ORIGINAL RESEARCH

Comparative Genome Analysis of *Scutellaria baicalensis* and *Scutellaria barbata* Reveals the Evolution of Active Flavonoid Biosynthesis

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Abstract  *Scutellaria baicalensis* (*S. baicalensis*) and *Scutellaria barbata* (*S. barbata*) are common medicinal plants of the Lamiaceae family. Both produce specific flavonoid compounds, including baicalein, scutellarein, norwogonin, and wogonin, as well as their glycosides, which exhibit antioxidant and antitumor activities. Here, we report chromosome-level genome assemblies of *S. baicalensis* and *S. barbata* with quantitative chromosomal variation (2n = 18 and 2n = 26, respectively). The divergence of *S. baicalensis* and *S. barbata* occurred far earlier than previously reported, and a whole-genome duplication (WGD) event was identified. The insertion of long terminal repeat elements after speciation might be responsible for the observed chromosomal expansion and rearrangement. Comparative genome analysis of the congeneric species revealed the species-specific evolution of chrysin and apigenin biosynthetic genes, such as the *S. baicalensis*-specific tandem duplication of genes encoding phenylalanine ammonia lyase and chalcone synthase, and the *S. barbata*-specific duplication of genes encoding 4-CoA ligase. In addition, the paralogous duplication, colinearity, and expression diversity of CYP82D subfamily members revealed the functional divergence of genes encoding flavone hydroxylase between *S. baicalensis* and *S. barbata*. Analyzing
Introduction

Plant-specific flavonoids, including flavones, flavonols, anthocyanins, proanthocyanidins, and isoflavones, play important functions in plants. These functions include flower pigmentation, ultraviolet protection, and symbiotic nitrogen fixation [1–3]. Flavonoid metabolites also have biological and pharmacological activities on human health, including antibacterial and antioxidant functions, and the treatment of cancer, inflammatory, and cardiovascular diseases [3]. The genus Scutellaria, which belongs to the Lamiaceae family, consists of common herbal plants enriched in bioactive flavonoids. Approximately 300–360 Scutellaria species have the characteristic flower form of upper and lower lips [4,5]. Nonetheless, only two Scutellaria species, S. baicalensis and S. barbata, are recorded in the Pharmacopoeia of the People’s Republic of China. The roots of S. baicalensis and dried herbs of S. barbata are the basis of the traditional Chinese medicine (TCM) Huang Qin and Ban Zhi Lian, respectively, which have been used as heat-clearing and detoxifying herbs for thousands of years [6]. The main biologically active compounds in Scutellaria are derivatives of chrysin and apigenin, such as baicalein, scutellarein, and wogonin, as well as their glycosides, which include baicalin, scutellarin, and wogonoside [7–10]. The demonstration that baicalin activates carnitine palmitoyltransferase 1 in the treatment of diet-induced obesity and hepatic steatosis [11,12] has generated extensive interest in the potential antilipemic effect of this compound.

Illuminating the chemodiversity and biosynthesis of the active constituents of Scutellaria will provide a foundation for investigating the use of Huang Qin and Ban Zhi Lian in TCM, and the production of these natural products via synthetic biology [13]. In S. baicalensis, the biosynthetic genes of the root-specific compounds baicalein and wogonin have been functionally identified, providing an important basis for studies of the biosynthesis and regulation of the natural products [14,15]. Recently, the in vivo production of baicalein and scutellarein in Escherichia coli and Saccharomyces cerevisiae was achieved based on the guidance of synthetic biology [16,17]. However, the discovery and optimization of biological components are important limitations to the metabolic engineering of these compounds. Salvia miltiorrhiza (Lamiaceae family) genome has provided useful information on secondary metabolism for the rapid functional identification of biosynthetic and regulatory genes [18–23]. In contrast, the genomes of the Scutellaria genus remain unclear, and the reliance on transcriptome data from short-read sequencing has restricted gene discovery and analyses of genome evolution, including studies of gene family expansion and contraction, evolution of biosynthetic genes, and identification of regulatory elements [24].

Morphological differences are present at the macroscopic level between S. baicalensis and S. barbata. Differentiation of these species are characterized mainly by the fleshy rhizome and branched stem of S. baicalensis and the fibrous root and erect stem of S. barbata (Figure 1A). The active compounds baicalein, wogonin, and scutellarein are differentially distributed in the roots and aerial parts of S. baicalensis and S. barbata. Here, we performed de novo sequencing and assembly of the S. baicalensis and S. barbata genomes using a long-read strategy and high-through chromosome conformation capture (Hi-C) technology. The chromosome-level genomes of S. baicalensis and S. barbata revealed their divergence time, chromosomal rearrangement and expansion, whole-genome duplication (WGD), and evolutionary diversity of flavonoid biosynthesis. The data provided important insights for the molecular assisted breeding of important TCM resources, genome editing, and increased understanding of the molecular mechanisms of the chemodiversity of active compounds.

Results and discussion

High-quality assembly of two Scutellaria genomes

The size of the S. baicalensis genome was predicted to be 440.2 ± 10 Mb and 441.9 Mb by using the flow cytometry and the 21 k-mer distribution analysis (approximately 0.96% heterozygosity), respectively (Figure S1). The genome survey of S. barbata revealed a 404.6 Mb genome size and 0.28% heterozygosity via the 21 k-mer distribution analysis (Figure S1). Third-generation sequencing platforms, including PacBio and Oxford Nanopore technologies, have been confirmed to have important advantages in de novo assembly and in processing data with complex structural variation due to high heterozygosity and repeat content [25–27]. Thus, 52.1 Gb Oxford Nanopore technology (ONT) reads (~120×) with an N50 of 16.3 kb from S. baicalensis and 51.7 Gb single molecule, real-time sequencing (SMRT) reads from the PacBio platform (~130×) with an N50 of 9.8 kb from S. barbata were produced to assemble highly contiguous genomes (Table S1). The low-quality long reads were further corrected and trimmed to yield 20.2 Gb ONT reads with an N50 of 35.5 kb from S. baicalensis and 18.0 Gb SMRT reads with an N50 of 15.3 kb from S. barbata using the Canu pipeline.

