**Title page**

A phylogeny-based analysis of bioactive metabolites in *Scutellaria* reveals multiple species with significant medicinal potential

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**Footnotes**

**Abstract (250 word limit)**

The *Scutellaria* genus contains multiple plant species used extensively in traditional medicines due to their various anti-inflammatory, sedative, and neuroprotective effects. Bioactive 4´-hydroxyflavones and 4´-deoxyflavones have been identified as a significant source of these effects. *S. baicalensis*,one of the most well-known species of *Scutellaria*, accumulates 4´-deoxyflavones mainly in its roots in addition to 4´-hydroxyflavones. Although the biochemistry of *S. baicalensis* responsible for this organ-specific pattern has been studied, the *Scutellaria* genus contains more than 470 species of plants, many of which have not been chemically analyzed. The primary goal of this work was to investigate the chemodiversity of *Scutellaria*, and use this information to identify patterns in flavone accumulation across the genus, and to highlight species with significant medicinal value and biotechnology potential. We first compared metabolite profiles of aerial parts to a phylogenetic tree constructed from chloroplast genome sequences for 51 species of *Scutellaria*. From this initial profiling, we selected 13 species for further organ-specific and genome size analysis. We found that across the species we selected, 4´-hydroxyflavones and 4´-deoxyflavones accumulated independently, and that the 4´-deoxyflavone pathway was very well conserved. Additionally, we identified several species with significant 4´-deoxyflavone accumulation in their aerial tissues, suggesting a divergence from *S. baicalensis* with regards to regulation of pathway. From the species we selected for further profiling, *S. racemosa*, *S. dependens*, *S. wrightii*, and *S. suffrutescens* stood out as candidates for medicinal study due to their high flavone accumulation, and we also found *S. racemosa* and *S. dependens* to have relatively small genomes.

**Key words**

Chemodiversity, flavone, skullcap, medicine, biotechnology

**INTRODUCTION**

Introduction to medicinal plants and biotechnology as a solution to mass cultivation

Belonging to the mint family Lamiaceae, the *Scutellaria* genus contains multiple species of plants renowned for their medicinal properties. *S. barbata* is commonly used in traditional Eastern medicines to treat swelling and inflammation, and multiple reports have recently been published describing its effectiveness in cancer treatments (Shang et al., 2010; Q. Wang et al., 2018). *S. lateriflora* is used in traditional Native American treatments as a nerve tonic and sedative, with recent studies demonstrating its anticonvulsant and anxiolytic properties (Awad et al., 2003; Zhang et al., 2009). Perhaps the most well-known species is *S. baicalensis* due to its extensive use in traditional Eastern remedies. More commonly called Huang Qin in Chinese medicine, the roots of *S. baicalensis* are prescribed to treat a variety of ailments, including edema, dysentery, pneumonia, jaundice, and more (T. Zhao et al., 2019). In clinical studies, *S. baicalensis* root extracts have been found to exhibit antibacterial, anticancer, neuroprotective, antioxidant, and other beneficial health effects (Saralamma et al., 2017; Tao et al., 2018; Zhu et al., 2016).

These beneficial effects can be largely attributed to the bioactive metabolites which these *Scutellaria* species accumulate in high concentrations (Karimov & Botirov, 2017; Q. Zhao, Chen, et al., 2016). 4´-hydroxyflavones, which include apigenin and its derivatives, have been isolated from multiple *Scutellaria* species, but are also widely distributed throughout multiple families in the plant kingdom. 4´-deoxyflavones however, which includes chrysin and its derivatives, have been demonstrated to be mostly specific to the *Scutellaria* genus (Q. Zhao, Zhang, et al., 2016). Only several species of plants outside of the *Scutellaria* genus have been found to be capable of synthesizing this class of flavones (Kato et al., 1992; V. M. Rao et al., 2009; Y. K. Rao et al., 2002). The specific biological activities of many flavones from both classes has been studied (Lin et al., 2012; Salehi et al., 2019; Shang et al., 2010). In addition, the accumulation patterns of these flavones have been characterized for several more well-known *Scutellaria* species, such as the previously mentioned *S. barbata*, *S. lateriflora*, and *S. baicalensis* (Cole et al., 2008; L. Wang et al., 2020).

In *S. baicalensis*, an organ-specific accumulation pattern can be observed, where 4´-hydroxyflavones accumulate in the aerial parts at higher concentrations than in the roots, and 4´-deoxyflavones accumulate in the roots at higher concentrations than in the aerial parts. The biosynthetic pathway responsible for this organ-specific accumulation of flavones has been largely elucidated (Q. Zhao et al., 2018; Q. Zhao, Zhang, et al., 2016). Specifically, after the formation of cinnamic acid, the pathway diverges into a 4´-hydroxyflavone pathway, and a 4´-deoxyflavones pathway. In the 4´-hydroxyflavone pathway, a cinnamate 4-hydroxylase (C4H) uses cinnamic acid to form 4-coumarate. The ligation of 4-coumarate with coenzyme A (CoA) by 4-coumarate CoA ligase (4CL) forms 4-coumaroyl-CoA, which then undergoes several additional reactions to form apigenin, the first 4´-hydroxyflavone in the pathway. Further glycosylation, hydroxylation, and methylation of apigenin generates a variety of specialized 4´-hydroxyflavones. In contrast to the 4´-hydroxyflavone pathway, the 4´-deoxyflavone pathway begins with the immediate ligation of cinnamic acid with CoA by a specialized isoform of CoA ligase-like (CLL). This forms cinnamoyl-CoA, which then undergoes several additional reactions to form chrysin, the first 4´-deoxyflavone in the pathway. Glycosylation, hydroxylation, and methylation reactions then decorate chrysin to form a variety of specialized 4´-deoxyflavones (Q. Zhao, Zhang, et al., 2016). In addition to being well-characterized biochemically, a reference genome for *S. baicalensis* was published in 2019 (Q. Zhao et al., 2019).

Although many studies have focused on the biochemistry of *S. baicalensis*, the *Scutellaria* genus contains more than 470 species, distributed nearly worldwide (Yoonkyung & Kim, 2021). Because metabolite profiles for most of these species are not well-studied, it is unknown how well conserved the 4´-hydroxyflavone and 4´-deoxyflavone pathways are in the genus. It’s also unknown how well the flavone organ-specific accumulation pattern observed in *S. baicalensis* is conserved. Thus, the limited number of *Scutellaria* species that have been chemically analyzed leaves the possibility of an uncharacterized species having a medicinally significant flavone accumulation profile. In this case, the species may be a strong candidate for biotechnology efforts for the mass production of medicinal flavones.

