**Title:** An analysis of phylogenetic and phytochemical diversity in *Scutellaria* to identify species with medicinal potential

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*Scutellaria baicalensis* is a medicinal plant whose root extracts have been widely used in Asian medicine for more than 2,000 years. Flavonoids in these extracts possess anti-cancer, antioxidant, antiviral, and neuro-psychologic properties. Because of interest in the medicinal properties of these flavonoids, the reference genome of *S. baicalensis* has been recently completed. Although *S. baicalensis* has been well-studied, the *Scutellaria* genus contains more than 470 other species, the majority of which not analyzed. This study aims to extend the current knowledge of *Scutellaria* by analyzing flavonoid profiles for a large set of species representing the diversity in the genus.Targeted metabolite analysis of fresh and dried samples was completed with High Performance Liquid Chromatography (HPLC) to quantify 15 flavones. A phylogenetic tree of these species was constructed from chloroplast genomic data andusedto identify “medicinal hotspots” – clades of species accumulating high concentrations of medicinally relevant flavones. Based on these results, a subset of species were selected for organ-specific metabolite profiling and genome size analysis. A comparison of phytochemical profiles for these species indicates significant diversity in site and identity of flavone accumulation when compared to *S. baicalensis*. Inconsistences in site of accumulation between the proposed flavonoid biosynthesis pathway for *S. baicalensis* and chemical analysis results imply significant differences in the pathway must exist for several species. Flow cytometry results revealed 7 of the 8 species analyzed have similarly sized genomes as *S. baicalensis*. This similarity in genome size can facilitate the use of the reference genome of *S. baicalensis* as a tool to study genetic data collected from other species. Whole genome sequencing was also performed on 4 species with similarly sized genomes as *S. baicalensis* to evaluate interspecies variation in genome structure. Researchers studying *Scutellaria* can use the results of this work to identify previously uncharacterized species with medicinal potential and target these species for further development. Additionally, the comparative metabolite and phylogenetic analyses included in this study will help researchers to better understand the evolutionary history of the *Scutellaria* genus.

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