

THE COMPLETE CHLOROPLAST GENOME OF A MEDICINAL PLANT, *Inula grandis* (Asteraceae)

Farkhodjon MINGBOEV*, Gulzoda ERMATOVA**, Ibromkhimjon ERGASHOV*,
Nasibakhon NARALIEVA**, Ziyoviddin YUSUPOV*

* Institute of Botany, Academy of Sciences of Uzbekistan, Tashkent, Uzbekistan

** Department of Ecology and Botany, Andijan State University, Andijan, Uzbekistan

Corresponding author: Ziyoviddin Yusupov, Institute of Botany, Academy of Sciences of Uzbekistan, Durmon yuli street 32, Tashkent, Uzbekistan,
e-mail: yusupov@mail.kib.ac.cn

Abstract. The genus *Inula* (Asteraceae) includes numerous medicinally important species, but phylogenetic relationships within the *Inula* complex remain difficult to resolve using morphological characters alone. In this study, we assembled and annotated the complete chloroplast genome of *Inula grandis* using Illumina paired-end sequencing data and compared it with 24 publicly available plastome accessions representing 13 additional species of *Inula*, *Carpesium*, *Pentanema*, and *Limbarda*. The chloroplast genome of *I. grandis* was 151,160 bp in length and exhibited the typical quadripartite structure consisting of a large single-copy region, a small single-copy region, and two inverted-repeat regions. Comparative analysis showed that the LSC/IR and IR/LSC boundaries were generally conserved, whereas greater variation was detected at the IRb/SSC junction. Sliding-window analysis identified several highly variable regions that may provide candidate markers for future phylogenetic and DNA-barcoding studies; however, their discriminatory power requires validation using broader taxon and population sampling. Maximum-likelihood analysis placed *I. grandis* with several *Carpesium* accessions, whereas most sampled *Inula* accessions were recovered in a separate lineage together with *Pentanema britanicum* and two accessions identified as *Carpesium abrotanoides*. These findings reveal discordance between plastome relationships and currently recognized generic boundaries within the *Inula* complex. Because the present analysis is based exclusively on chloroplast genomes and includes limited taxon sampling, no formal taxonomic changes are proposed. Broader sampling based on verified voucher specimens and the integration of nuclear genomic and morphological data are required to clarify evolutionary relationships within the group.

Keywords: Asteraceae; DNA barcoding; *Inula grandis*; molecular markers; phylogenetic analysis.

INTRODUCTION

The *Inula* complex, belonging to the tribe Inuleae of the family Asteraceae, comprises a morphologically diverse group of genera distributed mainly across Eurasia and Africa [2, 3, 9]. *Inula grandis* Schrenk ex Fisch. & C.A.Mey. is a perennial Central Asian species occurring in Uzbekistan and neighboring countries. The species is regarded as a medicinally important plant, and its underground organs are used as a source of medicinal plant material in Central Asia [19]. Despite its regional importance, genomic information for *I. grandis* remains limited.

The taxonomic delimitation of *Inula* and its allied genera has long been controversial because many taxa exhibit overlapping morphological characters. Molecular phylogenetic analyses based on nuclear ribosomal ITS and chloroplast DNA regions demonstrated that *Inula* in its traditional broad circumscription is not monophyletic. Species historically assigned to *Inula* were recovered together with representatives of *Carpesium*, *Pentanema*, *Telekia*, *Chrysophthalmum*, and several other related genera within the broader *Inula* complex [9]. These findings demonstrated that traditional classifications based primarily on morphology do not fully reflect the evolutionary relationships within the group.

Using expanded nuclear and plastid datasets, Gutiérrez-Larruscain et al. [14] recovered both *Inula* and *Pentanema* as paraphyletic and concluded that the generic boundaries within the *Inula* complex required revision. Based on molecular, morphological, and karyological evidence, they proposed an expanded circumscription of *Pentanema* and reinstated several segregate genera to maintain monophyletic taxonomic

units. More recently, Liu et al. [18] demonstrated that *Carpesium* is monophyletic only after the exclusion of *C. abrotanoides* and established the new genus *Cladocarpesium* to accommodate that species. Together, these studies show that generic delimitation within the *Inula* complex remains an active area of systematic research and that conclusions derived from a single genomic compartment should be interpreted cautiously.