The contiguous assembly of the S. baicalensis and S. barbata genomes was performed using the optimized SMARTdenovo and × Pilon polishing (50× Illumina reads) packages. For S. baicalensis, the contig-level genome assembly, which was 377.0 Mb in length with an N50 of 2.1 Mb and a maximum contig length of 9.7 Mb, covered 85.3% of the estimated genome size (Table S2). The S. baicalensis genome identified 91.5% of the complete Benchmarking Universal Single-Copy Orthologs (BUSCO) gene models and had an 88.7% DNA mapping rate, suggesting a high-quality genome assembly. For S. barbata, the contiguous contig assembly of 353.0 Mb with an N50 of 2.5 Mb and a maximum contig of 10.5 Mb covered 87.2% of the predicted genome size (Table S2). The S. barbata genome identified 93.0% of the complete BUSCO gene models and had a 95.0% DNA mapping rate. The high-quality genome assemblies of S. baicalensis and S. barbata showed the great advantage of single molecule
sequencing, with assembly metrics that were far better than those of other reported genomes of Lamiaceae species, i.e., *S. miltiorrhiza* [22] and *Mentha longifolia* [28].

Given the assembly continuity, with a contig N50 of over 2 Mb for the *S. baikalensis* and *S. barbata* genomes, Hi-C technology was applied to construct chromosome-level genomes [29]. In total, 99.8% and 98.8% of the assembled *S. baikalensis* and *S. barbata* contigs were corrected and anchored to 9 and 13 pseudochromosomes (2n = 18 for *S. baikalensis*, 2n = 26 for *S. barbata*) using a Hi-C interaction matrix with N50 values of 40.8 Mb and 23.7 Mb, respectively. The strong signal along the diagonal of interactions between proximal regions suggested the high-quality of the Hi-C assemblies for the *S. baikalensis* and *S. barbata* genomes (Figure S2).

The *S. baikalensis* genome comprised 33,414 protein-coding genes and 2833 noncoding RNAs (ncRNA). For the *S. barbata* genome, 41,697 genes and 1768 ncRNAs were annotated (Table S3). Consistent with the genome assembly quality assessment, orthologs of 93.2% and 94.3% of the eukaryotic BUSCOs were identified in the *S. baikalensis* and *S. barbata* gene sets, respectively, suggesting the completeness of the genome annotation (Table S3). The gene-based synteny between *S. baikalensis* and *S. barbata* showed chromosome number variation and structural rearrangement (Figure 1B, Figure S3, Table S4). In addition, the alignment at the DNA sequence level also showed the large-scale structural variations between the *S. baikalensis* and *S. barbata* genomes (Figure S4).

### Chromosome rearrangements and expansion after speciation

Transposable elements (TEs) accounted for approximately 55.2% (208,004,279) and 53.5% (188,790,851) of the *S. baikalensis* and *S. barbata* genomes, respectively (Tables S5 and S6). Furthermore, 57.6% and 59.9% of these TEs were long terminal repeat (LTR) elements, respectively. We identified 1225 and 1654 full-length LTR elements, including Gypsy (342 and 310) and Copia (354 and 618) elements, in the *S. baikalensis* and *S. barbata* genomes, respectively (Table S7). However, there were differences in the insertion time of LTR elements, i.e., the LTRs (1.41 million years ago; MYA) in *S. baikalensis* are more ancient than those in *S. barbata* (0.88 MYA), assuming a mutation rate of \( \mu = 1.3 \times 10^{-8} \) (per bp per year) (Figure S5, Table S7). The recent insertion and activation of LTRs might be key factors in the generation of chromosome rearrangements and expansion of *S. barbata* [30,31]. The ribosomal RNAs (rRNAs) and simple sequence

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**Figure 1** Genome colinearity reveals the chromosome rearrangement in *Scutellaria*.<br>
**A.** Morphological differences between the aerial parts of *S. baikalensis* and *S. barbata*.<br>
**B.** Comparison of nucleotide sequences of 9 *S. baikalensis* chromosomes (Sbai1–Sbai9; gray bars) and 13 *S. barbata* chromosomes (Sbar1–Sbar13; colored bars). Mapped regions with >90% sequence similarity over 5 kb between the two species were linked. The red and black dots represent up-regulated genes (Log2 FC > 1, FPKM > 10) in the root tissue compared to other tissues (stem, leaf, and flower) in *S. baikalensis* and *S. barbata*, respectively.<br>
**C.** Content distribution of flavone compounds in different tissues of *S. baikalensis* and *S. barbata*, including root, stem, leave, and flower, determined by UPLC. FC, fold change; FPKM, fragments per kilobase of exon model per million reads mapped; UPLC, ultraperformance liquid chromatography; R, root; S, stem; L, leaf; F, flower.
Shared WGD events in Lamiaceae

Conserved sequences, including orthologs and paralogs, can be used to deduce evolutionary history based on whole-genome comparisons. Here, orthologous groups of amino acid sequences from 11 angiosperms were identified, yielding a total of 19,479 orthologous groups that covered 291,192 genes. Among these, 120,459 genes clustering in 6837 groups were conserved in all examined plants. Computational analysis of gene family evolution (CAFE) showed that 1180 and 1853 gene families were expanded in the S. baicalensis and S. barbata lineages, respectively, while 1599 and 1632 gene families were contracted, respectively (Figure S8, Table S10). Functional exploration of Scutellaria-specific genes indicated that domains related to secondary metabolic biosynthesis, such as transcription factors, cytochrome P450s, and O-methyltransferase were markedly enriched.

