



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

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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

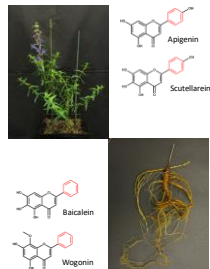
- Several species more well-studied because of their medicinal uses



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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)



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Scutellaria contains >470 species

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

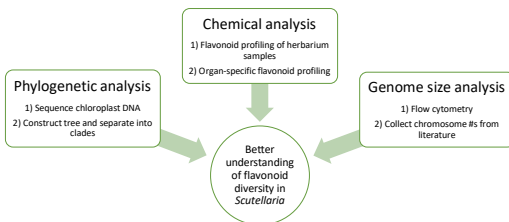
An improved understanding of flavonoid diversity in *Scutellaria* can:

- 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



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Approach

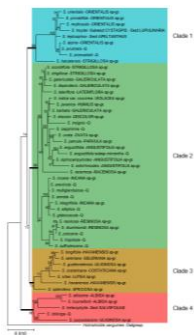


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Phylogenetic analysis

- 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

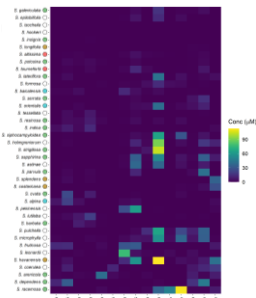
Unpublished phylogenetic data provided by Yoonkyung Lee and Sangtae Kim



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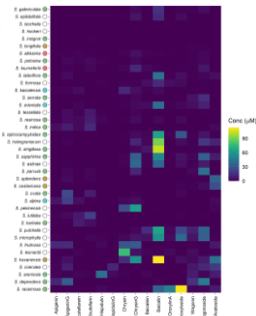
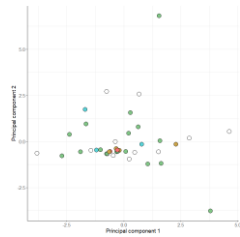
Chemical analysis

- 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

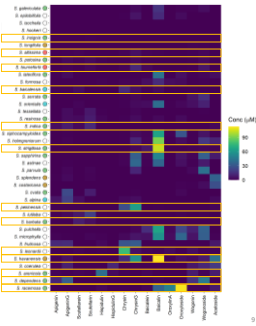


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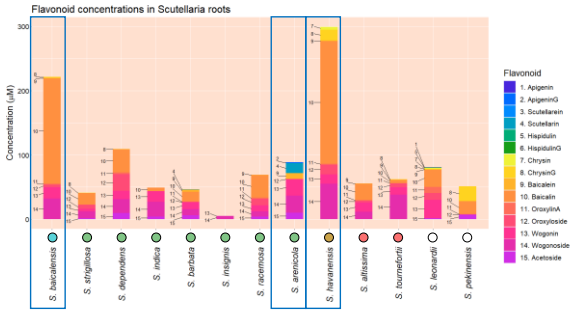
Chemical analysis



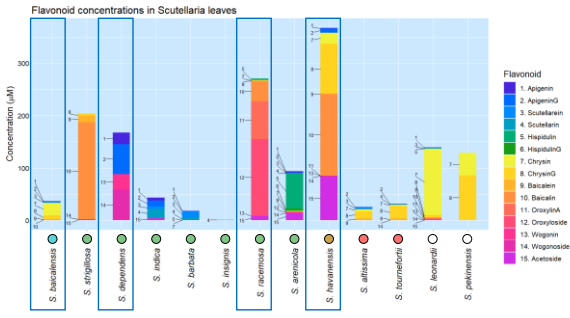
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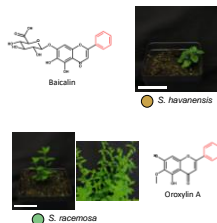
Genome size analysis

Species	Estimated genome size (Gbp)		Chromosome number	
	Measured in this study	Published previously	Published previously	
<i>S. baicalensis</i>	0.54	0.36 (Yu et al., 2020) 0.41 (Zhai et al., 2018) 0.41 (Cole et al., 2008)	2n = 18 (Yu et al., 2020) 2n = 18 (Zhai et al., 2019)	
<i>S. angustata</i>	0.44	0.38 (Lee & Kim, 2017)		
<i>S. dependens</i>	0.44	0.38 (Lee & Kim, 2017)		
<i>S. indica</i> var. <i>coccinea</i>	0.52	0.36 (Yu et al., 2020)	2n = 26 (Yu et al., 2020)	
<i>S. angustata</i>	0.44	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. amurensis</i>	0.85			
<i>S. havanensis</i>	0.37			
<i>S. alba</i>	0.39			
<i>S. baicalensis</i>	0.36			
<i>S. leucantha</i>	0.50			
<i>S. pallidiflora</i> var. <i>alba</i>	0.38			

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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



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