Chloroplast genomes provide an informative source of molecular characters for comparative genomics, species identification, molecular-marker development, and phylogenetic inference. Angiosperm plastomes generally exhibit a conserved quadripartite structure consisting of a large single-copy region, a small single-copy region, and two inverted-repeat regions [6, 15, 29]. Although their overall organization is relatively conserved, sequence divergence, gene-content variation, and shifts in inverted-repeat boundaries may provide useful characters for distinguishing closely related taxa. Complete plastome sequences also contain substantially more phylogenetically informative characters than individual chloroplast markers. However, the chloroplast genome represents a single, generally uniparentally inherited linkage group, and plastome-based relationships may differ from nuclear species histories because of hybridization, introgression, lineage sorting, or other evolutionary processes [9, 14].

Complete chloroplast genomes have been reported for several species currently or historically associated with *Inula* and *Carpesium*, providing information on plastome organization, nucleotide variation, and phylogenetic relationships [24, 30]. Nevertheless, a detailed comparative plastome analysis centered on *I. grandis* and incorporating representatives of the major

lineages of the *Inula* complex remains lacking. Consequently, the plastome-based position of *I. grandis* relative to *Carpesium*, *Pentanema*, and other sampled members of the complex has not been adequately characterized.

Therefore, the objectives of this study were to: (i) assemble and annotate the complete chloroplast genome of *I. grandis*; (ii) characterize its genome size, gene content, and quadripartite organization; (iii) compare the inverted-repeat and single-copy junctions among selected members of the *Inula* complex; (iv) identify highly variable plastome regions that may serve as candidate molecular markers; and (v) assess the plastome-based phylogenetic placement of *I. grandis*. The resulting data are expected to provide a genomic resource for future studies of species identification and evolutionary relationships within the group. Because the present analysis is based primarily on chloroplast genomes and includes sequences obtained from public databases, its taxonomic implications are interpreted as provisional and should be evaluated using broader taxon sampling, verified voucher specimens, nuclear genomic data, and morphological evidence.

This research will contribute to the growing body of work aimed at clarifying the taxonomic boundaries of *Inula* species, particularly those with significant medicinal potential [14, 23, 24, 30]. By providing complete plastome data and comparative phylogenetic analyses, this study provides a genomic framework for future integrative studies of *Inula grandis* and its relatives [3, 5, 11, 12, 27, 31].

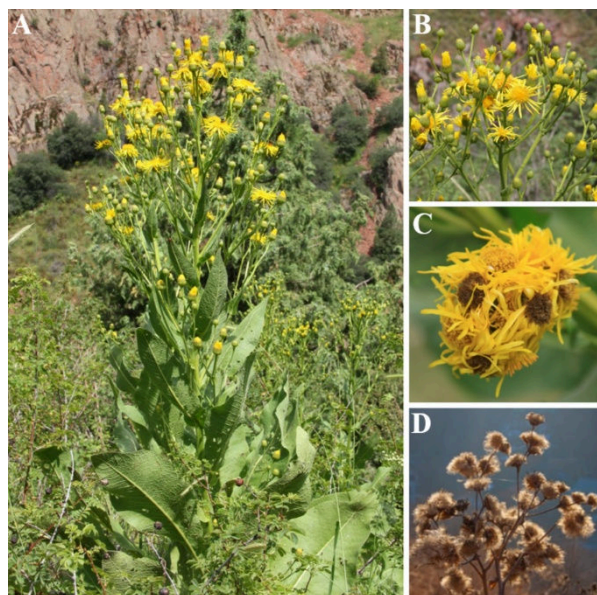


Figure 1. Various individuals of *Inula grandis* in their natural habitat. A - Flowering individual, flowering plant. Uzbekistan, Tashkent region, southern slope of the Chatkal Range, Ohangaron River basin, Kattasoy Gorge, above the "Yangiobod" tourist base, approximately 1500 m a.s.l., rocky-loamy slope, among sparse juniper forests. B - Flowering individual. C - Flowering individual. D - Apex of a fruiting plant (All photos taken by N. Beshko).