Therefore, to better characterize flavone diversity in *Scutellaria*, we performed a phylogenetic-based analysis of 14 flavones, and one other metabolite across 76 species of *Scutellaria*. A subset of 13 species was then selected for additional chemical and genome size analysis. With the results from this method, we identified several species which have significant medicinal potential and could serve as targets for biotechnology improvement.

**MATERIALS AND METHODS**

***Chloroplast genome sequencing and phylogenetic tree construction –***

***Plant materials and growth conditions for fresh tissue samples –***

Viable seeds were obtained for *S. altissima*, *S. baicalensis*, *S. leonardii*, *S. tournefortii*, *S. wrightii,* and *S. racemosa*. Seeds for all these species, except *S. wrightii* and *S. racemosa*, were ordered from retailers. *S. wrightii* seeds were harvested from a mature plant obtained from Far South Wholesale Nursery (Austin, Texas, USA). *S. racemosa* mature plants were taken from a field in Hattiesburg, Mississippi, USA and further grown in indoor conditions at the University of Florida before harvesting seeds. To improve germination rate, seeds were first incubated in a 100 µM solution of gibberellic acid for 1 hour with gentle shaking. Seeds were then planted on moist soil, and watered every 5-8 days. Plants were grown at the University of Florida (Gainesville, Florida, USA) in indoor, climate-controlled conditions at 21-23°C under fluorescent lighting with a light intensity of 140 mE m-2s-1 in a 16 hour light/ 8 hour dark photoperiod. Organ-specific tissue samples were taken at six weeks after germination.

Tissue samples for *S. suffrutescens* were taken from fully mature plants having open flowers obtained from Far South Wholesale Nursery (Austin, Texas, USA) where they were cultivated in outdoor greenhouse conditions. Approximately one week before tissue samples were taken, the plants were moved to indoor, climate-controlled conditions.

The species of *S. insignis*, *S. indica var. coccinea*, *S. barbata*, *S. strigillosa*, *S. dependens*, and *S. pekinensis* var*. alpina* were collected from the field in Korea and transplanted in the greenhouses of the Sungshin Women’s University, Korea. grown at Sungshin Women’s University (Seoul, Republic of Korea). Fresh tissue samples from mature plants were then frozen, and shipped to the University of Florida for metabolite analysis.

Voucher specimens of fresh plants that were used in this study were deposited in FLAS or SWU herbaria. Dried herbarium vouchers for all other species studied here were obtained from FLAS and NY herbaria. Voucher information for all plant material used in this study is provided in Appendix S2.

***Metabolite extraction and quantification –***

*Herbarium tissue samples –*

14 flavones and one other metabolite were extracted and quantified from the aerial tissues of herbarium vouchers of 67 unique *Scutellaria* species. The flavones quantified included six 4´-hydroxyflavones, which were apigenin, apigenin-7-glucuronide (apigenin 7-G), scutellarein, scutellarin, hispidulin, and hispiduloside. The remaining eight flavones were 4´-deoxyflavones, which were chrysin, chrysin-7-glucuronide (chrysin 7-G), baicalein, baicalin, oroxylin A, oroxyloside, wogonin, and wogonoside. Acteoside was the final metabolite quantified. Tissue samples were first weighed with an analytical balance to determine their dry weight. An extraction buffer of 80% High Performance Liquid Chromatography (HPLC) grade methanol added to each so that the following ratio was achieved: 10 mg dry tissue/1 mL solvent. Samples were sonicated for 1 hour at room temperature. The extraction buffer from each sample was withdrawn and further diluted by adding 80% HPLC grade methanol so that the following ratio was achieved: 1 mg tissue/1 mL solvent. To remove any remaining tissue particles, the diluted extraction buffer was centrifuged at 15,000 rpm for 5 minutes and ran through a syringe filter with a pore size of 0.45 µM. Metabolite concentrations in this final solution were quantified with a Thermo Scientific (Massachusetts, USA) UltiMate 3000 HPLC system. Metabolites were separated with a 3 x 100 mm Acclaim RSLC 120 C18 column, and eluted by a mixture of 0.1% formic acid (A) and 100% acetonitrile (B) with the following gradient: -8 to 0 min, 5% B; 2 min, 25% B; 2 to 6 min, 25% B; 9 min, 50% B; 9 to 11 min, 50% B; 15 min, 95% B; and 15 to 23 min, 95% B. A flowrate of 0.5 mL/min was used and the column oven temperature set to 40°C. Calibration mixes of 0.1, 0.5, 1, 5, 10, 25, 50, and 100 ppm were used to convert peak areas to concentrations in ppm. Chemical standards used to prepare the calibration mixes were purchased in powdered form from ChemFaces (Wuhan, China) or MilliporeSigma (Massachusetts, USA), and dissolved in dimethylsulfoxide (DMSO) to generate stocks of 1000, 2000, or 4000 ppm. These stocks were diluted with 50% methanol and mixed to generate calibration mixes of the varying desired concentrations. Using the peak areas of these calibration mixes and the molecular weight of each metabolite, concentrations in µmol/g dry weight were calculated for experimental samples. To roughly account for the difference in water weight between herbarium and fresh tissues so that comparisons could be made, all measured metabolite concentrations for herbarium tissue samples were divided by 10. Thus, all final concentrations for dried tissue samples are expressed in units of µmol/0.1 g dry weight, which is approximately equivalent to µmol/g fresh weight.

*Fresh tissue samples –*

The same set of 15 metabolites were extracted and quantified from the root, stem, and leaf tissues of 13 *Scutellaria* species. Tissue samples for each organ were collected in triplicate from mature plants. A mixture of young and mature tissues were selected for each sample so that the average chemical state of the entire plant was represented. Root tissue samples were gently washed to remove soil. The fresh weight of all tissue samples was determined with an analytical balance immediately after harvesting. For the species with tissue samples that were frozen and shipped, fresh weight was measured before freezing. The metabolite extraction and quantification method closely follows that used for the herbarium samples. However, the initial extraction buffer was added to achieve a ratio of 30 mg tissue/1 mL solvent instead of 10 mg tissue/1 mL solvent, and then after sonication, diluted to achieve a ratio of 5 mg tissue/1 mL solvent instead of 1 mg tissue/1 mL solvent. Measured metabolite concentrations were then divided by 5, and the molecular weight of each metabolite was used to calculate final concentrations in units of µmol/g fresh weight.

