Comparative Chloroplast Genome Analysis of Medicinally Important Veratrum (Melanthiaceae) in China: Insights into Genomic Characterization and Phylogenetic Relationships

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Abstract

Background: Veratrum is a genus of perennial herbs that are widely used as traditional Chinese medicine for emetic, resolving blood stasis and relieve pain. However, the species classification and the phylogenetic relationship of the genus Veratrum have long been controversial due to the complexity of morphological variations. Knowledge on the infrageneric relationships of the genus Veratrum can be obtained from their chloroplast genome sequences and increase the taxonomic and phylogenetic resolution.

Methods: Total DNA was extracted from ten species of Veratrum and subjected to next-generation sequencing. The cp genome was assembled by NOVOPlasty. Genome annotation was conducted using the online tool DOGMA and subsequently corrected by Geneious Prime. Then, genomic characterization of the Veratrum plastome and genome comparison with closely related species was analyzed by corresponding software. Moreover, phylogenetic trees were reconstructed, based on the 29 plastomes by maximum likelihood (ML) and Bayesian inference (BI) methods.

Results: The whole plastomes of Veratrum species possess a typical quadripartite structure, ranging from 151,597 bp to 153,711 bp in size and comprising 135 genes. The gene order, content, and genome structure were nearly identical with a few exceptions across the Veratrum chloroplast genomes. The total number of simple sequence repeats (SSRs) ranged from 31 to 35, and of large sequence repeats (LSRs) ranged from 65 to 71. Seven highly divergent regions (rpoB-trnC, tmT-trnL, trnS-trnG, psbC-psbZ, psbl ycf1, and ndhF) were identified that can be used for DNA barcoding in the genus of Veratrum. Phylogenetic analyses based on 29 plastomes strongly supported the monophyly of Veratrum. The circumscription and relationships of infrageneric taxa of Veratrum were well evaluated with high resolutions.

Conclusions: Our study identified and analyzed the cp genome features of ten Veratrum species, and suggested high effectiveness of chloroplast complete genome in resolving generic circumscription in Veratrum. These results will facilitate the identification, taxonomy, and utilization of Veratrum plants as well as contribute to the genetic diversity study of Melanthiaceae simultaneously.

Background

The genus Veratrum L. is one of the most important groups in the family Melanthiaceae (Liliorae), with approximately 17–45 species of perennial herbaceous plants [1–5]. It is widely distributed in the temperate to arctic zones of the Northern Hemisphere, the majority of which are native to Eastern Asia [1, 2, 6]. There are roughly 13 species and one variety of Veratrum plants in China, several species were used in medicine for more than 1700 years, including V. nigrum, V. schindleri, V. maackii and others [4, 5, 7, 8]. For instance, the dried roots and rhizomes of V. nigrum (Li-lu in Chinese) have been used to treat aphasia arising from apoplexy, wind-type dysentery, scabies, jaundice, and chronic malaria [7, 8]. Other species V. taliense, V. stenophyllum, V. mengtzeanum, and V. grandiflorum that are the source of folk medicine “Pimacao” in China, has been used for treating bruises, rheumatic pain and wound hemostasis [8–10]. Furthermore, “Pimacao” has a high economic value and is one of the main components of Yunnan Baiyao, as well as the principal drug of Yilizhitong pill [10, 11]. The major active ingredient isolated from roots of the above Veratrum plants is steroidal alkaloids, which pharmacological activities mainly focus on decreasing blood pressure, anti-platelet aggregation and anti-thrombosis, and have anti-inflammatory, analgesic and antitumor effect [11–14]. However, Veratrum plants also contain toxic components such as cevanine-ester alkaloids [13–15]. In human nausea, bradycardia, hypotension and apnea develop shortly after ingestion, in some cases resulting in death [12, 13, 15]. Our previous investigation found that some closely related species are occasionally mixed with Veratrum medicinal varieties as adulterants undermining the security and efficacy of the Veratrum containing medicinal products. Thus, securing accurate identification is urgent for the utilization of Veratrum medicinal materials safely and effectively.

Veratrum has a controversial taxonomic history and has been combined with Melanthium totally or in part [1, 16–19]. Since Linnaeus (1753) first circumscription of Veratrum, many subgenera, sections, and subsections have been proposed [1, 16–27]. The first subgeneric division of Veratrum was suggested by Baker (1880) [21]. Using perianth coloration as a diagnostic trait, he divided the genus into informal groups: strips V. albi (perianth white-green) and strips V. nigr (perianth purple-black) [21]. Loeseler split the genus Veratrum into three subgenera and two sections including 48 species consisting of elements of Melanthium [22–24]. Nakai modified Loeser’s infrageneric classification into two sections, omitting the rank of subgenera, and divided each section into two subsections [25, 26]. Recently, Veratrum has been circumscribed broadly (including Melanthium) and divided into two sections (sect. Veratrum and sect. Fuscoveratrum) and two subsections (subsect. Pseudoantl and subsect. Asiaveratrum) [1]. This modified infrageneric classification established a framework for resolving phylogenetic relationships within Veratrum [1, 6].