In addition, 235 single-copy genes were identified in all tested plants. They were used to construct a phylogenetic tree, which indicated that these two Scutellaria species were most closely related to S. miltiorrhiza with an estimated divergence time of 41.01 MYA. S. baicalensis and S. barbata were grouped into one branch, with an estimated divergence time of approximately 13.28 MYA (Figure 2A). The phylogenetic tree also supported the close relationship between Lamiaceae (S. baicalensis, S. barbata, and S. miltiorrhiza) and Pedaliaceae (Sesamum indicum) with a divergence time of approximately 49.90 MYA (Figure 2A) [35]. Previous research reported that the divergence time of S. baicalensis and S. barbata based on the matK and CHS (chalcone synthase) genes was approximately 3.35 MYA [36]. However, a genome-wide analysis identified 8 and 3 CHS genes in S. baicalensis and S. barbata, respectively. The expansion and evolution of CHS negatively impacted the estimation of diversification history between these Scutellaria species.

Based on sequence homology, 17,265 orthologous gene pairs with synteny were identified between the S. baicalensis and S. barbata genomes. The distribution of synonymous substitution rates (Ks) peaked at approximately 0.16, representing the speciation time of S. baicalensis and S. barbata (Figure 2B, Table S11). The mean Ks values of orthologous gene pairs with synteny and the divergence time among S. baicalensis, S. barbata, S. miltiorrhiza, S. indicum, and Vitis vinifera [37] revealed the estimated synonymous substitutions per site per year as 1.30 × 10^{-8} for the test species (Table S11). In total, 7812, 7168, 6984, and 7711 paralogous gene pairs were identified, and the distribution of Ks values peaked at approximately 0.87, 0.86, 1.02, and 0.67 in S. baicalensis, S. barbata, S. miltiorrhiza, and S. indicum, respectively (Figure 2B, Table S11). Based on the phylogenetic analysis, the WGD event occurred prior to the divergence of S. baicalensis, S. barbata, S. miltiorrhiza, and S. indicum. The divergence time of the Lamiaceae and Pedaliaceae shared WGD event was determined to be approximately 46.24–60.71 MYA (Table S11). The distribution of the Ks values of paralogous genes showed that no WGD events have occurred since the divergence of S. miltiorrhiza, S. baicalensis, and S. barbata. Comparison of the S. baicalensis and S. barbata genomes with an ancestral eudicot karyotype (AEK) genome [38] and with the V. vinifera genome, also supported the structural rearrangement between the S. baicalensis and S. barbata genomes, and the shared WGD event after whole-genome triplication (WGT)-γ event of V. vinifera (Figure 2C, Figure S9). The genome synteny analysis indicated two copies of syntenic blocks from Lamiaceae and Pedaliaceae species per corresponding V. vinifera block, which confirmed the recent WGD event before the divergence of S. baicalensis, S. barbata, and S. indicum (Figure S10).

Organ-specific localization of bioactive compounds

Baicalein, scutellarein, norwogonin, wogonin, and their glycosides (baicalin, scutellarin, norwogonoside, and wogonoside) are the main bioactive compounds in S. baicalensis and S. barbata. We collected samples from the root, stem, leaf, and flower tissues of S. baicalensis and S. barbata to detect the accumulation of active compounds. Baicalein, norwogonin, wogonin, baicalin, norwogonoside, and wogonoside accumulation of active compounds in the roots of these species (Figure 1C, Figure S11, Table S12), providing a potential basis for the co-expression analysis of biosynthetic genes [23].
Among them, 31.5% (12,320) and 40.6% (19,153) of the transcriptome were not expressed (FPKM < 1) in any of the tested tissues. Based on the scripts were not expressed (FPKM < 1) in any of the tested tissues. Based on the expression levels of 3421 genes and their orthologous genes from clusters 8, 20, 32, 33, 34, 39, and 47 in the roots of *Scutellaria* species. *S. baikalensis* and *S. barbata*. Speciation time was estimated based on the reported divergence time for *Arabidopsis thaliana* (98–117 MYA). The phylogenetic tree based on the concatenated method using 235 single-copy orthologous genes from 11 angiosperms was constructed. The basal angiosperm *Amborella trichopoda* was chosen as the outgroup. The red branches represent two *Scutellaria* species, *S. baikalensis* and *S. barbata*. The orange ovals represent the reported WGT events. The purple and red ovals represent the reported WGD events and the newly identified WGD event in this study, respectively. The reported WGT/WGD events represent the WGT/WGD events identified in previous studies, including the WGT–WGD events in core eudicots, WGT event in *Salvia miltiorrhiza*, and WGD events in *Sesamum indicum*, *A. thaliana*, *P. trichocarpa*, *Oryza sativa*, and *Brachypodium distachyon*. The gray box indicates the shared WGD event in *S. baikalensis*, *S. barbata*, *S. miltiorrhiza*, *S. indicum*, and *V. vinifera*. The density of paralogs and orthologs of syntenic blocks for the paralogs and orthologs of *S. baikalensis*, *S. barbata*, *S. miltiorrhiza*, *S. indicum*, and *V. vinifera*. The gray box indicates the shared WGD event in *S. baikalensis*, *S. barbata*, *S. miltiorrhiza*, *S. indicum*, and *V. vinifera*. The comparison with AEK chromosomes. The syntenic AEK blocks are painted onto the AEK chromosomes separately. MYA, million years ago; WGT, whole-genome triplication; WGD, whole-genome duplication; AEK, ancestral eudicot karyotype.