***Phylogeny-metabolite comparison by multiple correspondence analysis –***

Comparisons between phylogenetic clade and metabolite profile were made using a multiple correspondence analysis-based approach. This analysis used HPLC data for the 15 metabolites extracted from aerial tissue samples of 76 *Scutellaria* species. 67 of these tissue samples were herbarium vouchers, and the remaining 9 were fresh tissue. To reduce bias resulting from mixing data from herbarium and fresh tissue samples, all metabolite concentrations were converted into a binary format where only the presence or absence of a metabolite was considered. The multiple correspondence analysis was conducted in R with the “MCA” function from the FactoMineR package with all settings left at their default values (ver. 2.3). 80% confidence ellipses were drawn from the covariance matrix calculated with the “covMcd” function from the robustbase package (ver. 0.93-6).

***Estimation of genome size with flow cytometry –***

Seeds of *Solanum lycopersicum L*. ‘Stupické polní rané’ (2C = 1.96 pg), and *Glycine max Merr.* ‘Polanka’ (2C = 2.50 pg) were requested from Dr. Jaroslav Doležel (Institute of Experimental Botany, Olomouc, Czech Republic) who suggested them as size-standards for flow cytometry (Doležel et al., 2007). Leaves of these plants were used as size standards for genome-size estimation. In each estimation, a standard sample was selected based on the previously reported genome size information in *Scutellaria* (Y. Lee & Kim, 2017).

The genome sizes of 8 species of *Scutellaria* were estimated using flow cytometry as described in Doležel et al. (2007). Fresh leaves from a standard plant and a sample for estimation (each ca. 5 mm²) were co-chopped using a razor blade in a petri dish with DAPI Prep DNA Staining Solution (SONY, Biotechnology Inc., USA) and incubated two minutes for staining. Cell sorter SH800 (SONY, Biotechnology Inc., USA) was used to measure the fluorescence of the stained cells and ensure each sample measured more than 5,000 particles. Each analysis was repeated three or more times using different leaves or different individuals, and their average and standard deviation were calculated. The 2C-value was estimated based on the relative counts between G1 (growth 1 stage on the cell division) peak from a standard plant and that from a sample for the estimation. The genome size (bp) was estimated based on relative rate between 1C-value and number of bases: 1C (pg) DNA = 0.978 × 109 bp (Doležel et al., 2007).

**RESULTS**

***Phylogeny of selected species as revealed by chloroplast genome sequences – (Fig 1)***

***Aerial tissue metabolite diversity and comparison with phylogeny –***

Recent studies have elucidated the organ-specific flavone biosynthesis pathway of S. baicalensis, and characterized several enzymes functioning in specific steps (Q. Zhao et al., 2018, 2019; Q. Zhao, Zhang, et al., 2016) (Fig. 2, Appendix S1; see Supplemental Data with this article). Based on this proposed pathway, we selected 15 metabolites for further study, including seven unique flavones and their corresponding glycosides, as well as acteoside (also known as verbascoside), a phenylethanoid glycoside common across many Lamiaceae species (Alipieva et al., 2014). Using high performance liquid chromatography (HPLC), we analyzed the levels of these 15 metabolites from aerial tissue samples of 76 species of *Scutellaria* (Fig. 3A, Appendix S3). 51 of the 76 species were included in our phylogenetic analysis. 67 of the tissue samples were from herbarium vouchers with one replicate, and the remaining 9 from fresh tissue sampled in triplicate. Herbarium voucher labels for all species analyzed are provided in Appendix S2. To roughly account for the difference in water weight between herbarium and fresh tissues, the fresh weight of herbarium tissues was estimated by multiplying their dry weight by 10. Thus, concentrations for dried tissue samples are expressed in units of µmol/0.1 g dry weight, which is approximately equivalent to µmol/g fresh weight. Aerial tissues were chosen for this analysis because they were more readily available from herbariums than root tissues, and because preliminary results indicated that, between species, aerial metabolite profiles were much more diverse than root metabolite profiles. More diversity in metabolite profile would facilitate the metabolite-phylogeny comparison method we planned to apply.

The most commonly occurring metabolites were scutellarin and chrysin 7-G, which we detected in 52 of the 76 species. The rarest flavone we quantified was hispiduloside, which was detected in only one species, *S. coerulea*. In general, we detected the 7-glucuronide form of each metabolite (chrysin 7-G, wogonoside, apigenin 7-G, baicalin, scutellarin, and oroxyloside) more often and in greater amounts, than its aglycone counterpart (chrysin, wogonin, apigenin, baicalein, scutellarein, and oroxylin A). This evidences that the 7-glucuronide form is a more stable, storage form. The exception was hispiduloside and hispidulin, as hispidulin was detected in 27 species, but hispiduloside in only one. out of the eight most commonly occurring metabolites, six were 4´-deoxyflavones (chrysin 7-G, wogonoside, baicalin, wogonin, chrysin, and oroxyloside), and only two were 4´-hydroxyflavones (scutellarin and apigenin 7-G). This result suggests that the 4´-deoxyflavone biosynthetic pathway is more well conserved across the *Scutellaria* genus than the 4´-hydroxyflavone pathway. However, it is also possible that the 4´-deoxyflavones we quantified are more stable than the 4´-hydroxyflavones, and as a result, were less likely to be degraded over time in the herbarium vouchers. Additionally, our quantification of eight unique 4´-deoxyflavones but only six unique 4´-hydroxyflavones likely affected this result.

As this data was generated from aerial tissue samples, our finding of 4´-deoxyflavones in all but 8 species suggests that 4´-deoxyflavones are not strictly root specific. Matching with that observed in *S. baicalensis* by (Q. Zhao, Zhang, et al., 2016), it’s likely that the enzymes involved in 4´-deoxyflavone biosynthesis are simply much more active in the roots, but are still expressed at some basal level in the aerial tissues. This hypothesis is supported by our detection of low concentrations of several 4´-deoxyflavones, including chrysin, baicalein, wogonin, and their 7-glucuronide forms, in our *S. baicalensis* tissue sample. Alternatively, it’s possible that 4´-deoxyflavones are being synthesized in the roots and transported to the aerial tissues.