Morphologically, the key characteristics of Veratrum vary greatly depending on habitat, environment, and developmental stages, and the range of those variations often overlap among the taxa [1, 22–24, 28]. As a result, some species and its closely related species constitute a taxonomically complex group that is difficult to be clearly distinguished based on morphological traits alone such as V. maackii complex group [1, 6]. V. maackii has been divided into numerous varieties by different authors, including V. japonicum (broader leaves; relatively large flowers), V. schindleri (broader leaves; short-pedicellate flowers) and so on [1, 4, 5, 25, 26, 29–31]. Shimizu pointed that V. japonicum was a variety of V. maackii and was recognized by WCSP (World Check List of Selected Plant Families; http://www.theplantlist.org). In Flora Reipublicae Popularis Sinicae (FRPS), V. japonicum and V. schindleri were treated as two distinct species from V. maackii [4]. In addition, V. japonicum was treated as a synonym of V. schindleri in Flora of China (FOC) [5]. At the same time, because of its similar characters, such as black-purple perianth, basal leaves, and bulb layers disintegrating into reticulated fibers, V. maackii has been historically placed either in the V. nigrum or treated as its subspecies [32].

Veratrum species were a subject of many molecular analyses [1, 2, 6, 33–35]. Kim et al. conducted maximum parsimony and Bayesian inference based on ITS and cpDNA regions (matK, psbA-trnH, rpl16, and trnS-G) to re-examine the taxonomic status and phylogenetic relationships within Veratrum in Korea and Japan [33]. An analysis using the sequences of ITS, trnL-F, and atpB-rbcL indicated that Veratrum possibly originated in East Asia and radiated across the Northern Hemisphere, but most of the species were not well distinguished [6]. Previous studies have significantly advanced the phylogeny and taxonomy of genus Veratrum. However, due to limited resolution of molecular phylogeny and insufficient sampling of Asiatic species, phylogenetic relationships among the
species of the main clades (sections and subsections), particularly among the species from East Asia, are still poorly understood [1, 2, 6]. These shortcomings motivated our study.

The chloroplast genome of higher plants is relatively conservative in its structure, being a double-stranded circular molecule of 120–160 kb in length and comprising a large single-copy (LSC) region and a small single-copy (SSC) region, separated by two identical copies of inverted repeats (IRs) regions [34–36]. The cp genome has been widely used for evolutionary, taxonomic and species diversity studies due to such features as highly conserved genome structure, maternal inheritance, low to moderate evolutionary rate and low effective population sizes [36, 37]. The cp genomes have been showed to be effective in resolving problematic phylogenetic relationships at different taxonomic levels [38–41]. Up to now, however, the plastomes of only a few *Veratrum* species have been sequenced, and the data accumulated are still deficient for the clarification of the internal relationships of the family [35, 42–44]. Hence, we attempted to explore more *Veratrum* and its related species phylogenetic relationships with chloroplast genomics.

Here, we sequenced, assembled and annotated the complete cp genomes of ten *Veratrum* species using the next-generation sequencing platform, and performed the first comprehensive analysis of *Veratrum* species from China. This study aimed to: (1) establish and characterize the newly sequenced plastomes of ten *Veratrum* species; (2) examine the variations of SSRs and LSRs among these plastomes plus two previously published plastomes of *Veratrum*; (3) discover the most variable regions that could be used as DNA barcodes for *Veratrum*; (4) and reconstruct phylogenetic relationships among the *Veratrum* species using the plastome sequences.

**Materials And Methods**

**Plant material and DNA extraction**

Ten species, *V. dahuricum*, *V. grandiflorum*, *V. japonicum*, *V. maackii*, *V. nanchuanense*, *V. nigrum*, *V. oblongum*, *V. schindleri*, *V. stenophyllum* and *V. taliense* were collected in their native habitats in Yunnan, Fujian, Liaoning and Sichuan of China and used in this study. Fresh leaves were taken from healthy, mature individuals and dried with allochroic silica gel. From 3 to 5 individuals per species with flowers or fruits were collected and preserved as voucher specimens for morphological analysis and taxonomic identification. All voucher specimens were deposited in the Herbarium of Yunnan University of Chinese Medicine (YNUCM), China (Table S1). Total genomic DNA extraction was carried out using a modified CTAB protocol [45]. The quality and quantity of the DNA extracts for next-generation sequencing were determined using 1.0% agarose gel electrophoresis, and Nanodrop™ 2000 spectrophotometer (Thermo Fisher Scientific, USA), respectively.

**Genome sequencing, assembly and annotation**

Paired-end library was constructed by purified DNA and then sequenced on the Illumina HiSeq 2500-PE platform (Illumina, Inc., United States). High quality reads were obtained by removing the low-quality reads and connector sequence of using NGS QC Toolkit with default parameters [46]. Filtered reads of ten *Veratrum* species were assembled de novo using NOVOPlasty with cp genome of its close relative species, *V. patulum* (NC_022715), as the reference [43,47]. Annotation was performed with the online annotation tool DOGMA [48] and subsequently corrected using Geneious Prime® 2020.1.1 (Biomatters Ltd., Auckland, New Zealand). The chloroplast genome maps were drawn through OGDRAW [49]. Finally, the annotated chloroplast genomes of the ten *Veratrum* species were submitted to Genbank (Table 1).