Transcriptome analysis of these four tissues from *S. baikalensis* and *S. barbata* included calculation of the fragments per kilobase of exon model per million reads mapped (FPKM) values of 39,121 and 47,200 genes, respectively. Among them, 31.5% (12,320) and 40.6% (19,153) of the transcripts were not expressed (FPKM < 1) in any of the tested tissues. Based on k-means clustering, all the expressed genes from *S. baikalensis* and *S. barbata* were classified into 48 clusters (Figures S12 and S13). The expression levels of 3421 genes from clusters 8, 20, 32, 33, 34, 39, and 47 in *S. baikalensis*, and 3675 genes from clusters 2, 4, 21, 25, 27, 31, and 40 in *S. barbata* were higher in the roots than in the other organs. The biosynthetic genes involved in the synthesis of flavonoids specific flavones and glycosides, containing genes encoding the chalcone synthase, the chalcone isomerase, and the flavone synthase. The main active compounds in the medicinal plants *S. baikalensis* and *S. barbata* are flavonoids. The chrysin biosynthetic genes in *S. baikalensis* encoding 4-CoA ligase (4CL), CHS, chalcone isomerase (CHI), and CYP700, O-methyltransferase, glycosyltransferase, and glycosyl hydrolases were enriched in the roots of *S. baikalensis* and *S. barbata* (Tables S13 and S14).

Conserved evolution of the chrysin and apigenin biosynthesis in *Scutellaria*

The main active compounds in the medicinal plants *S. baikalensis* and *S. barbata* are flavonoids. The chrysin biosynthetic genes in *S. baikalensis* encoding 4-CoA ligase (4CL), CHS, chalcone isomerase (CHI), and flavone synthase (FNSII) have been cloned and functionally identified [14]. However, the gene locations, gene numbers, and evolution of this pathway in the *S. baikalensis* and *S. barbata* genomes remain unclear. Here, we identified the same number of chrysin and apigenin biosynthetic genes in the *S. baikalensis* and *S. barbata* genomes and determined the expression levels of these genes, including 4CL (9 and 14), CHS (8 and 3), CHI (1 and 1), and FNSII (3 and 3), in different tissues (Figure 3A and B, Tables S15 and S16). Eighteen orthologous gene pairs were found between the *S. baikalensis* and *S. barbata*
Scutellarein

S. baicalensis

SbaPAL

thetic pathways indicated that the specific expansion of the Ks species. The might have occurred after the separation of these found, suggesting that expansion via tandem duplication Sbar4CLL9-2 S. barbata (Figure 3C, Figure S14, Table S17).

S. baicalensis were expanded compared to those in genomes, and the Ka/Ks value (average 0.13) indicated purifying selection on flavone biosynthesis during evolution [39] (Figure 3B, Table S17). The PAL and CHS gene numbers in S. baicalensis were expanded compared to those in S. barbata. Conversely, a duplication event of 4CL genes in S. barbata was found, suggesting that expansion via tandem duplication might have occurred after the separation of these Scutellaria species. The Ks values of 18 orthologous gene pairs of S. baicalensis and S. barbata in the chrysin and apigenin biosynthetic pathways indicated that the specific expansion of the SbaiPAL (SbaiPAL1 and SbaiPAL2), SbaiCHS (SbaiCHS2, SbaiCHS3, SbaiCHS4, and SbaiCHS5), and Sbar4CL (Sbar4CL1-1, Sbar4CL1-2, Sbar4CL1-3, Sbar4CL1-4, Sbar4CLL9-2, and Sbar4CLL9-3) genes had occurred via tandem duplication, after the speciation of S. baicalensis and S. barbata (Figure 3C, Figure S14, Table S17).

Sbai4CLL7 and SbaiCHS1 are reportedly related to the biosynthesis of specific 4’-deoxyflavones with cinnamic acid as a substrate in S. baicalensis [14]. Compared to S. miltiorrhiza, the 4CLL7 genes from the Scutellaria genus showed gene expansion, and the gene duplication of Sbai4CLL7-1 and Sbai4CLL7-2 occurred before the speciation of S. baicalensis and S. barbata (Figure S13). Sbai4CLL7-1 and Sbar4CLL7-1 were not expressed in the tested transcriptomes, and the duplication of the Scutellaria-specific 4CLL7-2 allowed the evolution of substrate preferences for the catalysis of cinnamic acid. The initial step and central hub for flavone biosynthesis is the catalysis of CHS. Hence, the expression of CHS is required for the production of flavonoids, isoflavonoids, and other metabolites in plants [40]. Here, we also detected the highest expression levels of SbaiCHS1 and SbarCHS1 in all the tested samples. However, a recent expansion of CHS genes

Figure 3  Conserved flavonoid biosynthesis and species-specific gene expansion in Scutellaria

A. Genes related to the biosynthesis of flavones and their glycosides. The red ovals represent the hydroxyl groups that can be glucosylated by UGT. The dashed box means the glycoside. B. The expression profile and orthologous gene pairs of flavone biosynthetic genes in S. baicalensis and S. barbata. C. Tandem duplication and phylogenetic analysis of CHS genes. The phylogenetic tree was constructed based on maximum likelihood method. PAL, phenylalanine ammonia lyase; C4H, cinnamate 4-hydroxylase; 4CL, 4-CoA ligase; CHS, chalcone synthase; CHI, chalcone isomerase; FNSII, flavone synthase II; F6H, flavone 6-hydroxylase; F8H, flavone 8-hydroxylase; UGT, UDP-glycosyltransferase; F8OMT, flavone 8-O-methyltransferase.
has occurred in *S. baicalensis*, and 4 additional paralogs of *ShaiCHS1* (*Shai7C10721*) were observed in chr7. Duplications of the *ShaiCHS2*, *ShaiCHS3*, *ShaiCHS4*, and *ShaiCHS5* genes occurred after the speciation of *S. baicalensis* and *S. barbata* (Figure 3C). The nucleotide and amino acid sequences of *ShaiCHS2* and *ShaiCHS3* were identical, but *ShaiCHS5* contained a variant K316 deletion. The divergence of *ShaiCHS1* and *SharCHS1* occurred before the separation of *S. miltiorrhiza* and the *Scutellaria* species, suggesting a conserved function of CHS in flavone biosynthesis. In addition, the tandemly duplicated *ShaiCHS2S* genes were more highly expressed in the root of *S. baicalensis* than in other tissues (Figure 3B), suggesting that their species-specific evolution might be related to the biosynthesis of flavones and their glycosides, which are enriched in root.