Although the species in Fig. 3A are ordered based on the phylogenetic tree shown in Fig. 1, it is difficult to detect any clear relationship between phylogeny and metabolite profile. Therefore, to make any relationship more apparent, we used a multiple correspondence analysis (MCA) approach. MCA is a technique similar to principal component analysis (PCA), which seeks to summarize a multivariate dataset into only several variables. These variables, called principal components, are calculated to retain the maximum amount of variance possible that is present in the original dataset. MCA was chosen over PCA because it is more appropriate for data in a binary format, which the metabolite dataset was converted into prior to the analysis. This conversion to a binary format was completed by assigning concentration datapoint with a value of TRUE if the metabolite was detected in that species, and FALSE if it was not. A binary format was chosen for this use in this analysis to minimize the effects resulting from the varying ages of the herbarium samples, as well as our use of fresh tissue samples for several species.

No significant separation of species by clade was observed in the MCA plot, indicating that metabolite profile cannot be used to definitively determine the phylogenetic relationship of those species we included (Fig. 3B). This is supported by the relatively low percentage of variance in the original dataset that was able to be explained by the first two principal components (23.45% and 14.47%). The small number of species included in clade 5 limits detection of any patterns in metabolite accumulation. Confidence ellipses for both clades 2 and 4 were very large, reflecting the diversity in aerial metabolite profiles for the species in this clade. Although no conclusions besides these can be drawn from the confidence ellipses of clades 2, 4, and 5, several general patterns in metabolite profile are illustrated by the locations of the confidence ellipses for clades 1 and 3.

Some grouping of species in clade 3 to the upper left side of the plot can be observed, possibly because of trace accumulation of 4´-hydroxyflavones in many of these species, Globally, apigenin 7-G, hispidulin, and scutellarein were detected in 59.21%, 38.16%, and 22.37% of all species analyzed, respectively, but in 69.23%, 69.23%, and 38.46% of species in clade 3. This increase in detection rate of 4´-hydroxyflavones can be confirmed as a cause for the slight grouping of clade 3 species in Fig. 3B by considering the associated variable loading plot (Fig. 3C). This plot illustrates the role that each metabolite plays in determining the position of points in Fig. 3B. The variable loading plot shows that a positive detection of 4´-hydroxyflavones can drive the movement of species in Fig. 3B. to the upper half of the plot area, which is where multiple clade 3 species cluster. Additionally, the plot indicates that the negative detection of 4´-deoxyflavones can shift species in Fig. 3B left, and that a negative detection of baicalin will have the most significant effect in this regard. Accordingly, we detected baicalin in 57.89% of all species, but in only 23.08% of clade 3 species.

A similar method of analysis can be applied to clade 1, which has a confidence ellipse centered towards the bottom left of the plot area in Fig. 3B. The variable loading plot shows that this position corresponds to a negative detection of both 4´-deoxyflavones and 4´-hydroxflavones. With regards to 4´-deoxyflavones, we detected chrysin and chrysin 7-G in only 14.29% and 28.57% of species in clade 1, but globally, in 44.59% and 67.57% of all species analyzed. For 4´-hydroxyflavones, Fig 3C illustrates that negative detection of apigenin 7-G will strongly drive species towards the lower half of the MCA plot. Matching this result, we detected apigenin 7-G in only 14.29% of species in clade 1, but in 59.21% of all species.

Although differentiation of clades by metabolite profile is not possible, the variable loadings calculated in our MCA form several significant patterns that are illustrated in the variable loading plot. First, flavones of the same class and detection (i.e. TRUE or FALSE) cluster together in the same region of the plot: TRUE 4´-deoxyflavones on the positive PC1 axis, FALSE 4´-deoxyflavones on the negative PC1 axis, TRUE 4´-hydroxyflavones on the positive PC2 axis, and FALSE 4´-hydroxyflavones on the negative PC2 axis. The exception to this pattern is scutellarein, which despite being a 4´-hydroxyflavone, is positioned on the PC2 axis. This may be a result of its commonness obscuring the development of any pattern across the species we examined. The grouping of other 4´-deoxyflavones and 4´-hydroxyflavones however, indicates that in most species, accumulation of a flavone of a given class is positively correlated with accumulation of other flavones from that same class. In addition, because flavones of different classes are positioned on axes perpendicular to each other, accumulation of one class of flavone is usually not correlated with accumulation of flavones from the other class. In other words, in the aerial tissues of *Scutellaria* species that we analyzed, 4´-deoxyflavone accumulation was independent of 4´-hydroxyflavone accumulation, and vice versa.

***Organ-specific metabolite diversity –***

From the initial set of 76 species selected for aerial tissue metabolite profiling, we identified 13 species with interesting accumulation patterns to investigate further. Representative images of these species are provided in Appendix S4. At least one species was selected from four of the five clades identified in our phylogenetic analysis. Due to limited access to plant material, no species were selected from clade 1. The selected species were grown fresh, and tissue samples taken in triplicate from the roots, stems, and leaves of mature plants. We then quantified concentrations of the same 15 metabolites as in our aerial tissue analysis.

Based on our root-specific metabolite profiling results, the 4´-deoxyflavone pathway appears to be very well conserved across all the species we selected (Fig. 4, Table 1). We detected at least two 4´-deoxyflaonves in all of the species we analyzed, and at least four in all but two species, *S. suffrutescens* and *S. insignis*. *S. suffrutescens* accumulated high concentrations of baicalein and baicalin, and *S. insignis* accumulated only wogonin and wogonoside at relatively low concentrations as compared to those in other species.

Interestingly, although chrysin is proposed to serve as a precursor for all the 4´-deoxyflavones we quantified, we only detected chrysin in the root tissues of three species, and its glycosylated form, chrysin 7-G, in seven. This rarity in detection is possibly a result of chrysin rapidly being converted into downstream products before it accumulates to a level detectable by our HPLC method.

The absence of 4´-hydroxyflavones in the root tissues of all but four species indicates the specificity of the 4´-hydroxyflavone biosynthetic pathway to the aerial tissues of the plant, in line with that described for *S. baicalensis* (Q. Zhao, Zhang, et al., 2016). *S. wrightii* is notable because of its large accumulation of baicalein and baicalin, multiple times that of *S. baicalensis*. We also found *S. suffrutescens* to accumulate greater concentrations of baicalein and baicalin than *S. baicalensis*.