**Repeat Sequence Analysis**

Simple sequence repeats (SSRs) were detected using IMEX with the search parameters set to 10, 5, 4, 3, 3, and 3 for mono-, di, tri, tetra-, penta- and hexa-nucleotides, respectively [51]. REPuter software was used for the identification of palindromic, forward, reverse and complement repeats present in the genome, whereby the Hamming distance was set as 3 and the minimum repeat size was 30 bp [50].

**Genome comparison and structural analysis**

Relative synonymous codon usage (RSCU) in these genes was assessed using MEGA X with default parameters [52,53]. Twelve species were compared and visualized using mVISTA with the Shuffle-LAGAN mode [54,55]. The borders of large single copy (LSC), small singles copy (SSC), and inverted repeat (IR) regions in the genomes of the twelve species were compared and examined. In addition, DnaSP v.5.0 was employed to analyze nucleotide variability among the twelve species of *Veratrum* [56]. The step size was set to 200 bp, with a 600 bp window length.

**Phylogenetic analyses**

To examine the phylogenetic relationships of *Veratrum* species, 27 plastomes representing phylogenetic diversity in the family Melanthiaceae and two species of Liliales (*Lilium henryi* and *Smilax china*) used as outgroup were included in the phylogenetic analysis (Table S1). All the plastomes were aligned using MAFFT integrated with Geneious Prime. A maximum-likelihood (ML) tree was constructed by RAxML using the general time-reversible (GTR) with gamma distribution (+G) nucleotide substitution model and 1,000 bootstrap replicates for each branch node [57]. Bayesian inference (BI) analyses were conducted using MrBayes v 3.2.6 [58]. The Markov Chain Monte Carlo (MCMC) algorithm was run for 1,00,000 generations and the trees were sampled every 1000 generations. The remaining analysis parameters were set as defaults. The first 25% of the trees were discarded as a burn-in and remaining trees were used to generate the consensus tree, including clade posterior probability (PP).
Results

Chloroplast Genome Features

A total of 12 chloroplast genomes representing majority of *Veratrum* species distributed in China were analyzed (Table 1, Table S1). Among them, 10 plastomes were newly sequenced and assembled in this study. *V. mengtzeanum* (MN589932) and *V. patulum* (NC_022715) (synonym of *V. oxysepalum*) were used as supplemental species for comparative analysis. The complete chloroplast genome of *Veratrum* species ranged from 151,597 bp (*V. maackii*) to 153,711 bp (*V. grandiflorum*) in length (Table 1, Fig. 1). The LSC region ranged 81,822-83,372 bp and SSC region ranged 17,473-17,628 bp, which were separated by two IR regions (26,145-26,359 bp) (Table 1). The overall Guanine-Cytosine (GC) content of twelve *Veratrum* cp genomes ranged 35.7-35.8%, which is similar to that of other Melanthieae species [38,43,44]. And the GC content of the IRs (42.9-43.0%) was higher than that of LSC (35.7-35.8%) and SSC (31.3-31.5%) regions in twelve *Veratrum* species (Table 1).

Table 1
Summary of complete chloroplast genomes of twelve *Veratrum* species

| Genome Characteristic | Accession number | Length (bp) | Gene number | GC content (%) | Protein-coding | rRNA | Full | LSC | SSC | IR | Full | LSC | SSC | IR |
|----------------------|------------------|-------------|-------------|----------------|----------------|------|------|-----|-----|-----|------|-----|-----|-----|
| *V. dahuricum*       | MN699635         | 153,688     | 83,363      | 17,607         | 26,359         | 135  | 83   | 8   | 38  | 8   | 37.7 | 35.7 | 31.4 | 42.9|
| *V. grandiflorum*    | MN613592         | 153,711     | 83,367      | 17,628         | 26,358         | 135  | 83   | 8   | 38  | 8   | 37.7 | 35.7 | 31.4 | 42.9|
| *V. japonicum*       | MN613594         | 151,897     | 81,885      | 17,533         | 26,212         | 135  | 84   | 8   | 38  | 8   | 37.7 | 35.7 | 31.3 | 42.9|
| *V. maackii*         | MN613590         | 153,688     | 83,368      | 17,608         | 26,358         | 135  | 83   | 8   | 38  | 8   | 37.7 | 35.7 | 31.4 | 42.9|
| *V. nanchuanense*    | MN613591         | 151,799     | 81,823      | 17,473         | 26,151         | 135  | 84   | 8   | 38  | 8   | 37.7 | 35.7 | 31.4 | 42.9|
| *V. nigrum*          | MN613595         | 151,767     | 81,997      | 17,480         | 26,145         | 135  | 84   | 8   | 38  | 8   | 37.7 | 35.7 | 31.4 | 42.9|
| *V. oblongum*        | MN613593         | 151,768     | 81,862      | 17,530         | 26,188         | 135  | 84   | 8   | 38  | 8   | 37.7 | 35.8 | 31.4 | 42.9|
| *V. schindleri*      | MN613588         | 152,028     | 82,122      | 17,558         | 26,180         | 135  | 84   | 8   | 38  | 8   | 37.8 | 35.8 | 31.5 | 43.0|
| *V. stenophyllum*    | MN613589         | 152,028     | 82,122      | 17,558         | 26,180         | 135  | 84   | 8   | 38  | 8   | 37.8 | 35.8 | 31.5 | 43.0|
| *V. taliense*        | MN604405         | 152,040     | 82,122      | 17,558         | 26,180         | 135  | 84   | 8   | 38  | 8   | 37.8 | 35.8 | 31.5 | 43.0|
| *V. mengtzeanum*     | MN589932         | 153,699     | 83,372      | 17,607         | 26,360         | 135  | 83   | 8   | 38  | 8   | 37.7 | 35.7 | 31.4 | 42.9|

