The complete plastomes of seven *Peucedanum* plants: comparative and phylogenetic analyses for the *Peucedanum* genus

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**Abstract**

**Background:** The *Peucedanum* genus is the backbone member of Apiaceae, with many economically and medically important plants. Although the previous studies on *Peucedanum* provide us with a good research basis, there are still unclear phylogenetic relationships and many taxonomic problems in *Peucedanum*, and a robust phylogenetic framework of this genus still has not been obtained, which severely hampers the improvement and revision of taxonomic system for this genus. The plastid genomes possessing more variable characters have potential for reconstructing a robust phylogeny in plants.

**Results:** In the current study, we newly sequenced and assembled seven *Peucedanum* plastid genomes. Together with five previously published plastid genomes of *Peucedanum*, we performed a comprehensively comparative analyses for this genus. Twelve *Peucedanum* plastomes were similar in terms of genome structure, codon bias, RNA editing sites, and SSRs, but varied in genome size, gene content and arrangement, and border of SC/IR. Fifteen mutation hotspot regions were identified among plastid genomes that can serve as candidate DNA barcodes for species identification in *Peucedanum*. Our phylogenetic analyses based on plastid genomes generated a phylogeny with high supports and resolutions for *Peucedanum* that robustly supported the non-monophyly of genus *Peucedanum*.

**Conclusion:** The plastid genomes of *Peucedanum* showed both conservation and diversity. The plastid genome data were efficient and powerful for improving the supports and resolutions of phylogeny for the complex *Peucedanum* genus. In summary, our study provides new sights into the plastid genome evolution, taxonomy, and phylogeny for *Peucedanum* species.

**Keywords:** Apiaceae, *Peucedanum*, Plastome evolution, Phylogenomics, DNA barcoding

**Background**

*Peucedanum* L. is one of the largest genera of Apiaceae [1–3], which was once placed in the tribe Peucedaneae [1, 4, 5], but now in the tribe Selineae [2]. The genus comprises 100-120 species worldwide that are widely distributed in Eurasia and South Africa (and sometimes Australia) [2, 3, 6], with Europe and East Asia as distribution centers [7]. Of those, forty species are distributed in China with 33 of them endemic [3].

The genus *Peucedanum* is taxonomically notorious within Apiaceae family, especially described as “*Peucedanum* problem” by Downie et al. [8]. Its members are characterized by dorsally compressed mericarps with slightly prominent dorsal ribs, narrowly winged lateral ribs, as well as a broad commissure [2, 3]. However, the
genus is extremely heterogenous and exhibits great diversity in life-forms, leaf and fruit structures, and chemical constituents [9]. Hence, several researchers are prone to divide this genus into smaller and presumably more natural units. For example, Pimenov and Leonov [5] suggested that all members of *Peucedanum* except 8-10 species included in sect. *Peucedanum* should be transferred to other genera. Based on morphological and phytochemical evidences, Reduron et al. [10] separated the genera *Cervaria* Wolf, *Imperatoria* L., *Oreoselinum* Mill., *Pteroselinum* Rchb., *Thysselinum* Adans., *Xanthoselium* Schur and *Holandrea* Reduron from *Peucedanum*. Winter et al. [11] established three new genera (*Afroscladium* P.J.D. Winter, *Nanobubon* Magee and *Notobubon* B.-E. van Wyk) to accommodate the African peucedanoid species and transferred 24 *Peucedanum* species into *Afroligusticum* C. Norman, *Cynorrhiza* Eckl. & Zeyh., and *Lefebvrea* A. Rich. However, due to the varied morphological features of leaf division, bracteoles, and mericarps, distinguishing separate genera from *Peucedanum* is extremely difficult [2, 3]. Therefore, the generic limits of *Peucedanum* based on morphological characters faces challenges.