MATERIALS AND METHODS

Plant material, DNA extraction and sequencing

Fresh leaves of *Inula grandis* Schrenk ex Fisch. & C.A.Mey. were collected in May 2024 from a natural population in the Ugam–Chatkal area, Bo‘stonliq District, Tashkent Region, Uzbekistan (41.623588° N, 69.954821° E) (Fig. 1). The plant material was taxonomically identified by N. Beshko at the National Herbarium of Uzbekistan. A voucher specimen was deposited in the National Herbarium of Uzbekistan (TASH000529). The collected leaf material was immediately dried in silica gel and stored at room temperature until DNA extraction.

Total genomic DNA was extracted from silica-dried leaf tissue using a modified cetyltrimethylammonium bromide method following Doyle and Doyle [8]. High-throughput sequencing was performed on an Illumina NovaSeq 6000 platform using 150-bp paired-end reads. Adapter sequences and low-quality reads were removed using Trimmomatic v0.39 [4]. The filtered reads were used for de novo assembly of the chloroplast genome with GetOrganelle v1.7.5 [16].

Chloroplast genome annotation and visualization

The assembled chloroplast genome was annotated in Geneious Prime v2025.1.2 using the chloroplast genome of *Inula hupehensis* (GenBank accession MN418395) as a reference. Gene boundaries, start and stop codons, intron–exon junctions, and genes duplicated in the inverted-repeat regions were manually inspected and corrected where necessary. The circular chloroplast genome map was generated using OrganellarGenomeDRAW [13].

The complete chloroplast genome sequence of *I. grandis* was deposited in GenBank under accession number PQ389803.

Comparative analysis of chloroplast genomes

Twenty-four complete chloroplast genome sequences representing species of *Inula*, *Carpesium*, *Pentanema*, and *Limbarda* were downloaded from the NCBI GenBank database. Together with the newly sequenced plastome of *I. grandis*, the comparative dataset included 25 accessions representing 14 species. The species names and GenBank accession numbers used in the analyses are provided in Supplementary Table 1.

The boundaries between the large single-copy region, small single-copy region, and the two inverted-repeat regions were compared among the selected plastomes. The LSC/IRb, IRb/SSC, SSC/IRa, and IRa/LSC junctions were visualized using IRscope [1]. Gene positions and distances from the junctions were subsequently checked in Geneious Prime v2025.1.2.

Nucleotide diversity analysis

The complete chloroplast genome sequences were aligned using MAFFT v7 [17]. The resulting alignment was inspected and manually adjusted where necessary. Nucleotide diversity values were calculated using DnaSP v6.12.03 [22]. Sliding-window analysis was conducted with a window length of 800 bp and a step

size of 200 bp. Regions showing comparatively high nucleotide diversity were considered candidate variable regions for future phylogenetic and DNA-barcoding studies.

Phylogenetic analysis

Phylogenetic relationships among the sampled taxa were reconstructed using complete chloroplast genome sequences. The aligned dataset was analyzed using the maximum-likelihood method implemented in RAXML v8.2.12 [25]. Branch support was evaluated using 1,000 bootstrap replicates. *Limbarda crithmoides* was selected as the outgroup. The resulting phylogenetic tree was visualized and edited using iTOL v7, and bootstrap support values were displayed at the corresponding nodes.

RESULTS

The complete chloroplast genome of *Inula grandis* was assembled as a circular molecule of 151,160 bp. It exhibited the typical quadripartite structure, consisting of a large single-copy (LSC) region of 82,774 bp, a small single-copy (SSC) region of 18,484 bp, and two inverted-repeat regions (IRa and IRb) of 24,951 bp each.

The overall GC content of the chloroplast genome was 38%.

The plastome contained 131 genes, including 87 protein-coding genes, 36 transfer RNA genes, and eight ribosomal RNA genes. Genes located within the inverted-repeat regions were present in two copies. The circular chloroplast genome map of *I. grandis*, including gene positions, transcriptional directions, functional categories, and GC-content variation, is presented in Figure 2.