New sequences from this study are in boldface.

The gene content, order, and structure were similar in the twelve *Veratrum* cp genomes. Most of the examined plastomes have 84 protein-coding genes, 38 tRNAs and eight rRNAs (Table 1). However, there were 83 protein-coding genes in *V. grandiflorum*, *V. nanchuanense*, *V. nigrum*, and *V. patulum* because of the complete loss of *infA* gene. The LSC region contains 61 protein-coding genes and 21 tRNA genes, whereas the SSC region contains 12 protein-coding genes and one tRNA gene. Six protein-coding and eight tRNA genes are located in the IR regions. Seventeen of the genes contained introns, eight coding genes (*rpl2, rpoC1, ndhA, ndhB, petD, petP, atpA*) and six tRNA genes (*trnA UGC, trnG UCC, trnI GAU, trnK UUU, trnV UAC*) with a single intron, and three coding genes (*rps12, clpP ycf3*) with two introns (Table 2). The *rpl2* gene was a unique trans-spliced gene with the two duplicated 3' end exons in the IR regions and a 5' end exon in the LSC region. Both *ycf15* and *ycf68* in twelve plastomes of *Veratrum* species contain many internal stop codons, indicating that these sequences represent pseudogenes.
### Table 2
Genes in the chloroplast genome of *Veratrum* species

| Category                     | Group of Genes                      | Name of Genes                                                                 |
|------------------------------|-------------------------------------|-------------------------------------------------------------------------------|
| **Self-replication**         | Large subunit of ribosomal          | *rpl2*<sup>2</sup>;<sup>14</sup>;*rpl16*<sup>2</sup>;*rpl20*<sup>2</sup>;*rpl23*<sup>2</sup>;<sup>32</sup>;<sup>33</sup>;<sup>36</sup> |
|                              | Small subunit of ribosomal          | *rps2*<sup>2</sup>;*rps3*<sup>a</sup>;*rps7*<sup>a</sup>;*rps12*<sup>b,c,d</sup>;*rps14*<sup>1</sup>;*rps15*<sup>14</sup>;*rps16*<sup>18</sup>;*rps19*<sup>19</sup> |
|                              | DNA dependent RNA polymerase        | *rpoA*;<sup>a</sup>*rpoB*;<sup>a</sup>*rpoC1*<sup>a</sup>*rpoC2*                                                         |
|                              | rRNA genes                          | *rrn4.5*<sup>c</sup>*rrn5*<sup>c</sup>*rrn16*<sup>c</sup>*rrn23*<sup>c</sup>                                                   |
|                              | tRNA genes                          | *trnA-UGC*<sup>a,c</sup>*trnC-GCA*<sup>c</sup>*trnD-GUC*<sup>a</sup>*trnE-UUC*<sup>c</sup>*trnF-GAA*<sup>c</sup>*trnG-GCC*<sup>c</sup>*trnH-GUC*<sup>c</sup>*trnI-CAU*<sup>c</sup>*trnI-GAU*<sup>a,c</sup>*trnK-UUU*<sup>c</sup>*trnL-CAA*<sup>c</sup>*trnL-UAG*<sup>c</sup>*trnM-CAU*<sup>c</sup>*trnN-GUU*<sup>c</sup>*trnP-UGG*<sup>c</sup>*trnQ-UUG*<sup>c</sup>*trnR-ACG*<sup>c</sup>*trnR-UCU*<sup>c</sup>*trnS-CCA*<sup>c</sup>*trnS-GCU*<sup>c</sup>*trnS-GGA*<sup>c</sup>*trnS-UGA*<sup>c</sup>*trnT-GGU*<sup>c</sup>*trnT-UGU*<sup>c</sup>*trnV-GAC*<sup>c</sup>*trnV-UAC*<sup>c</sup>*trnW-CCA*<sup>c</sup>*trnY-GUA*                                                            |
| **Photosynthesis**            | Photosystem I                       | *psaA*<sup>b</sup>*psaB*<sup>c</sup>*psaC*<sup>c</sup>*psaD*<sup>c</sup>                                                         |
|                              | Photosystem II                      | *psbA*<sup>b</sup>*psbB*<sup>c</sup>*psbC*<sup>c</sup>*psbD*<sup>c</sup>*psbE*<sup>c</sup>*psbF*<sup>c</sup>*psbH*<sup>c</sup>*psbI*<sup>c</sup>*psbJ*<sup>c</sup>*psbK*<sup>c</sup>*psbL*<sup>c</sup>*psbM*<sup>c</sup>*psbN*<sup>c</sup>*psbO*<sup>c</sup>*psbP*<sup>c</sup>*psbQ*<sup>c</sup>*psbR*<sup>c</sup>*psbS*<sup>c</sup>*psbT*<sup>c</sup>*psbU*<sup>c</sup>*psbV*<sup>c</sup>*psbW*<sup>c</sup>*psbX*<sup>c</sup>*psbY*<sup>c</sup>*psbZ*<sup>c</sup> |
|                              | NadH oxidoreductase                 | *ndhA*<sup>a</sup>*ndhB*<sup>c</sup>*ndhC*<sup>c</sup>*ndhD*<sup>c</sup>*ndhE*<sup>c</sup>*ndhF*<sup>c</sup>*ndhG*<sup>c</sup>*ndhH*<sup>c</sup>*ndhI*<sup>c</sup>*ndhJ*<sup>c</sup>*ndhK*<sup>c</sup> |
|                              | Cytochrome b6/f complex             | *petA*<sup>a</sup>*petB*<sup>a</sup>*petD*<sup>a</sup>*petE*<sup>a</sup>*petG*<sup>a</sup>*petL*<sup>a</sup>*petN*<sup>a</sup>*petO*<sup>a</sup>*petP*<sup>a</sup>*petQ*<sup>a</sup>*petR*<sup>a</sup>*petS*<sup>a</sup>*petT*<sup>a</sup>*petU*<sup>a</sup>*petV*<sup>a</sup>*petW*<sup>a</sup>*petX*<sup>a</sup>*petY*<sup>a</sup>*petZ*<sup>a</sup> |
|                              | ATP synthase                        | *atpA*<sup>a</sup>*atpB*<sup>a</sup>*atpC*<sup>a</sup>*atpD*<sup>a</sup>*atpE*<sup>a</sup>*atpF*<sup>a</sup>*atpH*<sup>a</sup>*atpI*<sup>a</sup> |
|                              | Rubisco                             | *rbcL*                                                                         |
| **Other genes**              | Maturase                            | *matK*                                                                         |
|                              | Translational                       | *infA*                                                                         |
|                              | Protease                            | *clpP*                                                                         |
|                              | Envelope membrane protein           | *cemA*                                                                         |
|                              | Subunit of acetyl-CoA               | *accD*                                                                         |
|                              | c-type cytochrome synthesis gene    | *ccsA*                                                                         |
| **Unknown**                  | Conserved Open reading               | *ycf1*;<sup>a</sup>*ycf2*<sup>c</sup>*ycf3*<sup>b</sup>*ycf4*<sup>c</sup>*ycf15*<sup>c</sup>*ycf68*<sup>c</sup> |