A robust phylogenetic framework could provide a valuable information to aid the generic delimitation of *Peucedanum*. Previously, a few molecular phylogenies of *Peucedanum* based on single or multiple locus DNA sequence data, such as nuclear ribosomal DNA internal transcribed spacer (ITS), plastid DNA *rpl*16 and *rps*16 intron, have been performed, yet these analyses failed to recognize *Peucedanum* as a monophyletic group [2, 12–16]. This phenomenon infers that re-evaluating the generic limits of *Peucedanum* may be essential. Nevertheless, weak supports and low resolutions of these phylogenetic trees could not provide sufficient information to support the improvement of taxonomy for *Peucedanum*. Therefore, additional molecular data are urgent to reconstruct a strong phylogeny.

In addition, several species of *Peucedanum* are highly appreciated as traditional medicinal herbs due to their versatile therapeutic properties [17]. Among them, *Peucedanum praeruptorum* Dunn, known as “Baihu Qianhu”, is an excellent representation. The dried root of *P. praeruptorum* has been utilized as traditional Chinese medicine for more than 1500 years, which is generally used to treat respiratory diseases, pulmonary hypertension, chest pain, as well as symptomatic coughs and dyspnea [18]. However, most *Peucedanum* species exhibit abundant intraspecific variations in morphology that make it difficult to accurately identify species. In order to assure medicinal quality, it is, therefore, necessary to develop specific DNA marker for *Peucedanum* species authentication.

The plastid genome (plastome) is one of the three DNA genomes (with nuclear and mitochondrial genomes) in plants. The genome is uniparentally inherited, lacks recombination, and possesses highly variable characters in flowering plants; hence, it has the potential to significantly improve the supports and resolutions of the phylogeny [19–22]. Furthermore, a typical plastome comprises two inverted repeats regions (IRs) of 22-25 kb separated by the large single copy region (LSC) of 82-90 kb and small single copy region (SSC) of 15-20 kb and generally encodes 110-130 unique genes [23, 24]. Comparative analysis of plastome could reveal the diversity of plastome in structural organization, gene arrangement and content that deepens our understanding of adaptive evolution for plant lineages and identify suitable mutation hotspots for species authentication [21, 25, 26]. Hence, with the development of next-generation sequencing and bioinformatics technologies, plastomes have been extensively and successfully used for plant phylogenetic analyses and development of specific DNA barcodes in recent years [25–32].

Currently, although six plastomes of *Peucedanum* species were submitted in GenBank [33–36], the plastid phylogenomic analysis of the genus has not been conducted. In this study, we newly sequenced the plastomes of seven *Peucedanum* taxa. In conjunction with the previously reported five plastomes of *Peucedanum*, we carried out a comprehensive analysis of plastomes for this taxonomically difficult plant group. Our aims were to: (1) investigate the plastome features of *Peucedanum* plants; (2) screen out suitable mutation hotspot regions from plastome as candidate DNA barcodes for species identification of *Peucedanum*; (3) test the power of plastome for improving the supports and resolutions of phylogeny in the complex *Peucedanum* genus. Overall, our results will well lay the foundation for the phylogenetic and taxonomic studies of *Peucedanum*.

Results

Plastome features of *Peucedanum*

Illumina sequencing generated 36,875,778–44,140,972 paired-end clean reads for the seven *Peucedanum* samples. Among them, 712,889 to 6,125,929 reads were mapped to the final assembly. Based on these data, we obtained seven high-quality *Peucedanum* plastomes, with coverage ranging from 730.073× to 6,266.178× (Table S1).