The chloroplast genomes included in the comparative analysis ranged in size from 150,754 bp in *Inula japonica* to 152,592 bp in *I. racemosa*. The lengths of the LSC regions ranged from 82,428 to 83,642 bp, whereas the SSC regions ranged from 18,422 to 18,590 bp. The lengths of the individual IR regions varied from 24,921 to 25,180 bp. Thus, differences in total plastome length were associated with variation in both the single-copy regions and the positions of the IR boundaries.

The organization of the LSC/IRb junction (JLB) was generally conserved among the examined plastomes. The *rps19* gene was positioned near the end of the LSC region, whereas *rpl2* was located within IRb. Minor differences were observed in the distances of these genes from the boundary.

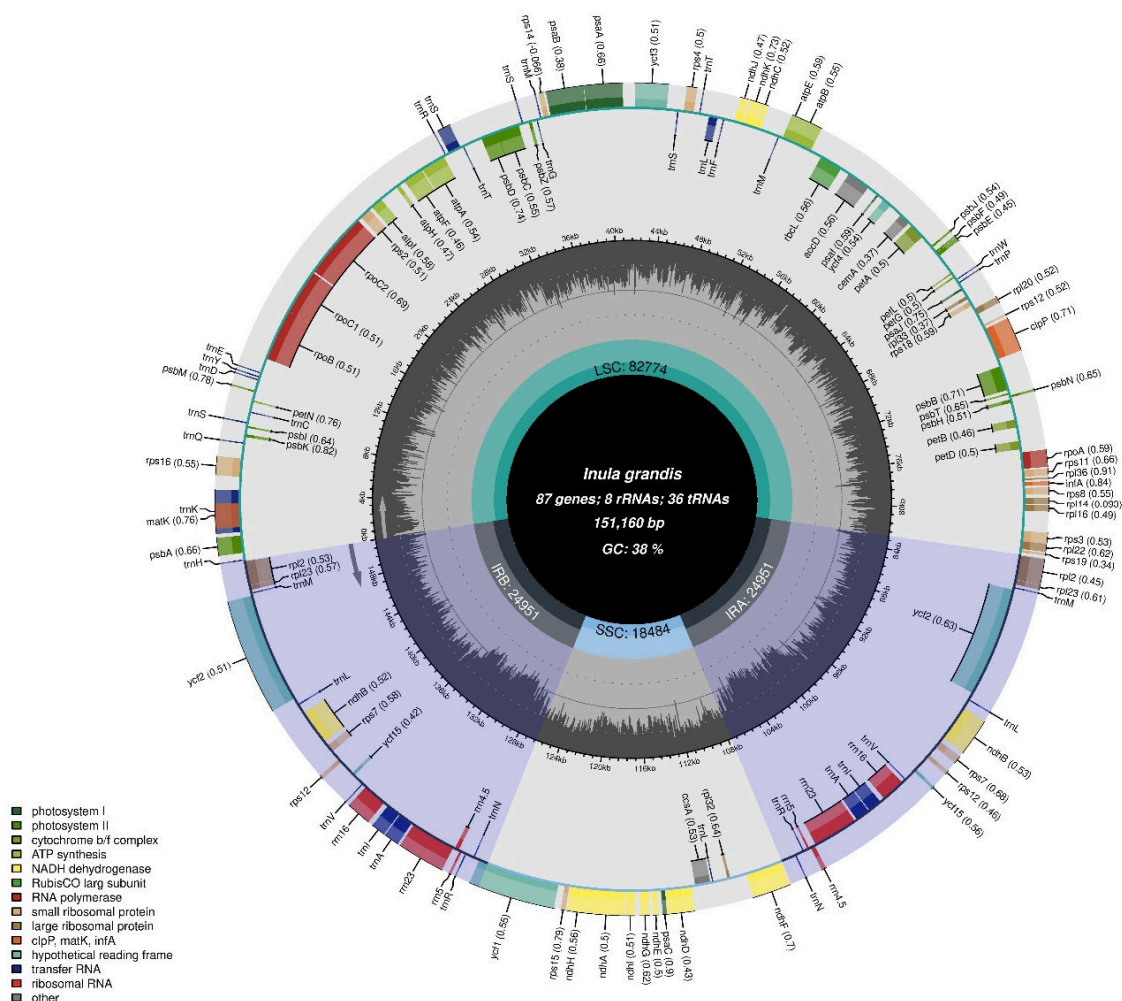


Figure 2. Chloroplast genome map of species within the genus *Inula*. Genes located within the circle are transcribed in a clockwise direction, while those outside the circle are transcribed counterclockwise. The inner dark grey circle indicates the GC content, while the light grey circle represents the AT content.

The organization of the LSC/IRb junction (JLB) was generally conserved among the examined plastomes. The *rps19* gene was positioned near the end of the LSC region, whereas *rpl2* was located within IRb. Minor differences were observed in the distances of these genes from the boundary.

Greater variation was detected at the IRb/SSC junction (JSB). The position of the *ndhF* gene differed among the examined accessions, and in several plastomes it extended across or was located immediately adjacent to the JSB boundary. A truncated copy of *ycf1* was also detected near this junction in many of the examined genomes, although its position and length varied among accessions.