<sup>a</sup>Gene containing a single intron; <sup>b</sup>Gene containing two introns; <sup>c</sup>Gene with two copies; <sup>d</sup>Trans-splicing gene.

### SSRs and LSRs of *Veratrum* chloroplast genomes

Numerous simple sequence repeats (SSRs) loci were found through the IMEx analysis in twelve analyzed plastomes, ranging from 63 SSRs in *V. taliense* to 78 SSRs in *V. oblongum* (Fig. 2A, Table S2). The most common types of SSRs were mono-nucleotide repeats (65%), followed by di-nucleotide (18%), tetra-nucleotide repeats (8%) and tri-nucleotide repeats (5%). No hexa-nucleotide repeats were found in any of the analyzed plastomes (Fig. 2A). Among these, the type number of mono-, di-, tri-, tetra-, penta-, and hexa- nucleotides SSRs are 3, 2, 5, 8, 7, and 2, respectively (Fig. 2B). Most SSRs (97%) were located in LSC and SSC regions, while the inverted regions had very few repeats (3%) (Fig. 2C). The SSRs were more abundant in non-coding than in coding regions (64% vs. 36%) (Fig. 2D).

A total of 403 long sequence repeats (LSRs) including 125 forward, 188 palindromic and 22 reverse repeats were detected in the twelve plastomes (Fig. 3A, Table S3). Repeat numbers varied from 31 in *V. oblongum* to 35 in *V. grandiorum*, *V. nanchuanense*, *V. patulum*, and *V. dahuricum* (Fig. 3A). LSRs mainly ranged 30-47 bp in length, whereas only one palindromic repeat was longer than 54 bp in *V. dahuricum*, *V. grandiorum*, *V. nanchuanense* and *V. patulum* (Fig. 3B). Further analysis revealed that most of the LSRs were located in the LSC region, with a small portion distributed throughout the SSC and IR regions (Fig. 3C). In the first location, 39% of the repeats are in the non-coding region (Fig. 3D).