Although root-specific metabolite profiles were relatively consistent across the 13 species we selected, aerial tissue-specific profiles were much more varied, with the 4´-hydroxyflavone pathway conserved to greatly varying degrees. In our leaf and stem tissue samples, we were able to detect at least one 4´-hydroxyflavone in all 13 species. Nine species accumulated apigenin, a precursor for all other 4´-hydroxyflavones analyzed, or its 7-glucuronide, apigenin 7-G. One of these species (*S. dependenens*) did not accumulate any 4´-hydroxyflavones downstream from apigenin. Out of the eight species in which we detected apigenin or its 7-glucuronide, we were able to detect scutellarein or its 7-glucuronide, scutellarin, in seven. Scutellarein is immediately downstream of apigenin in the proposed 4´-hydroxyflavone pathway, and is also a precursor for the final set of 4´-hydroxyflavones we analyzed, hispidulin and its 7-glucuronide, hispiduloside. We identified five species that accumulated apigenin, scutellarein, and hispidulin, or their 7-glucuronidated forms. Of the 4´-hydroxyflavones, hispiduloside was exceptionally rare, as we detected it in only one species, *S. racemosa*. *S. racemosa* accumulated only a small amount of hispiduloside in its stems.

Our detection of at least one 4´-deoxyflavone in the leaves of 11 of the 13 species we selected suggests that 4´-deoxyflavones are not root-specific to the same degree that 4´-hydroxyflavones are aerial tissue-specific. One explanation is provided by considering the flavone profiles of *S. wrightii*, S*. baicalensis*, *S. altissima*, and *S. tournefortii*. We detected higher concentrations of many of the same 4´-deoxyflavones in the roots of these species as compared to the leaves. A mix of 4´-hydroxyflavones from the leaves, and 4´-deoxyflavones from the roots, can also be observed in the stems. Therefore, in these species, it’s possible that some amount of 4´-deoxyflavones being synthesized in the roots are being transported to the aerial parts. Alternatively, biosynthetic enzymes acting in the 4´-deoxyflavone pathway of these species are potentially more active in the roots, but are also active at a much lower level in the leaves. Chrysin and chrysin 7-G are the only 4´-deoxyflavones which don’t seem to follow this pattern of accumulation due to their scarcity in the root tissues.

There are several species which do not follow a root-heavy accumulation pattern for 4´-deoxyflavones. We found *S. racemosa* to accumulate oroxylin A and oroxyloside at significantly greater concentrations in its leaves as compared to in its roots. *S. strigillosa* is also a notable exception due to its high accumulation of baicalin in its leaves relative to its roots. In addition, we found *S. dependens* to accumulate higher concentrations of wogonin and wogonoside in its leaves are compared to its roots. Finally, *S. suffrutescens* accumulated similar concentrations of baicalein and baicalin in all three organs that we sampled. In these species, it is likely that at least some biosynthetic enzymes in the 4´-deoxyflavone pathway are active in the aerial parts of the plant, instead of or in addition to, in the roots.

In general, acteoside does not seem to share the same organ specificity as the flavones we analyzed. We detected acteoside in the roots of seven species, but also in the stems or leaves of five out of these seven species. In these species that accumulated acteoside in both their roots and aerial parts, concentrations were very similar. This pattern of accumulation aligns well with other studies which have detected acteoside in both the roots and aerial parts of many species belonging to the Lamiales order (Alipieva et al., 2014).

Several general patterns of accumulation become apparent by considering the phylogeny of the 13 species we selected, as was shown in Fig. 1. First, three species within clade 2 (*S. insignis, S. indica var. coccinea*, and *S. barbata*) display a very similar flavone profile. The root specificity of 4´-deoxyflavones, and aerial tissue specificity of 4´-hydroxyflavones is very well conserved in these species. Additionally, the concentrations of accumulated flavones in all three organs are similar, and relatively low as compared to other species that we analyzed. Matching this similarity in accumulation profile, *S. insignis, S. indica var. coccinea*, and *S. barbata* are positioned nearby each other in our phylogenetic tree.

In contrast to this similarity, the other three species we selected from clade 2 (*S. racemosa*, *S. strigillosa*, and *S. dependens*) display very diverse accumulation patterns, especially in their aerial tissues. The root specificity of 4´-deoxyflavones is not well conserved in these species. Not only did we detect multiple 4´-deoxyflavones in leaf and stem tissues, but we also found that each species accumulates significantly higher concentrations of several 4´-deoxyflavones in its aerial tissues as compared to its roots. For *S. racemosa*, these 4´-deoxyflavones were oroxylin A and oroxyloside, for *S. strigillosa* baicalein and baicalin, and for *S. dependens* wogonin and wogonoside.

Although *S. wrightii* accumulated a slightly more diverse set of metabolites, both species we selected from clade 3 showed similar overall patterns of accumulation. The most apparent difference is the high concentrations of baicalin accumulated in the leaves of *S. suffrutescens* relative to *S. baicalensis*. In the roots of *S. wrightii*, and in all three organs of *S. suffrutescens*, we found baicalein and baicalin concentrations to be similar to or several times higher than that in the roots of *S. baicalensis*.

Another pattern in metabolite profile can be observed between those species in clades 4 and 5. *S. baicalensis*, the only species which we selected from clade 4, displays an organ-specific accumulation pattern that is closely matched by *S. tournefortii* and *S. altissima* in clade 5. These three species accumulate a similar set of 4´-deoxyflavones in their roots. However, the high accumulation of baicalin by *S. baicalensis* sets it apart from *S. tournefortii* and *S. altissima*. Aerial tissue accumulation for all three species was very similar. We detected limited concentrations of only several 4´-hydroxyflavones in our aerial tissue samples, but also several 4´-deoxyflavones accumulated in the roots of each species.

***Genome size estimations –***

Genome sizes for eight species of *Scutellaria* were estimated with flow cytometry by comparison of 2C-values to a standard plant. To facilitate comparison, we also collected genome size, chromosome number, and ploidy level data for several species from literature (Table 2). Unfortunately, we did not include *S. wrightii* or *S. suffrutescens* in our analysis, and no previous publications have reported genome size, chromosome number, or ploidy level data.