Overall size of plastomes ranged from 142,494 bp (*P. angelicoides* Wolff ex Kretschm.) to 156,899 bp (*P. insolens* Kitag.) for the twelve *Peucedanum* samples (Table 1). All of them showed typically quadripartite structure, including a pair of inverted repeats regions (IRs, 12,594-27,495 bp), a large single copy region...
Table 1 Comparison of plastome features among Peucedanum plants

| Taxon                  | Total length (bp) | LSC (bp) | SSC (bp) | IR (bp) | Total GC content (%) | Total genes (unique) | Protein coding genes (unique) | rRNA genes (unique) | tRNA genes (unique) |
|------------------------|-------------------|----------|----------|---------|----------------------|----------------------|-------------------------------|---------------------|---------------------|
| P. ampiatium           | 147,403           | 92,526   | 17,519   | 18,679  | 37.6                 | 114                  | 80                           | 4                   | 30                  |
| P. angelicoides        | 142,494           | 99,934   | 17,372   | 12,594  | 37.4                 | 114                  | 80                           | 4                   | 30                  |
| P. chujaense           | 147,839           | 93,335   | 17,590   | 18,457  | 37.4                 | 114                  | 80                           | 4                   | 30                  |
| P. delavayi            | 155,552           | 85,276   | 17,394   | 26,441  | 37.6                 | 113                  | 79                           | 4                   | 30                  |
| P. harry-smithii var. grande | 147,046          | 92,135   | 17,627   | 18,642  | 37.6                 | 113                  | 80                           | 4                   | 29                  |
| P. insolens            | 156,899           | 84,492   | 17,417   | 27,495  | 37.7                 | 113                  | 79                           | 4                   | 30                  |
| P. japonicum           | 147,967           | 93,265   | 17,572   | 18,565  | 37.5                 | 114                  | 80                           | 4                   | 30                  |
| P. mashanense          | 154,230           | 86,957   | 16,665   | 25,304  | 37.4                 | 114                  | 80                           | 4                   | 30                  |
| P. longshengense       | 152,288           | 86,645   | 17,571   | 24,036  | 37.5                 | 114                  | 80                           | 4                   | 30                  |
| P. praeruptorum        | 147,197           | 92,161   | 17,610   | 18,713  | 37.6                 | 113                  | 80                           | 4                   | 29                  |
| P. terebinthaceum      | 147,925           | 93,368   | 17,571   | 18,493  | 37.5                 | 114                  | 80                           | 4                   | 30                  |

(LSC, 84,492-99,934 bp), and a small single copy region (SSC, 16,665-17,627 bp) (Fig. 1, Table 1). The total GC content of the twelve plastomes ranged from 37.4% to 37.7% (Table 1). The twelve plastomes encoded 113-114 unique genes, including 79-80 protein-coding genes, 29-30 tRNA genes, and four rRNA genes (Table 1, Table S2). The ycf15 gene was lost in P. delavayi Franch. and P. insolens; the trnT-GGU gene was absent in P. praeruptorum and P. harry-smithii var. grande (K.T.Fu Shan et Sheh (Table S2).

In order to analyze the codon usage of Peucedanum plastomes, 79 protein-coding genes were extracted and connected for each plastome. These sequences were 66,552-68,130 bp in length and encoded 22,184-22,710 codons. The Leu was encoded by the highest number of codons (2,347-2,404), while the Cys was the least (234-666 bp) (Fig. 2). In addition, relative synonymous codon usage (RSCU) values of all codons ranged from 0.32 to 2.01 in the twelve plastomes (Table S3). Specifically, RSCU values of 30 codons were greater than 1.00 in all plastomes, whereas the codon AUA with RSCU > 1.00 was only detected in P. insolens plastomes (Fig. 2). All codons with RSCU > 1.00 were ended with A/U, except UUG (Fig. 2).

The potential RNA editing sites for 35 protein-coding genes of the twelve plastomes were detected. A total of 56-60 potential RNA editing sites were identified (Table S4, Fig. S1). All detected RNA editing sites were Cytosine to Uracil (C-U) conversion and most of them occurred in the second codon position (42-45), followed by the first codon position (12-16), but no sites situated in the third codon position (Fig. S1A). Moreover, the ndhB gene contained the highest number of RNA editing sites ranging from 10 to 11 (Fig. S1B).