### Codon Usage
The frequency of the codon usage present in the plastome of 27 Melanthiaceae species and two Liliales species was computed using the nucleotide sequence of protein-coding genes. The results showed the genes in the plastome are encoded by 23,963 (Smilax china) to 29,006 (Paris rugosa) codons with the RSCU (relative synonymous codon usage) values ranging from 0.297 (AGC) to 1.988 (AGA) (Fig. 4, Table S4). No codon bias (RSCU=1) can be shown by methionine (AUG) and trypotphan (UGG), encoded by only one codon. Leucine (10.0–10.4%) and cysteine (1.2% of each species) are the most and the least abundant amino acids except for stop codons (0.3%-0.4%) (Table S5). We found that the coding sequence of a protein-coding gene in the Veratrum cp DNA is preference A:T base, the same as the third position of the codon.

### Comparative analysis of twelve Veratrum chloroplast genomes

The alignment of the sequenced Veratrum plastomes having 154,858 bp in length revealed high sequence similarity, ranging from 96.46% (V. nigrum and V. patulum) to 99.99% (V. stenophyllum and V. taliense) (Table 3). The visualization analysis of the alignment using mVISTA showed that the genomic structure, order, and orientation of these plastomes were highly conserved. Notably, IR regions exhibited less divergence than the SSC and LSC regions (Fig. 5). In addition, the non-coding region was more variable than the coding region, the highly divergent regions among the twelve plastomes appeared in the intergenic spacers, such as trnK UUU- trnQ UUG, trnS GCU-trnG UCC, rps19, psbC-psbZ, rps7-trnV GAC and ndhF-rpl32 (Fig. 5). Among coding regions, ycf1, rpl22 and petD genes were relatively divergent (Fig. 5).

| genus          | V. dahuricum | V. grandiflorum | V. japonicum | V. maackii | V. nanchuanense | V. nigrum | V. oblongum | V. schindleri | V. stenophyllum | V. taliense |
|----------------|--------------|-----------------|--------------|------------|----------------|-----------|-------------|---------------|----------------|-------------|
| V. dahuricum   | 99.906       |                 |              |            |                |           |             |               |                |             |
| V. grandiflorum|              |                 | 99.786       |            | 99.565         | 99.799   | 98.511      |               |                |             |
| V. japonicum   | 96.786       |                 |              | 98.543     | 96.111         | 96.51    | 98.675      |               |                |             |
| V. maackii     | 96.516       |                 |              | 99.925     | 99.964         | 96.799   | 96.511      |               |                |             |
| V. nanchuanense| 99.925       |                 |              | 99.964     | 96.799         | 96.511   | 98.675      |               |                |             |
| V. nigrum      | 96.513       |                 | 96.498       | 98.544     | 99.985         | 96.501   | 98.675      |               |                |             |
| V. oblongum    | 96.615       |                 | 96.602       | 98.663     | 99.529         | 96.113   | 99.529      |               |                |             |
| V. schindleri  | 96.834       |                 | 96.818       | 99.725     | 98.551         | 96.831   | 98.552      | 98.675        |                |             |
| V. stenophyllum| 97.005       |                 | 96.991       | 98.73      | 98.431         | 97.002   | 98.429      | 98.543         | 98.762         |             |
| V. taliense    | 97.012       |                 | 96.998       | 98.737     | 98.437         | 97.009   | 98.436      | 98.55         | 98.77          | 99.989      |
| V. mengtezana | 97.013       |                 | 96.998       | 98.742     | 98.436         | 97.008   | 98.435      | 98.551         | 98.771         | 99.84       |
| V. patulum     | 99.869       |                 | 99.871       | 96.738     | 96.466         | 99.887   | 96.463      | 96.558         | 96.769         | 96.947      |

Nucleotide diversity of highly variable regions was calculated with a sliding window to estimate the divergence level of different regions in the analyzed plastomes. Of these, the SSC region exhibited the highest divergence levels (0.01469) and IR regions had the lowest (0.00218). Meanwhile, all highly divergent fragments were found in the SC regions whereas no highly variable loci were found in the IR regions. Seven regions with the highest variability, including 4 intergenic regions (trnS GCU-trnG UCC, rpoB-trnC GCA, psbC-psbZ, and tmS GCU-tmG UCC) and three gene regions (psbl, ndhF, and ycf1), were identified as most promising gene fragments for species identification and studying Veratrum phylogeny (Fig. 6). The rpoB-trnC GCA intergenic region was the most variable (Pi=0.03576), followed by pabC-psbZ (Pi=0.03477), tmT UGU-tmL UAA (Pi=0.03278), psbl (Pi=0.02914), ycf1 (Pi=0.02896), ndhF (Pi=0.02097), and trnS GCU-tmG UCC (Pi=0.02533) (Table S6).

Although the IR region of the twelve chloroplast genomes was highly conserved, genomic structure and size varied in the twelve Veratrum cp genomes and the IR/SC border regions of these species were also different (Fig. 7). V. dahuricum, V. grandiflorum, V. nanchuanense and V. patulum exhibited larger than the other species in plastome size due to the increased IR length. Six genes (rpl22, rps19, trnH, rpl2, ycf1, and ndhF) were found in the LSC/IR and SSC/IR borders of the twelve plastomes. The rps19 gene was found to be 3 bp away from the JLB junction in V. dahuricum, V. grandiflorum, V. patulum and V. nanchuanense, while it was across the IRb/SSC border in other species. The SSC/IRb junction is located in the ycf71 region in the chloroplast genomes of all Veratrum species and extends a different length (5,372-5,408 bp) into the SSC region in all genomes; the IRb region includes 959 to 991 bp of the ycf1 gene. In addition, the tmH gene is located in the LSC region, 141-144 bp away from the IRa/LSC border in the twelve Veratrum chloroplast genomes species.