C4H is responsible for the biosynthesis of coumaroyl-CoA, which might be the restrictive precursor of the 4'-hydroxyl group involved in scutellarein biosynthesis. *ShaiC4H1* and *SharC4H1* were highly expressed in the stems, leaves, and flowers of *S. baicalensis* and *S. barbata* (Figure 3B, Figure S14). The high expression levels of these genes were positively correlated with the distribution of scutellarine, which is biosynthesized in the aerial parts of *S. baicalensis* and *S. barbata* (Figure 1C).

*ShaiFNSII2* has been reported to catalyze the formation of chrysin in *S. baicalensis* [14], and the coding gene was highly expressed in the root and stem. Its ortholog, *SharFNSII2*, was also highly expressed in the root of *S. barbata*. A genome colinearity analysis identified 566 orthologous gene pairs covering a region approximately 6 Mb in length across chr3 of *S. baicalensis* and chr13 of *S. barbata*, including the tandem duplication of *ShaiFNSII1–ShaiFNSII2* and *SharFNSII1–SharFNSII2*. This duplication occurred before the speciation of *S. baicalensis* and *S. barbata* (Figure S14). The majority of the FNSII region (approximately 85%) in *S. baicalensis* and *S. barbata* was assigned to the A compartment, indicating high transcriptional activity. The genome syntenies of the FNSII region between *S. baicalensis* and *S. barbata* suggested the conserved evolution of flavone synthase.

Functional divergence of flavone hydroxylase genes between *S. baicalensis* and *S. barbata*

CYP450 superfamily members, such as C4H (*CYP73A* family), FNSII (*CYP93B* family), flavone 6-hydroxylase (*F6H*, *CYP82D* family), and flavone 8-hydroxylase (*F8H*, *CYP82D* family), perform key modifications in flavone biosynthesis. *ShaiCYP82D1* has been reported to have 6-hydroxylase activity on chrysin and apigenin to produce baicalein and scutellarein, respectively, and *ShaiCYP82D2* can catalyze chrysin to norwogonin in *S. baicalensis* [15] (Figure S15). Here, we identified 418 and 398 CYP450 gene members, and 17 and 24 physical clusters of CYP450s (5 gene clusters per 500 kb) in the *S. baicalensis* and *S. barbata* genomes, respectively (Figures S16 and S17), suggesting a high frequency of CYP gene tandem duplication. Among them, 18 CYP82D members containing *ShaiCYP82D1–9* and *SharCYP82D1–9* were identified in the *S. baicalensis* and *S. barbata* genomes. These genes might be responsible for the hydroxylation of chrysin and apigenin (Table S18). Consistent with a previous report, high expression of *ShaiCYP82D1* and *SharCYP82D2* in the root of *S. baicalensi-
We reported two chromosome-level genomes of the medicinal plants *S. baicalensis* and *S. barbata* through the combination of second-generation sequencing (Illumina platform), third-generation sequencing (PacBio and Oxford Nanopore platforms), and Hi-C technologies. This study confirmed and traced the divergence time of *S. baicalensis* and *S. barbata*, which occurred at 13.28 MYA, far earlier than previously reported [36]. Comparative genomic analysis revealed similar TE proportions in the *S. baicalensis* and *S. barbata* genomes, while the recent LTR insertion in *S. barbata* might be an important factor resulting in chromosomal rearrangement and expansion. A WGD event (approximately 42.64–60.71 MYA) shared among *S. baicalensis*, *S. barbata*, *S. miltiorrhiza*, and *S. indicum*. The tandem duplication of paralogs after the speciation of *S. baicalensis* and *S. barbata* might be the most important contributor to the divergent evolution of flavonoid biosynthetic gene families, such as *PAL*, *4CL*, *CHS*, *F6H*, and *F8H*. A determination of the distribution of flavone content and transcriptome analysis supported the functional divergence of flavonoid biosynthetic genes between *S. baicalensis* and *S. barbata*. The two high-quality genomes reported in this study will enrich genome research in the Lamiaceae and provide important insights for studies of breeding, evolution, chemodiversity, and genome editing.

**Materials and methods**

**Plant materials**

*S. baicalensis* and *S. barbata* plants were cultivated in the experimental field (40° N and 116° E) of the Institute of Medicinal Plant Development, Chinese Academy of Medical
Sciences & Peking Union Medical College, Beijing, China. Four independent tissues (root, stem, leaf, and flower) from *S. baicalensis* and *S. barbata* were extracted in three replicates. These tissues were used separately for the measurement of active compounds and RNA-seq. High-quality DNA extracted from young leaves was used to construct libraries for Illumina, ONT, and Sequel sequencing.

**Long-read sequencing and assemblies**

The high-molecular-weight (HMW) genomic DNA of *S. baicalensis* and *S. barbata* was extracted as described for megabase-sized DNA preparation [41]. HMW genomic DNA fragments (>20 kb) were selected using BluePippin. Long-read libraries were constructed following the protocols for the ONT (https://nanoporetech.com/) and PacBio Sequel platforms (https://www.pacb.com/). The ONT reads of *S. baicalensis* were generated using the ONT GridION X5 platform, and the library of *S. barbata* was sequenced using the Sequel platform. The raw ONT and SMRT reads were filtered via MinKNOW and SMRT Link, respectively. First, Canu (v1.7) was used to correct and trim the long reads from the ONT and Sequel platforms with the default parameters [42]. The corrected and trimmed ONT and SMRT reads were assembled using SMARTdenovo (https://github.com/ruanjue/smartdenovo). Finally, Illumina short reads were used to polish the assembled contigs three times using Pilon (v1.22).

The quality of the genome assembly was estimated by a search using BUSCO (v2.0) [43] and by mapping Illumina reads from the DNA and RNA libraries to the assembled genomes.