The total number of SSRs ranged from 58 to 89 among the twelve Peucedanum plastomes (Fig. 3, Table S5). Most of the SSRs distributed in the LSC region for all plastomes (Fig. 3A). Among these SSRs, the mononucleotide repeats were the most abundant (28-54), followed by the dinucleotides (14-21) (Fig. 3B). In addition, bases A and T were the dominant elements for all identified SSRs in the twelve plastomes.

**Plastome comparison and hotspots identification**

The borders of IRA/SSC, IRB/SSC, and IRB/LSC among the twelve Peucedanum plastomes were slightly conserved: the IRA/SSC junctions of most samples were located between ycf1 gene and ndhF gene, but expanded into ndhF gene in P. delavayi and P. angelicoides; the boundaries of IRB/SSC fell into ycf1 gene; the IRB/LSC borders of most samples were located between genes of trnL and trnH, but extremely expanded into psbA gene in P. angelicoides (Fig. 4). However, the junctions of IRA/LSC of plastomes within Peucedanum genus were divergent and could be classified into four different types. The junctions of IRA/LSC fell into the rps19 gene in P. delavayi and P. insolens, belonging to the type I; the IRA/LSC borders contracted to the intergenic region of trnL-trnH in P. angelicoides (type II) while moved to the intergenic regions of rpl2-trnL in P. mashanense Shan et Sheh and P. medicum Dunn (type III); the IRA/LSC borders of most remainder Peucedanum plants fell into the ycf2 gene, but contracted to the intergenic regions of ycf2-trnL in P. chujaense K. Kim, S.H. Oh, C.S. Kim & C.W. Park and P. terebinthaceum (Fisch.) Fisch. ex Turcz. (type IV) (Fig. 4).

The genes arrangement of the twelve Peucedanum plastomes was relatively conserved, except for an inversion of the trnY-trnD-trnE gene detected in P. japonicum.
Thunb. and *P. medicum* (Fig. 5). However, the whole plastome sequences shared low similarity among the twelve *Peucedanum* samples, identifying 7,350 variation sites in the 142,197 alignment positions (Fig. 6). According to the sequence divergences, the 15 mutation hot-spot regions were selected as candidate DNA barcodes, including five protein coding genes—*ccsA*, *matK*, *rpl22*, *rps8*, *ycf1*—which showed the Pi > 0.01200 (Fig. 7A) and 10 non-coding regions—*ccsA*-*ndhD*, *ndhF*-*rpl32*, *petA*- *psbI*, *psbA*-*trnK*, *rpl32*-*trnL*, *rps15*-*ycf1*, *rps2*-*rpoC2*, *trnH*-*psbA*, *trnK*-*rps16*, *ycf2*-*trnL*—which showed the Pi >0.03100 (Fig. 7B).
Phylogenetic analyses

The analyses of ML and BI generated the identical tree topology. The Fig. 8 illustrated the phylogeny, including two types of support values: BI posterior probabilities (PP) and ML bootstrap values (BS). Both analyses robustly supported that members of *Peucedanum* not clustered as monophyletic but fell into four clades: (1) *P. insolens* was placed in Arcuatopterus clade (PP = 1.00, BS = 100); (2) *P. delavayi* was sister to *Pterygopleurum neurophyllum* (Maxim.) Kitag., belonging to Acronema clade (PP = 1.00, BS = 100); (3) *P. angelicoides* clustered with *Semenovia transiliensis* Regel & Herder constituting Tordyliinae (PP = 1.00, BS = 100); (4) the remainders were included in Selineae (PP = 1.00, BS = 100). Most of the *Peucedanum* accessions fell into the tribe Selineae, while these samples were also not clustered in a clade. Within Selineae, three major lineages for *Peucedanum* accessions were recognized: *P. chujaense* and *P. terebinthaceum* formed a clade that was relatively distant from others (PP = 1.00, BS = 100); *P. mashanense* was clustered with *P. medicum* (PP = 1.00, BS = 100); *P. ampliatum* K.T. Fu, *P. praeruptorum*, *P. harry-smithii* var. *grande*, *P. japonicum*, and *P. longshengense* Shan et Sheh formed a clade (PP = 1.00, BS = 100), in which *P. longshengense* firstly diverged from the remainders (PP = 1.00, BS = 100), followed by *P. japonicum* (PP = 1.00, BS = 99), and the sub-clade *P. praeruptorum* + *P. harry-smithii* var. *grande* sister to *P. ampliatum* (PP = 1.00, BS = 100). In addition, the phylogenetic relationships among non-*Peucedanum* species inferred in this study were generally consistent with the previous work [37], but our results gave the higher support values for these relationships, showing PP = 1.00 and BS ≥ 96 for all nodes.
**Discussion**