At the SSC/IRa junction (JSA), the positions of *ycf1* and *ndhF* showed noticeable variation. In several plastomes, *ycf1* extended from the SSC region into IRa, whereas the distance between *ndhF* and the junction differed among taxa. These differences indicate that the IR/SSC boundaries were more variable than the LSC/IR boundaries.

The IRa/LSC junction (JLA) was comparatively stable. The *rpl2* gene was located within IRa, while *trnH-GUG* and *psbA* were positioned in or near the adjacent LSC region. Only minor differences in the distances between these genes and the JLA boundary

were observed. The comparative organization of the four chloroplast genome junctions is shown in Figure 3.

Sliding-window analysis revealed an uneven distribution of nucleotide diversity across the aligned chloroplast genomes. The π values ranged from 0 to 0.038. Most regions showed low to moderate nucleotide variation, whereas several distinct peaks were detected.

The highest nucleotide-diversity value was recorded in the region associated with *rpl32*, where π approached 0.038. Additional highly variable regions were detected around *rps16-psbK*, *rpoB*, *trnS-CGA-trnT-GGU*, and *ndhA-ycf1*. In these regions, π values generally ranged from approximately 0.020 to 0.030.

In contrast, broad portions of the plastome, particularly the intervals of approximately 96,000–118,000 bp and 140,000–165,000 bp, exhibited very low nucleotide diversity. These regions were comparatively conserved among the examined accessions. The identified highly variable regions may represent candidate loci for future phylogenetic, population-genetic, and DNA-barcoding studies, although their discriminatory efficiency requires further validation using broader taxonomic and population sampling. The distribution of nucleotide diversity across the chloroplast genomes is shown in Figure 4.