**Chromosome construction using Hi-C**

Young leaves from *S. baicalensis* and *S. barbata* were fixed and crosslinked, and Hi-C libraries were constructed and sequenced using Illumina as previously described [32,33]. The short reads were mapped to the assembled genome using BWA [44], and the valid interaction pairs were selected using HiC-Pro [45]. The draft assemblies of *S. baicalensis* and *S. barbata* were anchored to chromosomes (2n = 18 and 2n = 26, respectively) using LACHESIS with the following parameters: cluster min re sites = 62, cluster max link density = 2, cluster noninformative ratio = 2, order min n res in turn = 53, order min n res in shreds = 52 [29].

**Genome annotation**

The RepeatModeler (v1.0.9) package, including RECON and RepeatScout, was used to identify and classify the repeat elements of the *S. baicalensis* and *S. barbata* genomes. The repeat elements were then masked by RepeatMasker (v4.0.6). The long terminal repeat retrotransposons (LTR-RTs) in *S. baicalensis* and *S. barbata* were identified using LTR_Finder (v1.0.6) and LTR_retriever. Twenty-four samples from a total of eight different *S. baicalensis* and *S. barbata* tissues (root, stem, leaf, and flower) were subjected to RNA-seq using the Illumina NovaSeq platform. The clean reads from *S. baicalensis* and *S. barbata* were de novo assembled using Trinity (v2.2.0), and the coding regions in the assembled transcripts were predicted using TransDecoder (v2.1.0). The gene annotation of the masked *S. baicalensis* and *S. barbata* genomes was *ab initio* predicted using the MAKER (v2.31.9) pipeline, integrating the assembled transcripts and protein sequences from *S. baicalensis*, *S. barbata*, and *Arabidopsis thaliana* [46]. Non-coding RNAs and miRNAs were annotated by alignment to the Rfam and miRNA databases using INFERNAL (v1.1.2) and BLASTN, respectively. RNA-seq reads from different *S. baicalensis* and *S. barbata* tissues were mapped to the masked genome using HISAT2 (v2.0.5), and the different expression levels of the annotated genes were calculated using Cufflinks (v2.2.1) [47].

**Genome evolution analysis**

The full amino acid sequences of *S. baicalensis*, *S. barbata*, and nine other angiosperms were aligned to orthologous groups using OrthoFinder [48]. The basal angiosperm *Amborella trichopoda* was chosen as the outgroup. Single-copy genes were used to construct a phylogenetic tree using the RAxML package with PROTGAMMAJTT model and 1000 replicates (v8.1.13). The divergence time among 11 plants was predicted using r8s program based on the estimated divergence time *A. trichopoda–V. vinifera* (173–199 MYA) and *Populus trichocarpa–A. thaliana* (98–117 MYA). According to the phylogenetic analysis and divergence time, expansion and contraction of the gene families were identified using CAFE (v3.1) [49]. The paralogous and orthologous gene pairs from *S. baicalensis*, *S. barbata*, and *S. miltiorrhiza* were identified, and the *Ka*, *Ks*, and Ka/Ks values of *S. baicalensis–S. baicalensis*, *S. barbata–S. barbata*, *S. miltiorrhiza–S. miltiorrhiza*, *S. baicalensis–S. miltiorrhiza*, *S. baicalensis–S. barbata*, and *S. barbata–S. miltiorrhiza* were calculated using the SynMap2 and DAGchainer method of the CoGE Comparative Genomics Platform (https://genomesevolution.org/coge/). The detection of synteny and colinearity among *S. baicalensis*, *S. barbata*, and *S. miltiorrhiza* was performed using MCscan X(v1.1) [50]. The WGT–γ event in core eudicots, WGT event in *S. tuberosum*, and WGD events in *S. indicum*, *A. thaliana*, *P. trichocarpa*, *Oryza sativa*, and *Brachypodium distachyon* [51] were marked in our phylogenetic tree.

**Identification of gene families related to flavone biosynthesis**

The protein sequences of the *PAL*, *4CL*, *C4H*, *CHS*, *CHI*, and *FNSII* gene family members in *A. thaliana* were downloaded from the TAIR database, and those for *F6H* and *F8H* in *S. baicalensis* were obtained from a previous study [15]. These sequences were searched against the *S. baicalensis* and *S. barbata* protein sequences using BLASTP with an E value cutoff of 1E–10. The conserved domains of the protein sequences of candidate genes were further searched in the Pfam database using hidden Markov models [52]. Full-length protein sequences were used to construct phylogenetic trees using the maximum likelihood method with the Jones-Taylor-Thornton model and 1000 bootstrap replicates [53]. A detailed description of some materials and methods used is provided in the supplementary methods and results.
Data availability

The raw sequence data reported in this paper have been deposited in the Genome Sequence Archive [54] in the National Genomics Data Center, Beijing Institute of Genomics, Chinese Academy of Sciences / China National Center for Bioinformation (GSA: CRA001730) that are publicly accessible at http://bigd.big.ac.cn/hsa. The assembled genomes and gene structures were deposited to CoGe (https://genomevolution.org/coge/) with ID 54175 for Scutellaria baicalensis and ID 54176 for Scutellaria barbata. The assembled genomes and gene structures have also been deposited in the Genome Warehouse (GWHAOT0000000000 for S. baicalensis and GWHAOTP0000000000 for S. barbata), which are publicly accessible at https://bigd.big.ac.cn/gwh.

CRediT author statement

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Competing interests

The authors have declared no competing interests.