**Comparison of the plastomes in Peucedanum**

In this study, we sequenced and assembled seven plastomes of *Peucedanum* and performed a comprehensive comparative analyses of these plastomes with five other published plastomes of this genus obtained from GenBank. All *Peucedanum* plastomes showed a typically quadripartite structure, including a pair of inverted repeats regions separated by the large single copy region and small single copy region [33–36]. In addition, codon bias, RNA editing sites, and the distribution and constituent of SSRs were quite similar among twelve *Peucedanum* plastomes. These results suggested that *Peucedanum* plastome is conserved in terms of genome structure, codon bias, RNA editing sites, and SSRs. It is worth noting that this phenomenon is commonly found in other genera of flowering plants [38–40], which may be related to maintaining the stability of plastome function.

However, we also detected obvious diversity among the twelve *Peucedanum* plastomes. First, the overall sizes of plastomes varied from 142,494 bp (*P. angelioides*) to 156,899 bp (*P. insolens*) among *Peucedanum* plants. Second, the *ycf15* gene was lost in *P. delavayi* and *P. insolens*, whereas the *trnT-GGU* gene was absent in *P. praeruptorum* and *P. harry-smithii* var. *grande*. The loss of the *ycf15* gene has been detected in a wide diversity of lineages in the angiosperms [41–44], which may occur independently during the evolution of these lineages, hence, it may not provide relevant phylogenetic information. However, the loss of *trnT-GGU* gene was only observed in *P. praeruptorum* and *P. harry-smithii* var. *grande* and not identified in other members of Apiaceae [26, 37, 39], and thus it can be used as specific molecular marker to recognize this group. Third, the inversion of the *trnY-trnD-trnE* gene was detected in *P. japonicum* and *P. medicum*, which has been observed in *Angelica* L. species [26]. Finally, we observed extensive expansion and contraction of the IR regions among *Peucedanum* samples, recognizing four types of SC/IR border. All patterns have been observed in other genera of Apiaceae [26, 37, 39]. Overall, these plastome divergences detected among *Peucedanum* members further implied the non-monophyly of the *Peucedanum* genus.

![Comparison of the borders of the LSC, SSC, and IR regions among twelve Peucedanum plastomes](image-url)