Overall, genome sizes for the species we selected, including those values which we collected from literature, were similar, and ranged between 0.35 and 0.54 Giga base pairs (Gbp) (Cole et al., 2008; Y. Lee & Kim, 2017; Z. Xu et al., 2020; Q. Zhao et al., 2019). We estimated a slightly larger genome size as compared to previously published data for several species, including *S. barbata*, *S. racemosa*, *and S. baicalensis*. This is possibly a result of ... We also collected chromosome number and ploidy level data from literature to assess how well genome structure is conserved across the 13 species we selected. Despite the relatively tight range of genome sizes, chromosome numbers varied between 18 and 34 (Cole et al., 2008; Gill, 1981; Y. N. Lee, 1967; Lövkvist & Hultgård, 1999; Ranjbar & Mahmoudi, 2013; Takashi et al., 2003; Z. Xu et al., 2020; Q. Zhao et al., 2019). Four of the species for which ploidy level data has been published were diploid, and three were tetraploid (Gill, 1981; Hsieh & Huang, 1995; Y. N. Lee, 1967; Lövkvist & Hultgård, 1999; Ranjbar & Mahmoudi, 2013; Takashi et al., 2003). Although those species which were tetraploid had slightly higher chromosome numbers as compared to those which were diploid, there was seemingly no relationship between genome size and chromosome number nor ploidy level. In addition, there was no apparent relationship between phylogenetic clade and genome size, chromosome number, nor ploidy level.

**DISCUSSION**

The *Scutellaria* genus contains multiple species of plants which have been used extensively in traditional medicines. Flavones have been identified as the primary source of these plants’ medicinal effects, and a specific class of flavones, 4´-deoxyflavones, have been demonstrated to be mostly exclusive to the *Scutellaria* genus (Kato et al., 1992; V. M. Rao et al., 2009; Y. K. Rao et al., 2002). *S. baicalensis* is the most well studied *Scutellaria* species, and is known to accumulate 4´-hydroxyflavones in its aerial organs, and 4´-deoxyflavones in its roots (Q. Zhao, Zhang, et al., 2016). Aiming to further our understanding of the flavone biosynthetic pathway in *S. baicalensis*, multiple recent studies have demonstrated that this organ-specific accumulation pattern is a result of the differential expression of specialized enzyme isoforms (Q. Zhao et al., 2018, 2019; Q. Zhao, Zhang, et al., 2016). Although the biochemistry of *S. baicalensis* has been studied, it is unknown how well this biochemistry is conserved across the *Scutellaria* genus, which is presently known to contain more than 470 species (Yoonkyung and Kim, 2020). Thus, in this work, we chemically analyzed a diverse set of *Scutellaria* species with the goal of characterizing variation in metabolite accumulation across the genus, and identifying species with significant medicinal value and biotechnology potential. We first constructed a phylogenetic tree from chloroplast genome sequences for 51 species, and separated this tree into 5 clades. We then used the relationships described by this tree as a basis for comparison of metabolite profiles of these species.

From our analysis of aerial metabolite profiles of 76 species, we found that 4´-hydroxyflavones were less widespread across the *Scutellaria* genus than 4´-deoxyflavones. This was interesting considering that 4´-hydroxyflavone biosynthesis is significantly more common than 4´-deoxyflavone biosynthesis outside of *Scutellaria*. As most of our tissue samples for these 76 species came from dried herbarium vouchers of various ages, it’s possible that 4´-hydroxyflavones are simply less stable than 4´-deoxyflavones. However, the metabolite profiles collected from our fresh tissue samples of 13 species showed a similar pattern, as 4´-hydroxyflavones were considerably scarcer as compared to 4´-deoxyflavones. This result suggests that that the 4´-deoxyflavone pathway is more well conserved across the genus than the 4´-hydroxyflavone pathway. One potential explanation is that, with regards to their activities in the plant, 4´-hydroxyflavones serve more specific, accessory roles, while 4´-deoxyflavones fulfill more core roles. Sosa et al. (2004) reported that *Cistus landanifer*’s accumulation of apigenin, one of the 4´-hydroxyflavones we studied here, can deter herbivores through relaxation of mouth skeletal muscles. Hispidulin, another 4´-hydroxyflavone we quantified, was shown by Gallon et al. (2019) to have larvicidal properties against *Chlosyne lacinia* caterpillars. Thus, it’s possible that those species with limited 4´-hydroxyflavone accumulation face little herbivory pressure in their natural environments. However, from our organ-specific data, in each of the species with aerial parts in which we were unable to detect any 4´-hydroxyflavones (*S. strigillosa*, *S. suffrutescens,* and *S. pekinensis* var. *alpina*), we detected a significant accumulation of several 4´-deoxyflavones in their aerial parts instead. Perhaps these species have evolved to utilize 4´-deoxyflavones to fulfill the roles which 4´-hydroxyflavones do in other plant species. Unfortunately, as most studies of *Scutellaria* flavones have focused on their medicinal effects in animal models and not on their physiological purposes in plants, little is known about the specific relevance of 4´-deoxyflavones to plant growth, development, and stress response. Therefore, the causative factors for the differences in distribution of 4´-hydroxyflavones and 4´-deoxyflavones remains unknown.

The results of our MCA with 76 *Scutellaria* species demonstrated that in the aerial parts, 4´-hydroxyflavone and 4´-deoxyflavone accumulation occur largely independent of each other. This suggests that the layout of the flavone pathway for *S. baicalensis* proposed by Q. Zhao, Zhang, et al. (2016) can be extended to most of the species we studied here. In this pathway, separation of the 4´-hydroxyflavone and 4´-deoxyflavone pathways occurs immediately after the formation of cinnamic acid, upstream of any of flavones we quantified. 4´-hydroxyflavone biosynthesis begins with hydroxylation of cinnamic acid to 4-coumarate by a cinnamate-4-hydroxylase (C4H), followed by ligation of coenzyme A (CoA) by a 4-coumaroyl-CoA ligase (4CL). Instead of hydroxylation, 4´-deoxyflavones biosynthesis begins with the immediate ligation of cinnamic acid with CoA by CoA ligase-like (CLL). Our MCA results corroborate the hypothesis that after this initial differentiation, there is no interconversion of products between the 4´-hydroxyflavone and 4´-deoxyflavone pathways. This interconversion would require a dehydroxylase capable of removing a hydroxyl group from the B ring of flavones, an enzyme which has not been identified to exist in plants. Because we found 4´-hydroxyflavones and 4´-deoxyflavones to occur independently of each other, it’s unlikely that this enzyme exists in any of the species we analyzed here.