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Supplementary material

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References

[1] Winkel-Shirley B. Flavonoid biosynthesis. A colorful model for genetics, biochemistry, cell biology, and biotechnology. Plant Physiol 2001;126:485–93.
[2] Winkel-Shirley B. Biosynthesis of flavonoids and effects of stress. Curr Opin Plant Biol 2002;5:218–23.
[3] Grotewold E. The genetics and biochemistry of floral pigments. Annu Rev Plant Biol 2006;57:761–80.
[4] Shang XF, He XR, He XY, Li MX, Zhang RX, Fan PC, et al. The genus Scutellaria an ethnopharmaceutical and phytochemical review. J Ethnopharmacol 2010;128:279–313.
[5] Grzegorczyk-Karolak I, Wiktorek-Smagur A, Hnatuszko-Konka K. An untapped resource in the spotlight of medicinal biotechnology: the genus Scutellaria. Curr Pharm Biotechnol 2018;19:358–71.
[6] Chinese Pharmacopoeia Commission. Pharmacopoeia of the People’s Republic of China. Beijing, China: China Medical Science Press; 2015.
[7] Zhang Z, Lian XY, Li S, Stringer JL. Characterization of chemical ingredients and anticonvulsant activity of American skullcap (Scutellaria lateriflora). Phytomedicine 2009;16:485–93.
[8] Qiao X, Li R, Song W, Miao WJ, Liu J, Chen HB, et al. A targeted strategy to analyze untargeted mass spectral data: rapid chemical profiling of Scutellaria baicalensis using ultra-high performance liquid chromatography coupled with hybrid quadrupole orbitrap mass spectrometry and key ion filtering. J Chromatogr A 2016;1441:83–95.
[9] Yan BF, Xu WJ, Su SL, Zhu SQ, Zhu ZH, Zeng HT, et al. Comparative analysis of 15 chemical constituents in Scutellaria baicalensis stem-leaf from different regions in China by ultra-high performance liquid chromatography with triple quadrupole tandem mass spectrometry. J Sep Sci 2017;40:3570–81.
[10] Zhao Q, Chen XY, Martin C. Scutellaria baicalensis, the golden herb from the garden of Chinese medicinal plants. Sci Bull 2016;61:1391–8.
[11] Dai JY, Liang K, Zhao S, Jia WT, Liu Y, Wu HK, et al. Chemoproteomics reveals baicalin activates hepatic CPT1 to ameliorate diet-induced obesity and hepatic steatosis. Proc Natl Acad Sci U S A 2018;115:E5896–905.
[12] Guo HX, Liu DH, Ma Y, Liu JF, Wang Y, Du ZY, et al. Long-term baicalin administration ameliorates metabolic disorders and hepatic steatosis in rats given a high-fat diet. Acta Pharmacol Sin 2009;30:1505–12.
[13] Chen SL, Song JY, Sun C, Xu J, Zhu YJ, Verpoorte R, et al. Herbal genomics: examining the biology of traditional medicines. Science 2015;347:227–8.
[14] Zhao Q, Zhang Y, Wang G, Hill L, Weng JK, Chen XY, et al. A specialized flavone biosynthetic pathway has evolved in the medicinal plant, Scutellaria baicalensis. Sci Adv 2016;2:e1501780.
[15] Zhao Q, Cui MY, Levsh O, Yang D, Liu J, Li J, et al. Two CYP82D enzymes function as flavone hydroxylases in the biosynthesis of root-specific 4-deoxyflavones in Scutellaria baicalensis. Mol Plant 2018;11:135–48.
[16] Liu XN, Cheng J, Zhang GH, Ding WT, Duan LJ, Yang J, et al. Engineering yeast for the production of breviscapine by genomic analysis and synthetic biology approaches. Nat Commun 2018;9:448.
[17] Li JH, Tian CF, Xia YH, Mutanda I, Wang KB, Wang Y. Production of plant-specific flavones baicalin and scutellarein in an engineered E. coli from available phenylalanine and tyrosine. Metab Eng 2019;52:124–33.
[18] Xu ZC, Song JY. The 2-oxoglutarate-dependent dioxygenase superfamily participates in tanshinone production in Salvia miltiorrhiza. J Exp Bot 2017;68:2299–308.
[19] Cao WZ, Wang Y, Shi M, Hao XL, Zhao WW, Wang Y, et al. Transcription factor SmWRKY1 positively promotes the biosyn-
thesis of tanshinones in *Salvia miltiorrhiza*. Front Plant Sci 2018;9:554.

[20] Huang Q, Sun MH, Yuan TP, Wang Y, Shi M, Lu SJ, et al. The AP2/ERF transcription factor SmERF11L1 regulates the biosynthesis of tanshinones and phenolic acids in *Salvia miltiorrhiza*. Food Chem 2019;274:368–75.

[21] Sun MH, Shi M, Wang Y, Huang Q, Yuan TP, Wang Q, et al. The biosynthesis of phenolic acids is positively regulated by the IA-responsive transcription factor ERF115 in *Salvia miltiorrhiza*. J Exp Bot 2019;70:243–54.

[22] Xu HB, Song JY, Luo HM, Zhang YJ, Li QS, Zhu YJ, et al. Analysis of the genome sequence of the medicinal plant *Salvia miltiorrhiza*. Mol Plant 2016;9:949–52.

[23] Xu ZC, Peters RJ, Weirather J, Luo HM, Liao BS, Zhang X, et al. Full-length transcriptome sequences and splice variants obtained by a combination of sequencing platforms applied to different root tissues of *Salvia miltiorrhiza* and tanshinone biosynthesis. Plant J 2015;82:951–61.

[24] Xin TY, Zhang Y, Pu XD, Gao RR, Xu ZC, Song JY. Trends in herbogenomics. Sci China Life Sci 2019;62:288–308.

[25] Xu ZC, Xin TY, Bartels D, Li Y, Gu WC, Yao H, et al. Genome analysis of the ancient tracheophyte *Selaginella tamariscina* reveals evolutionary features relevant to the acquisition of desiccation tolerance. Plant Mol Biol 2018;118:983–94.

[26] Schmidt MH, Vogel A, Denton AK, Istance B, Wormit A, van de Geest H, et al. De novo assembly of a new *Solanium pennelli* accession using nanopore sequencing. Plant Cell 2017;29:2336–48.