**Fig. 4** Comparison of the borders of the LSC, SSC, and IR regions among twelve *Peucedanum* plastomes
Phylogeny inference
The utilization of a small number of DNA fragments for phylogenetic analysis may cause phylogenetic errors and thus result in the incongruent topology among different DNA sequences [45–47]. Hence, using few DNA sequences to infer the phylogeny of plant species might be frequently insufficient and inappropriate, especially at low taxonomic levels [26, 47]. The plastome sequence possesses highly variable characters and thus has the tremendous potential power to reconstruct the robust phylogeny at low taxonomic levels [19–22, 31]. Therefore, we performed plastid phylogenomic analyses for *Peucedanum* genus in this study. As expected, compared to previous phylogenetic studies by using single or multiple locus DNA sequences [2, 12–16], our phylogenetic analyses based on whole plastome sequences generated a robust phylogenetic framework for *Peucedanum* members, all nodes showing PP = 1.00 and BS ≥ 96. This result justifies that the plastome sequence is powerful and effective to improve the supports and resolutions of phylogeny for *Peucedanum* genus.
The Peucedanum genus was not recovered as monophyletic in our phylogenomic analyses, which was congruent with the previous studies that used ITS data and two plastid DNA regions (rpl16 and rps16 intron) [2, 12–16]. It is further supported by the great divergence of leaf epidermal morphologies [48], and fruit structures [49, 50] among Peucedanum members. These results justified that the Peucedanum genus is not a natural taxonomy unit. Therefore, the current taxonomy system of Peucedanum urgently needs to be improved and revised. Although the taxonomic treatment for Peucedanum members has not been performed in the current study due to the absence of the type species of Peucedanum (P. officinale L.), our results lay the foundations for the future taxonomic studies of Peucedanum.

The phylogenetic relationships among P. japonicum, P. praeruptorum, and P. terebinthaceum have long been controversial [14, 51, 52]. The phylogenetic analyses of Feng et al. [14] based on ITS sequences showed that P. praeruptorum was sister to P. japonicum that was relatively distant from P. terebinthaceum. However, the results of Ostroumova et al. [51] and Pimenov et al. [52] indicated that P. praeruptorum made a cluster with P. terebinthaceum being sister to P. japonicum. Our plastid phylogenomic analyses robustly supported that P. japonicum was sister to the clade consisting of P. ampliatum, P. praeruptorum and P. harry-smithii var. grande, in which the subclade of P. praeruptorum + P. harry-smithii var. grande diverged from P. ampliatum; P. terebinthaceum and P. chujaense clustered into a clade that was distant from all other Peucedanum members. The relationships recovered in the current study are different from those of previous studies [14, 51, 52]. With high supports and resolutions, our plastid-based phylogenetic analyses provide new sights into the inter-species relationship within Peucedanum.

**Potential DNA barcodes**

The accurate species identification has always been a serious challenge faced by taxonomists. The advent of DNA barcoding technology, which uses the short DNA sequences with sufficient variations to discriminate species [53], promises to resolve this difficulty. The mitochondrial gene cytochrome oxidase 1 has been proven to be effective and reliable as a standard DNA barcode for animal species identification [54–57]. However, in plants,
reliable species identification based on universal DNA barcodes, i.e., \textit{rbcL}, \textit{matK}, \textit{trnH-psbA}, is frequently problematic [58–62]. As expected, we found that the variation in \textit{rbcL} gene was relatively low (Pi = 0.00925) among \textit{Peucedanum} plants. Hence, this region may have limited power to discriminate \textit{Peucedanum} species.

Based on sequence variations, five protein coding genes (\textit{ccsA}, \textit{matK}, \textit{rpl22}, \textit{rps8}, \textit{ycf1}) and ten non-coding regions (\textit{ccsA-ndhD}, \textit{ndhF-rpl32}, \textit{petA-psbA}, \textit{psbA-trnK}, \textit{rpl32-trnL}, \textit{rps15-ycf1}, \textit{rps2-rpoC2}, \textit{trnH-psbA}, \textit{trnK-rps16}, \textit{ycf2-trnL}) were selected, which were potentially useful for species identification in \textit{Peucedanum} genus. Among them, \textit{matK} gene and \textit{trnH-psbA} region are members of universal DNA barcodes [62]; \textit{ccsA}, \textit{rpl22}, \textit{ycf1}, \textit{ccsA-ndhD}, \textit{ndhF-rpl32}, \textit{trnK-rps16}, and \textit{ycf2-trnL} have been chosen as promising DNA barcodes in other plants [26, 39, 63–65]; and \textit{petA-psbA}, \textit{rpl32-trnL}, and \textit{rps15-ycf1} regions have been widely used for phylogenetic analyses [66–70]. In a future study, we will test whether or not these sequences can serve as reliable DNA barcodes for species identification within \textit{Peucedanum} genus.