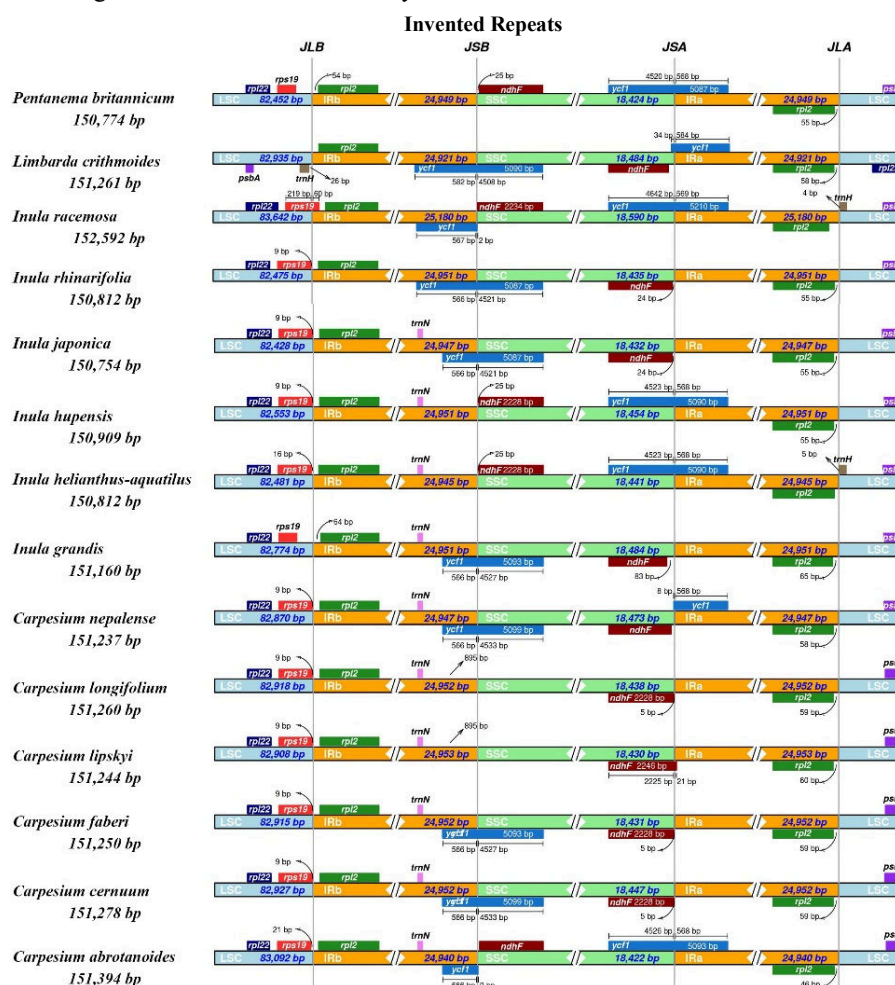


Figure 3. Comparative analysis of the LSC, IR and SSC boundary regions in the 14 chloroplast genomes of the genus *Inula*. The JLB represents the junction of LSC and IRb, JSB indicates the junction of SSC and IRb, JSA denotes the junction of SSC and IRa, and JLA signifies the junction of LSC and IRa.

Maximum-likelihood analysis based on complete chloroplast genome sequences resolved the examined accessions into two principal ingroup lineages, with *Limbarda crithmoides* used as the outgroup.

In the first principal lineage, *Inula grandis* was recovered as sister to a group containing most of the sampled *Carpesium* accessions. Within this lineage, the accession of *Carpesium abrotanoides* OM302256 occupied an early-diverging position, followed by *C. nepalense*. The two accessions of *C. cernuum* formed a sister pair, as did the two accessions of *C. faberi*. *Carpesium longifolium* was closely related to the two accessions of *C. lipskyi*, which also formed a well-supported pair.

The second principal lineage contained most of the sampled *Inula* accessions, two accessions identified as *Carpesium abrotanoides*, and two accessions of *Pentanema britannicum*. Within this lineage, *Inula japonica* MN974527 was recovered as sister to the two accessions of *I. linariifolia*. The two accessions of *I. racemosa* formed a closely related pair and were

associated with *C. abrotanoides* NC063321 and MT663326.

The two accessions of *Inula helianthus-aquaticus* were recovered together and were closely related to *I. hupehensis*. The remaining two accessions of *I. japonica*, NC063729 and MW115528, formed a separate pair from *I. japonica* MN974527. These accessions were closely associated with the two accessions of *Pentanema britannicum*, which formed a sister pair.

Multiple accessions assigned to *I. linariifolia*, *I. racemosa*, *I. helianthus-aquaticus*, *C. cernuum*, *C. faberi*, *C. lipskyi*, and *P. britannicum* were recovered as species-specific pairs. In contrast, the accessions identified as *I. japonica* and *C. abrotanoides* did not form single exclusive clades. In addition, the sampled accessions assigned to *Inula* and *Carpesium* were not recovered as mutually exclusive genus-level groups in the plastome phylogeny. The maximum-likelihood tree is presented in Figure 5.