As the 4´-hydroxyflavone and 4´-deoxyflavone pathways structurally parallel each other, studies in *S. baicalensis* have identified several biosynthetic steps which are completed by nonspecialized enzymes. These enzymes have similar catalytic activity in both 4´-hydroxyflavone and 4´-deoxyflavone pathways, and include chalcone isomerase (CHI), flavone-6-hydroxylase (F6H), and 7-O-glucosyltransferase (7GT) (Hirotani et al., 2000; Q. Zhao, Zhang, et al., 2016). However, work in *S. baicalensis* has also demonstrated the existence of specialized isoforms of several enzymes that preferentially act on the substrates of one pathway over the other. Q. Zhao, Zhang, et al. (2016) found that *S. baicalensis* uses a specialized isoform of chalcone synthase (CHS) in 4´-deoxyflavone synthesis, but also encodes a different isoform which only has activity in the 4´-hydroxyflavone pathway. In the same work, Q. Zhao, Zhang, et al. (2016) identified two isoforms of flavone synthase II (FNSII) in *S. baicalensis*. One isoform preferentially accepts substrates from the 4´-hydroxyflavone pathway, while the other exclusively acts in 4´-deoxyflavone synthesis. This specialization of enzyme isoforms at multiple steps in flavone biosynthesis allows for independent expression of the 4´-hydroxyflavone and 4´-deoxyflavone pathways in the different organs of *S. baicalensis*. Our detection of independence between 4´-hydroxyflavone and 4´-deoxyflavone accumulation suggests that this specialization of enzyme isoforms observed in *S. baicalensis* is likely present in most other species we analyzed. If a significant number of species we selected relied entirely on promiscuous enzymes equally capable of accepting substrates in both pathways, our MCA should have indicated a correlation between the products of both pathways. Therefore, in addition to the absence of a mechanism allowing for interconversion of substrates, the independence between 4´-hydroxyflavone and 4´-deoxyflavone accumulation we detected here is possibly a result of a divergence in function and specialization of enzyme isoforms, like that described in *S. baicalensis*.

Although the independence we observed between the two pathways throughout the species we analyzed resembled that of *S. baicalensis*, differing organ-specific patterns of accumulation suggest that the regulatory mechanisms controlling expression of flavone biosynthesis genes vary significantly across the genus. From our organ-specific metabolite analysis, we detected a metabolite profile for *S. baicalensis* that matched closely with previous publications (Q. Zhao, Chen, et al., 2016; Q. Zhao, Zhang, et al., 2016). High concentrations of 4´-deoxyflavones accumulated in the roots, and much lower concentrations of 4´-deoxyflavones and 4´-hydroxyflavones accumulated in the stems and leaves. As described by Q. Zhao, Zhang, et al. (2016), this root heavy accumulation of 4´-deoxyflavones is a result of root specific overexpression of several enzymes with activity exclusively, or near exclusively in 4´-deoxyflavone biosynthesis. In direct contrast to the root-favored metabolite profile of *S. baicalensis*, several of the species we selected accumulated higher concentrations of several 4´-deoxyflavones in their leaves as compared to their roots. These species included *S. racemosa*, *S. strigillosa*, *S. dependens,* and *S. suffrutescens*. In the aerial tissues of *S. racemosa S. strigillosa,* and *S. suffrutescens*, we detected only trace amounts of 4´-hydroxyflavones. This finding suggests an upregulation of one or several 4´-deoxyflavone specific biosynthetic genes in the aerial tissues of these species, rather than an upregulation of genes with similar activity in both 4´-hydroxyflavone and 4´-deoxyflavone biosynthesis. Interestingly, in the aerial tissues of *S. dependens*, we detected similar concentrations of both 4´-hydroxyflavones and 4´-deoxyflavones. This result suggests an upregulation of both 4´-deoxyflavone and 4´-hydroxyflavone specific biosynthetic genes, an upregulation of nonspecific enzymes with similar activity in both pathways, or a combination of both of these possibilities.

Despite chrysin being proposed as a common precursor to all 4´-deoxyflavones we analyzed here, our organ-specific profiling results illustrated its striking rarity in the roots of the 13 species we selected. Assuming that there are no alternative pathways for 4´-deoxyflavone synthesis, it appears that very quickly after its formation, chrysin is converted into downstream products, thereby preventing it from accumulating to significant, or even detectable levels. This efficient shuttling and conversion of chrysin suggests that many of the species we studied here utilize a metabolon during 4´-deoxyflavone biosynthesis. A metabolon is an ordered complex of multiple enzymes with activity in the same biosynthetic pathway. It often offers greater catalytic efficiency and control when compared to non-associated, free-floating enzymes (Nakayama et al., 2019). Metabolons acting in flavonoid biosynthesis have been described in multiple diverse plant species, including *Arabidopsis thaliana*, *Oryza sativa*, and *Glycine max* (Burbulis & Winkel-Shirley, 1999; Shih et al., 2008; Waki et al., 2016). Although metabolon formation between enzymes of the core flavonoid pathway (i.e. up to the formation of the first flavanone) has been studied in these and other species, the degree to which metabolons play a role in flavone biosynthesis remains largely unknown. Work by Fujino et al. (2018) in snapdragon (*Antirrhinum majus*) and torenia (*Torenia hybrida*) demonstrated that in addition to catalyzing the first committed step in flavone biosynthesis, FNSII serves to anchor the core flavonoid metabolon to the endoplasmic reticulum in the cells of these two lamiales plants. Our organ-specific profiling results indicate the possibility of a direct or indirect association of FNSII with a F6H, flavone-8-hydroxylase (F8H), or another enzyme able to accept chrysin as a substrate.

From the genome size data we generated and collected from literature, we found genome sizes for the species we analyzed to be vary between 0.35 and 0.54 Gigabase pairs (Gbp). This small size relative to other medicinal plants should be valuable for biotechnology efforts. For reference, sweet wormwood (*Artemisia annua*), known for its biosynthesis of the antimalarial drug artemisinin, has a published genome size of 1.74 Gbp (Shen et al., 2018). Although we found genome sizes to be relatively consistent across the species we analyzed, chromosome number appeared to be more variable . This can partially be explained by polyploidy, as those species which were reported to be tetraploid had slightly higher chromosome numbers as compared to those reported to be diploid. However, chromosome numbers in exclusively diploid species ranged between 18 and 26. Overall, the relatively tight range of genome sizes and wide range of chromosome numbers for the species we analyzed suggests significant variations in genome structure that cannot be explained by polyploidy alone.