**Conclusion**

This study is the first attempt to comprehensively investigate the plastome features and infer phylogeny by using plastome data for \textit{Peucedanum} genus. Comparative analyses found that plastomes of \textit{Peucedanum} are conserved in terms of genome structure, codon bias, RNA editing sites, and SSRs, but varied in genome size, gene content and arrangement, and border of SC/IR. The plastid phylogenomic analyses prove that plastome data are efficient and powerful for improving the supports and resolutions of \textit{Peucedanum} phylogeny and robustly support that
Peucedanum is not a monophyletic group. In addition, fifteen mutation hotspot regions are identified across the plastomes that can serve as potential DNA barcodes for species identification in Peucedanum. Overall, our study lays the foundations for the future phylogeny and taxonomy of Peucedanum.

Methods

**Plant material, DNA extraction, plastome sequencing and assembly**

The fresh young leaves of seven Peucedanum taxa were collected from the wild and the greenhouse in College of Life Sciences, Sichuan University, and then dried with silica gel. The formal identifications of all samples were undertaken by Professor Xingjin He (Sichuan University). The voucher specimens were deposited at the herbarium of Sichuan University (Chengdu, China) under deposition numbers of LCK2020001- LCK2020004, LZZ2020085, JQP19082303, and JQP19082505 (Table S6). Total DNA was extracted from ~20 mg silica-gel-dried leaves with the CTAB method [71]. Genomic DNA then was fragmented into 400 bp to construct the pair-end library, following the manufacturer's protocol (Illumina, San Diego, CA, USA). The libraries were sequenced on the Illumina NovaSeq platform at Personalbio (Shanghai, China). Raw data were filtered using fastP v0.15.0 (-n 10 and -q 15) to obtain high quality reads [72]. Then high-quality reads were used to assemble the whole plastome with NOVOPlasty v2.6.2 [73],
with the default parameters and rbcl sequence from *P. japonicum* (JF943288) as seed.

**Genomic annotation and feature analyses**
The assembled plastomes were annotated using web server CPGAVAS2 (http://www.herbalgenomics.org/cpgavas2) [74]. The start and stop codons and intron positions were manually corrected according to plastomes of congeneric species in *Geneious v9.0.2* [75]. The maps of annotated plastomes were drawn using the online program OrganellarGenomeDRAW (OGDRAW) [76].

Five whole plastomes of *Peucedanum* (*P. chujaense*, *P. delavayi*, *P. insolens*, *P. praeruptorum*, and *P. terebinthaceum*) were downloaded from NCBI. Together with newly sequenced plastomes, we investigated the codon usage of *Peucedanum* plastomes with the CodonW v1.4.2 program [77]. Then, we predicted the potential RNA editing sites of protein coding genes for the twelve *Peucedanum* plastomes by using the online program Predictive RNA Editor for Plants suite with a cutoff value of 0.8 [78]. Moreover, simple sequence repeats (SSRs) for each plastomes were detected with MISA (http://pgsc.ipk-gatersleben.de/misa/). The thresholds of repeat units were set as 10, 5, 4, 3, and 3, for mono-, di-, tri-, tetra-, penta-, and hexanucleotides, respectively.

**Genomic comparison**
We compared the boundaries of the LSC, SSC and IR regions among the twelve *Peucedanum* plastomes in *Geneious v9.0.2* [75]. Then, the DNA rearrangements among *Peucedanum* plastomes were detected by using Mauve Alignment [79] implemented in *Geneious v9.0.2* [75]. Furthermore, sequence divergence of *Peucedanum* plastomes was investigated using the mVISTA tool [80], with *P. ampliatum* set as the reference.