[27] Guo L, Winzer T, Yang XJ, Li Y, Ning ZM, He ZS, et al. The opium poppy genome and morpholin production. Science 2018;362:343–7.

[28] Vining KJ, Johnson SR, Ahkami A, Lange I, Parrish AN, Trapp AA, et al. Draft genome sequence of *Mentha longifolia* and development of resources for mint cultivar improvement. Mol Plant 2017;10:323–39.

[29] Burton JN, Adey A, Patwardhan RP, Qiu R, Kitman JO, Shendure J. Chromosome-scale scaffolding of *de novo* genome assemblies based on chromatin interactions. Nat Biotechnol 2013;31:1119–25.

[30] VanBuren R, Wai CM, Ou S, Pardo J, Bryant D, Jiang N, et al. Extreme haplotype variation in the desiccation-tolerant clubmoss *Selaginella lepidophylla*. Nat Commun 2018;9:13.

[31] Bennezen JL, Wang H. The contributions of transposable elements to the structure, function, and evolution of plant genomes. Annu Rev Plant Biol 2014;65:505–30.

[32] Liu C, Cheng YJ, Wang JW, Weigel D. Prominent topologically associated domains differentiate global chromatin packing in rice from *Arabidopsis*. Nat Plants 2017;3:742–8.

[33] Wang CM, Liu C, Roqueiro D, Grimm D, Schwab R, Becker C, et al. Genome-wide analysis of local chromatin packing in *Arabidopsis thaliana*. Genome Res 2015;25:246–56.

[34] Song C, Liu YF, Song AP, Dong GQ, Zhao HB, Sun W, et al. *Chrysanthemum nankinense* genome provides insights into the evolution and diversification of chrysanthemum flowers and medicinal traits. Mol Plant 2018;11:1482–91.

[35] Wang LH, Yu S, Tong CB, Zhao YZ, Liu Y, Song C, et al. Genome sequencing of the high oil crop sesame provides insight into oil biosynthesis. Genome Biol 2014;15:R39.

[36] Chiang YC, Huang BH, Liao PC. Diversification, biogeographic pattern, and demographic history of Taiwanese *Scutellaria* species inferred from nuclear and chloroplast DNA. PLoS One 2012;7:e50844.

[37] Jaillon O, Aury JM, Noel B, Pollicita A, Clepet C, Casagrande A, et al. The grapevine genome sequence suggests ancestral hexaploidization in major angiosperm phyla. Nature 2007;449:463–9.

[38] Murat F, Armero A, Pont C, Klugeophyc C, Salse J. Reconstructing the genome of the most recent common ancestor of flowering plants. Nat Genet 2017;49:490–6.

[39] Navarro A, Barton NH. Chromosomal speciation and molecular divergence–accelerated evolution in rearranged chromosomes. Science 2003;300:321–4.

[40] Zhang X, Abraham C, Colquhoun TA, Liu CJ. A proteolytic regulator controlling chalcone synthase stability and flavonoid biosynthesis in *Arabidopsis*. Plant Cell 2017;29:1157–74.

[41] Zhang M, Zhang Y, Scheuring CF, Wu CC, Dong JJ, Zhang HB. Preparation of megabase-sized DNA from a variety of organisms using the nuclei method for advanced genomics research. Nat Protoc 2012;7:467–78.

[42] Koren S, Walenz BP, Berlin K, Miller JR, Bergman NH, Phillippy AM. Canu: scalable and accurate long-read assembly via adaptive k-mer weighting and repeat separation. Genome Res 2017;27:722–36.

[43] Simao FA, Waterhouse RM, Ioannidis P, Kriventseva EV, Zdobnov EM. BUSCO: assessing genome assembly and annotation completeness with single-copy orthologs. Bioinformatics 2015;31:3210–2.

[44] Li H, Durbin R. Fast and accurate short read alignment with Burrows-Wheeler transform. Bioinformatics 2009;25:1754–60.

[45] Servant N, Varoquaux N, Lajoie BR, Viara E, Chen CJ, Vert JP, et al. HiC-Pro: an optimized and flexible pipeline for Hi-C data processing. Genome Biol 2015;16:259.

[46] Cantarel BL, Korf I, Robb SM, Parra G, Ross E, Moore B, et al. MAKER: an easy-to-use annotation pipeline designed for emerging model organism genomes. Genome Res 2008;18:188–96.

[47] Ghosh S, Chan CK. Analysis of RNA-seq data using TopHat and Cufflinks. Methods Mol Biol 2016;1374:339–61.

[48] Emmas DM, Kelly S. OrthoFinder: phylogenetic orthology inference for comparative genomics. Genome Biol 2019;20:238.

[49] De Bie T, Cristianini N, Demuth JP, Hahn MW. CAFE: a computational tool for the study of gene family evolution. Bioinformatics 2006;22:1269–71.

[50] Wang Y, Tang H, Debarry JD, Tan X, Li J, Wang X, et al. MScAnX: a toolkit for detection and evolutionary analysis of gene synteny and collinearity. Nucleic Acids Res 2012;40:e49.

[51] Van de Peer Y, Mizrachi E, Marchal K. The evolutionary significance of polyploidy. Nat Rev Genet 2017;18:411–24.

[52] El-Gebali S, Mistry J, Bateman A, Eddy SR, Luciani A, Potter SC, et al. The Pfam protein families database in 2019. Nucleic Acids Res 2019;47:D427–32.

[53] Kumar S, Stecher G, Li M, Knyaz C, Tamura K. MEGA X: molecular evolutionary genetics analysis across computing platforms. Mol Biol Evol 2018;35:1547–9.

[54] Wang YQ, Song FH, Zhu JW, Zhang SS, Yang YD, Chen TT, et al. GSA: genome sequence archive. Genomics Proteomics Bioinformatics 2017;15:14–8.