### Phylogenetic relationship
Plastome-based phylogenetic analysis showed identical topology for ML and BI methods (Figure 8). All the nodes in the phylogenetic tree were highly supported (BS ≥ 98% and PP ≥ 0.86). Consistent with the previous analyses, Melanthiaceae was monophyletic with five strongly supported groups corresponding to previously circumscribed tribes Parideae (Trilliaceae), Xerophylleae, Heloniadeae, Chionographideae and Melanthiaceae [1,2]. Within Melanthiaceae, Melanthiaceae was sister to the rest of the family, and Parideae (Trilliaceae) and Xerophylleae comprised a clade sister to the Heloniadeae and Chionographideae clades (BS=100, PP=1).

As shown in the cladogram, thirteen species of *Veratrum* formed one clade (Fig. 8, clade A) with highly support (BS=100%, PP=1) and this clade was subdivided into two sub-clades, labeled B and C. Clade B, corresponding to Loesener's section *Veratrum*, included *V. grandiflorum*, *V. nanchuanense*, *V. patulum* and *V. dahuricum* [22-24]. Clade C, corresponding to Loesener's section *Fuscoveratrum*, consisted of two subclades D and E, which were in accordance with the elements of Zomlefer's two subsections [1,2,22-24]. Within clade D, *V. taliense*, *V. stenophyllum* and *V. mengzeanum* were clustered together with high support. Clade E included remaining six species of *Melanthium* s.l. sensu Bodkin, the taxa of the *V. maackii*, *V. nigrum*, and relatives [18]. Two accessions of *V. japonicum*, one from South Korea (NC_041306) and another one from Yunnan, China didn't form a monophyletic clade while were clustered together with *V. schindleri* (Fig. 8, clade G) (Table S1).

**Discussion**

**Chloroplast Genome Features**

The *Veratrum* plastomes showed typical structural characteristics and genetic properties of the angiosperm plastome. The plastomes of *Veratrum* taxa are approximately 151 kb in length on average and organized into quadripartite regions with no structural variation among taxa. In total, 135 genes were identified, including 83-84 protein-coding genes, 38 tRNA genes, and 8 rRNA genes. Confirming previous reports [38,43] we have found the losses of the *rps16* gene in *Veratrum* species, which might be a specific feature of the *Veratrum* genus compared to the other genera of Liliales. In addition, it was found that *ycf68* and *ycf15* are pseudogenes not encoding any protein and apparently non-functional. We detected *infA* in four *Veratrum* plastomes (*V. grandiflorum*, *V. nanchuanense*, *V. nigirum* and *V. patulum*) and it contained an internal stop codons indicating that this sequence is from a pseudogene. It is believed that the most common gene loss in angiosperm, *infA* loss could result from transferring of the gene to the nucleus [59,60].

SSRs (1–6 repeating sequences) were distributed throughout the plastomes, have been used for analysis of population genetics due to their high variability and stable reproducibility [61-63]. Here, 762 SSRs were identified in the *Veratrum* species, which will be useful developing lineage-specific cpSSR markers and population genetics of the *Veratrum* species. With the increasing number of chloroplast genome sequences, many researchers have demonstrated that large repeat sequences play an important role in insertion/deletion mismatches and recombination of genomic variation [63]. Additionally, these repeat motifs might provide some informative sources to develop genetic markers for analysis on population genetics [64].

The structural integrity of the whole plastome is highly linked to the IR structure, and the changes in plastome structure are often associated with IR expansions and contractions [65]. In this study, a detailed comparison of four junctions of two IRs between twelve species of *Veratrum* were performed. There were some variations in the size and distribution of *psbI*, *ndhF*, *ycf1*, and *tmH* genes among the four boundaries. Overall, the two IR regions are highly conserved and structure variation was not significant in the twelve *Veratrum* plastomes.

**Identification of highly variable regions**

DNA barcodes and gene markers derived from divergence hotspots in the cp genome are reported to be efficient in species identification of closely related species in the plant kingdom [66]. The plastomes of twelve *Veratrum* species were relatively conserved, though each of them contained unique genetic information and variant sites. Previously two fragments (*ndhF*, and *tmS-trmG*) were suggested to be useful for the study of *Veratrum* phylogeny [33,42]. We detected several variant sites, namely genes *psbl*, *ycf1*, and *ndhF* and four intergenic spacer regions *rpoB-trnC*, *trnT-trnL*, *trnS-trmG*, and *psbC-psbZ* useful as potential barcoding regions. Future studies will clarify the efficacy of the above barcoding regions for species delimitation and identification in *Veratrum*.

**Phylogenetic inferences**

The topology of our phylogenetic tree for 27 species of Melanthiaceae (circumscribed based on APG II) was identical with the one of Zomlefer et al. and Kim et al. [35,42,67], and had improved resolution for previously defined five tribes. The monophyly of *Veratrum s.l.* (clade A) including *Melanthium* was confirmed with high support. Our results also suggest that broad circumscription of *Veratrum* advocated previously is appropriate [1,2].