**Identification of divergence hotspots**
In order to identify mutation hotspot regions, the protein coding genes, non-coding regions and intron regions of the twelve *Peucedanum* plastomes were extracted in *Geneious v9.0.2* [75] and aligned with MAFFT v7.221 [81]. Then, alignments with more than 200 bp in length were used to evaluate nucleotide diversity (Pi) using DnaSP v5.0 [82]. The thresholds of Pi for protein coding gene and non-coding region were set as 0.01200 and 0.03100, respectively.

**Phylogenetic analyses**
To infer the phylogenetic relationships among *Peucedanum* species, we reconstructed phylogenetic trees using 39 plastomes (Table S6, Table S7). *Cicuta virosa* L. and *Cryptotaenia japonica* Hassk. were chosen as outgroup to root the phylogenetic tree, according to the results of Wen et al. [37]. Sequence alignment was performed with the software MAFFT v7.221 [81], and adjusted and corrected manually when necessary. The unambiguous matrix was subjected to Maximum-Likelihood analyses (ML) and Bayesian Inference (BI). The ML phylogenetic tree was reconstructed in the program RAxML v8.2.8 [83] with 1000 replicates and GTRGAMMA model as the RAxML manual suggested. The BI analysis was performed by using MrBayes v3.2.7 [84] with the best-fit substitution model (TVM+I+G) determined by Modeller v3.7 [85]. Two independent Markov chains were run for 1,000,000 generations, sampling every 100 generations. The first 25% of trees were discarded as burn-in and the remaining were used to generate the consensus tree. Results of phylogenetic analyses were visualized and edited in FigTree v1.4.2 [86].

**Abbreviations**
BI: Bayesian inference; bp: Base pair; BS: Bootstrap value; CTAB: Cetyl trimethylammonium bromide; IR: Inverted repeat; ITS: Internal transcribed spacer; LSC: Large single copy; ML: Maximum Likelihood; Pi: Nucleotide diversity; PP: Posterior probability; rRNA: Ribosomal RNA; RSCU: Relative synonymous codon usage; SSC: Small single copy; SSR: Simple sequence repeat; tRNA: Transfer RNA.

**Supplementary Information**
The online version contains supplementary material available at https://doi.org/10.1186/s12870-022-03488-z.

**Additional file 1: Fig. S1.** Analyses of RNA editing sites in twelve *Peucedanum* plastomes. (A) numbers of RNA editing sites distributed in different codon positions; (B) numbers of RNA editing sites presented in genes.

**Additional file 2: Table S1.** Summary of Illumina sequencing of *Peucedanum*.

**Additional file 3: Table S2.** List of unique genes identified in plastomes of *Peucedanum*.

**Additional file 4: Table S3.** Codon usage and relative synonymous codon usage (RSCU) values of protein-coding genes of the twelve *Peucedanum* plastomes.

**Additional file 5: Table S4.** RNA editing sites detected in the twelve plastome of *Peucedanum*.

**Additional file 6: Table S5.** Numbers of SSR motifs identified in the twelve *Peucedanum* plastomes.

**Additional file 7: Table S6.** taxa newly sequenced in the present study with source, voucher and GenBank accession numbers.

**Additional file 8: Table S7.** Plastomes included in phylogenetic analyses with GenBank accession.

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**Authors’ contributions**
S-DZ and X-JH designed the research. C-KL, J-QL, and Q-PJ collected and analyzed the data; C-KL, S-DZ and X-JH prepared the manuscript. All authors read and approved the final manuscript.
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Availability of data and materials
The seven newly sequenced plastomes have been submitted into NCBI with accession numbers: OK336473-OK336479.

Declarations

Ethics approval and consent to participate
Collection of all samples completely complies with national and local legislation permission. Plant samples used in the study were not included in the list of national key protected plants and not collected from national park or natural reserve. According to national and local legislation, no specific permission was required for collecting these plants.

Consent for publication
Not applicable.

Competing interests
The authors declare that they have no competing interests.

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