During our analysis, several species stood out as valuable targets for further medicinal study. These species included *S. racemosa*, *S. dependens*, *S. wrightii*, and *S. suffrutescens*. *S. racemosa* accumulated concentrations of oroxylin A and its oroxyloside in its leaves that exceeded that in any organ of any other species we tested. This finding is medicinally significant because testing in rat models has demonstrated the neuroprotective effects of oroxylin A, making it a potential target for anti-Alzheimer’s disease drugs (Jeon et al., 2011, 2012). *S. dependens* is notable because of its high accumulation of wogonin and wogonoside in its leaves. Numerous studies have exhibited the usefulness of wogonin in the treatment of osteoarthritis, neurodegenerative diseases, and cancer (Huang et al., 2012; Khan et al., 2017; H. Lee et al., 2003). As this leaf-specific accumulation of 4´-deoxyflavones by both *S. racemosa* and *S. dependens* contrasts with that of *S. baicalensis*, studying these speciescould help uncover the regulatory mechanisms affecting the organ-specificity of the 4´-deoxyflavone pathway in *Scutellaria*. These factors, in addition to their relatively small genome sizes,make *S. racemosa* and *S. dependens* prime targets for biotechnology efforts. However, molecular study and transformation could be complicated by tetraploid nature of *S. dependens*. *S. wrightii* and *S. suffrutescens* are both notable due to their high accumulation of baicalin. Both baicalin and its aglycone form, baicalein, have been demonstrated to have anti-inflammatory, anti-cancer, hepatoprotective, and other medicinal effects (J. Xu et al., 2018; Zhou et al., 2018; Zhu et al., 2016). *S. wrightii* accumulated the majority of its baicalin in its roots, at concentrations more than double that in the roots of *S. baicalensis*. *S. suffrutescens* accumulated relatively equal amounts of baicalin in all three organs we sampled at concentrations which slightly exceeded that in the roots of *S. baicalensis*. Unfortunately, as no genome size, chromosome number, or ploidy level data has been published for these species, it is difficult to evaluate ease of molecular study. However, studying the significant baicalin accumulation of *S. wrightii* and *S. suffrutescens* could provide new insights into baicalin and baicalein biosynthesis.

**Acknowledgments**

**Author contributions**

**Data availability statement**

Chloroplast genome sequences?

**Supporting information**

Additional supporting information may be found online in the Supporting Information section at the end of the article.

Appendix S1. Proposed 4´-hydroxyflavone and 4´-deoxyflavone pathway with glycone structures included. Enzyme names in blue are specific isoforms that have been identified in *S. baicalensis*, and enzyme names in black are general names.

Appendix S2. Herbarium voucher information for all tissue samples used for metabolite measurements.

Appendix S3. Aerial metabolite concentrations measured by High Performance Liquid Chromatography (HPLC) for 76 Scutellaria species. Tissue samples for most species were prepared from herbarium vouchers, but tissue samples for species with a “\*” by their name were prepared from fresh leaf and stem tissue. Data is shown in units of µmol/g fresh weight. Fresh weight of herbarium samples was estimated by multiplying their dry weight by a factor of 10.

Appendix S4. Representative images of 13 species of *Scutellaria* selected for additional metabolite and genome size profiling. Scale bar in bottom left of images represents a length of 5 cm. Images without a scale bar did not have a ruler included in the image. Colored circles next to species names indicate the clade which the species belongs to, as indicated in Fig. 1.

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**Tables**

Table 1. Mean metabolite concentrations ± standard error (n=3) measured by High Performance Liquid Chromatography (HPLC) for 13 Scutellaria species. Tissue samples were prepared from fresh leaf, stem, or root tissues of mature plants. Units are µmol/g fresh weight.

Table 2. Genome size, chromosome number, and ploidy level data for 13 Scutellaria species. Genome sizes for 8 species were measured in this study using flow cytometry. Other genome size, and all chromosome number and ploidy level data was collected from literature. S. wrightii and S. suffrutescens were not included in the flow cytometry procedure, and genome size, chromosome number, nor ploidy level data has been published. Cell colors indicate phylogenetic clade, as shown in Fig. 1.

**Appendices**

List of appendices is provided in supporting information section.

**Figure Legends**

Figure 1. Maximum likelihood phylogenetic tree inferred from 3 chloroplast genome regions for 51 species of Scutellaria and 1 outgroup. The current infrageneric classification system suggested by Paton (1990) is indicated directly to the right of each species’ name. A “Q” indicates that the species is not included in the current infrageneric classification system. To facilitate downstream analysis, the tree is subdivided into 5 color-coded clades based on grouping of species within the tree.

Figure 2. Proposed 4´-hydroxyflavone and 4´-deoxyflavone pathway with aglycones only. Enzyme names in blue are specific isoforms that have been identified in *S. baicalensis*, and enzyme names in black are general names.

Figure 3. Aerial metabolite concentrations measured with High Performance Liquid Chromatography (HPLC) compared to phylogeny for 76 species of *Scutellaria*. (A) Heatmap of collected data. Data is shown in units of µmol/g fresh weight. Fresh weight of herbarium samples was estimated by multiplying their dry weight by a factor of 10. Species for which fresh tissue was used are indicated by an asterisk on the right side of the heatmap. Samples for all other species were prepared from herbarium vouchers. Colored circles next to species names indicate phylogenetic clade, as shown in Fig. 1. An empty circle indicates that the species was not included in the tree from Fig. 1. (B) Multiple Correspondance Analysis (MCA) individual results with overlaid 80% confidence ellipses generated from binarized metabolite data. Each colored circle represent a species, and the color of the circle represents phylogenentic clade, as shown in Fig. 1. The percentage of total variance explained by each principal component is shown next to each axis title. (C) Variable loadings from MCA. Each variable represents the prescence (indicated with “TRUE) or absence (indicated with “FALSE) of a metabolite, and are color-coded according to metabolite class.

Figure 4. Organ-specific metabolite data collected from 13 *Scutellaria* species via High Performance Liquid Chromatography (HPLC). Samples were taken in biological triplicate, and the average concentration of each metabolite calculated. Species on x-axis are ordered based on phylogenetic relationship determined from chloroplast genome data, and colored circles next to species names indicate phylogenetic clade, as shown in Fig. 1. An empty circle indicates that the species was not included in the tree from Fig. 1.