The phylogenetic topology for *Veratrum* is consist of previous infrageneric circumscriptions with clade B responding to sect. *Veratrum* and clade C responding to sect. *Fuscoveratrum* [1,2,22-24]. Morphologically, species of sect. *Veratrum* has cauley leaves, styles terminal on the fruiting carpels and bulb layers disintegrating into fibers. All species of clade B exhibited these characters. The species composition of the sect. *Veratrum* was compatible with the circumscriptions proposed by Nakai and Loesener [22-26]. Meanwhile, *V. nanchuanense*, with the unclear systematic position since its nomenclature [4,5], clustered with *V. grandiflorum* closely (Fig 8, clade B). Its morphological characteristics, such as leafy stems and pubescent many-branched inflorescences, are identical with the circumscriptions of Loesener's sect. *Veratrum* [22-24]. Therefore, we suggested *V. nanchuanense* was a member of the sect. *Veratrum*. Sect. *Fuscoveratrum* differs from the sect. *Veratrum* by its leaves that are mostly basal and reduced upward on the stem, styles sublaterally attached to the fruiting, and bulb layers disintegrating into reticulated fibers [25,26]. In this study, sect. *Fuscoveratrum* (Fig. 8, clade C) were separated into two subsections: subsect. *Pseudoanticlea* (Fig. 8, clade D) and subsect. *Asiaveratrum* (Fig. 8, clade E), and which is consistent with the infrageneric circumscription of Zomlefer [1].
V. stenophyllum, V. taliense, V. mengtzeanum and V. grandiflorum had been used as the original plant of traditional Chinese medicine namely “Pimacao” to treat bruise, rheumatic pain, wound hemostosis, which listed in the Standard of Chinese Herbal Pieces in Yunnan Province [9]. Phylogenetic analysis indicated that V. grandiflorum belongs to sect. Veratrum, while V. stenophyllum, V. taliense and V. mengtzeanum belong to sect. Fuscoveratrum. These species were placed into two distinct clades (Fig. 8, clades B and C). In general, closely related species also had similar chemical composition and efficacy, conversely, there could be different effects [68]. Thus, additional studies should be imperative to investigate the chemical composition and pharmacological effect of V. grandiflorum to solve the safety of medication concerns.

Till now, the taxonomic treatment of subsect. Asiaveratrum is uncertain, due to either the morphological synapomorphies or lack of resolution from molecular phylogenetic analysis based on sequences of the internal transcribed spacers (ITS) of the nuclear ribosomal DNA [1,6,33]. In previous studies, all species of subsect. Asiaveratrum formed an unresolved polytomy among V. maackii/V. nigrum, V. japonicum and V. schindleri. In this study, high resolutions were detected for these taxa. V. maackii and V. nigrum were closely related, and they formed the sister clade of V. oblongum with strong support (BS=100%, PP=0.859). Hence, we suggested the taxonomic treatment of V. nigrum to be a distinct species from V. maackii. The cladogram exhibited two accessions of V. japonicum formed paraphyly with one accession clustered together with V. schindleri (Fig. 8, clade G). Therefore, we advocate treating V. japonicum as the synonym of V. schindleri corresponding to the Flora of China [5].

Conclusions

In this study, the complete chloroplast genome was sequenced, assembled, and annotated for ten Veratrum species from China. The ten plastomes exhibited a typical circular quadripartite structure and shared a high similarity in gene order and genomic structure. SSRs, LSRs, and the seven highly variable loci were identified across the Veratrum plastid genomes, which could serve as potential markers for future study on phylogenetic and population genetic studies. The monophyly of Veratrum s.l. including Melanthium was confirmed and two sections were exhibited in the phylogenetic analysis. The circumscription and relationships of infrageneric taxa of Veratrum were well evaluated, too. We suggest V. nanchuanense was a member of the sect. Veratrum, and V. japonicum was the synonym of V. schindleri. In addition, V. nigrum and V. maackii should be treated as distinct species. Overall, the comparative complete chloroplast genome analysis in this study provides valuable insight for species clarification, phylogenetic construction for the genus Veratrum, and will also conducive to the phylogenetic studies of Melanthiaceae.

Abbreviations

cp: chloroplast; LSC: large single-copy; SSC: small single-copy; IR: inverse repeat; NCBI: National Center for Biotechnology Information database; tRNA: transfer RNA; rRNA: ribosomal RNA

Declarations

Ethics approval and consent to participate

Not applicable

Consent to publish

Not applicable

Availability of data and materials

All data generated or analyzed during the course of this study are included in this document or obtained from the appropriate author(s) at reasonable request.

Competing interests

The authors declare that they have no competing interests.

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Authors’ contributions

ZQ and GL conceived and designed the research. GL, CY, YZ and XT collected the leaf materials. YZ, LH and YL performed the experiments; YZ, YL and CY analyzed the data. YZ, LH and XT drafted the manuscript. GL revised the manuscript. All authors read and approved the final manuscript.

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