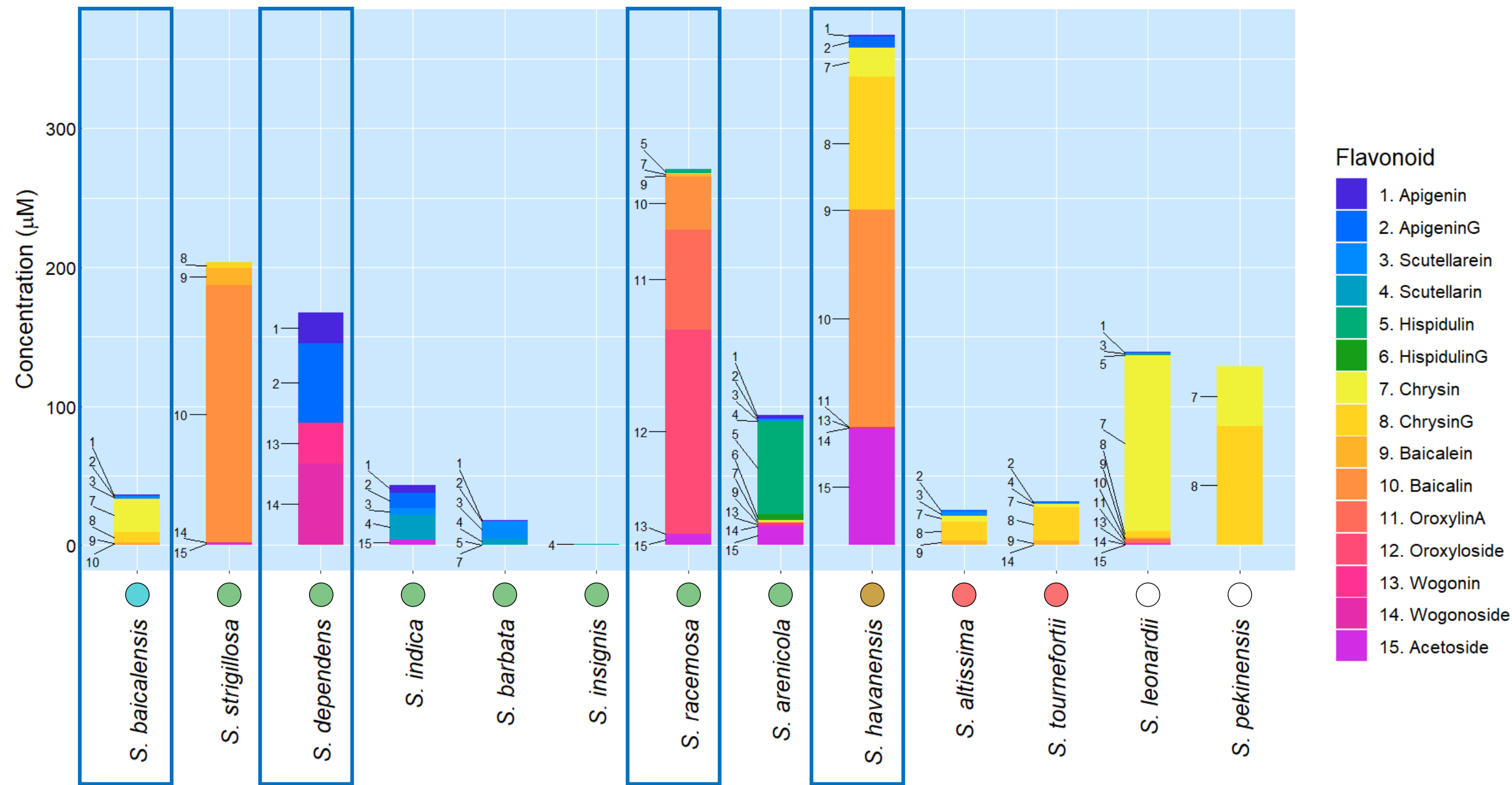
● *S. racemosa*



Flavonoid concentrations in Scutellaria roots



Flavonoid concentrations in Scutellaria leaves

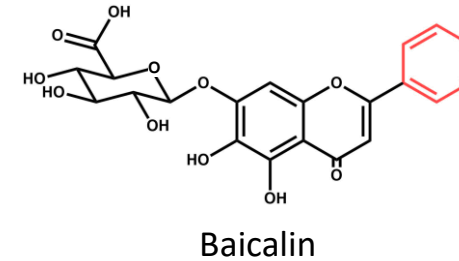


Genome size analysis

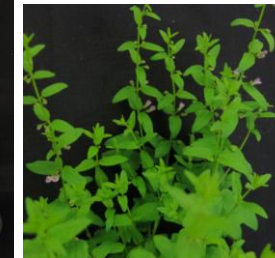
Species	Estimated genome size (Gbp)		Chromosome number
	Measured in this study	Published previously	Published previously
<i>S. baicalensis</i>	0.54	0.38 (Xu et al., 2020)	2n = 18 (Xu et al., 2020)
		0.41 (Zhao et al., 2019)	2n = 18 (Zhao et al., 2019)
		0.41 (Cole et al., 2008)	
<i>S. strigillosa</i>		0.38 (Lee & Kim, 2017)	
<i>S. dependens</i>	0.44		
<i>S. indica</i> var. <i>coccinea</i>		0.38 (Lee & Kim, 2017)	
→ <i>S. barbata</i>	0.52	0.35 (Xu et al., 2020)	2n = 26 (Xu et al., 2020)
<i>S. insignis</i>		0.46 (Lee & Kim, 2017)	
<i>S. racemosa</i>	0.44	0.37 (Cole et al., 2008)	2n = 18 (Cole et al., 2008)
<i>S. arenicola</i>	0.85		
<i>S. havanensis</i>	0.37		
<i>S. altissima</i>	0.39		
<i>S. tournefortii</i>	0.39		
<i>S. leonardii</i>	0.50		
<i>S. pekenensis</i> var. <i>alpina</i>	0.38		

Discussion & conclusion

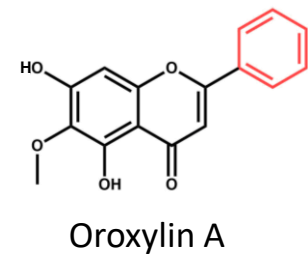
- Diversity in flavonoid accumulation indicates differences in biosynthetic pathway
- Several biotechnology targets identified
 - *S. havanensis* – Baicalin in roots and shoots
 - *S. racemosa* – Oroxylin A in shoots
- Weak relationship between phylogenetic and flavonoid data
- Future work – increase size of dataset, and transcriptomic and genomic analyses



● *S. havanensis*



● *S. racemosa*



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