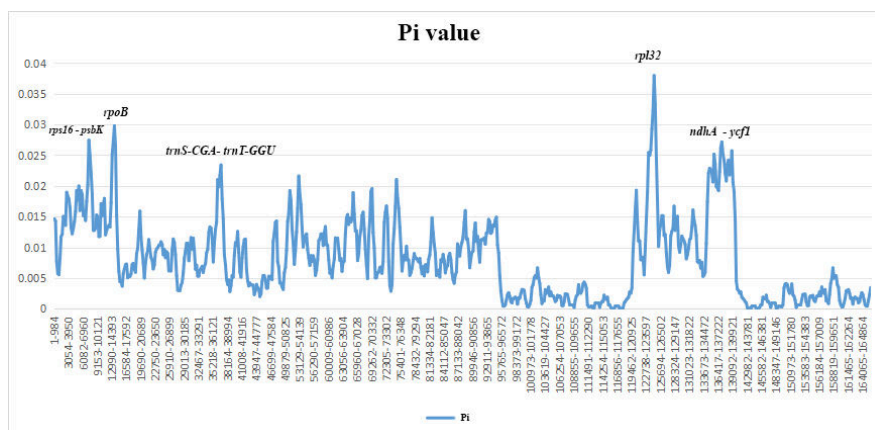


Figure 4. The nucleotide variability (Pi value) of the genomes of the genus *Inula* of the presented in a sliding window (window length: 800 bp; step size: 200 bp).

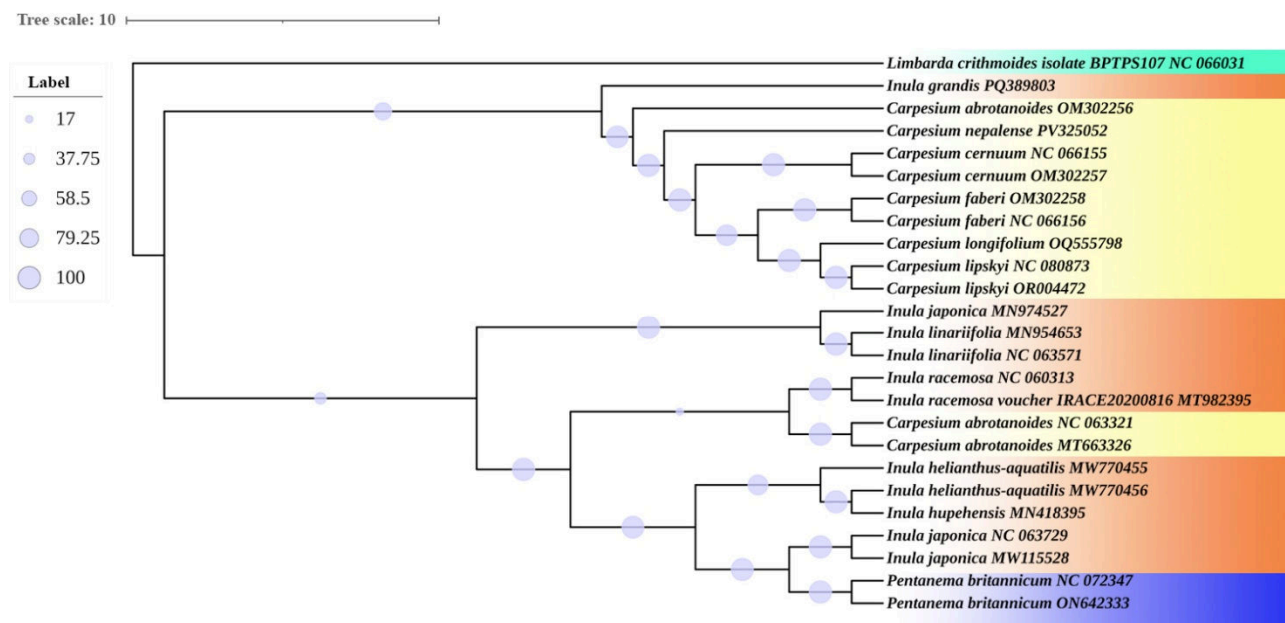


Figure 5. Phylogenetic tree of the *Inula* species based on the whole chloroplast genome using maximum likelihood (ML). Maximum support values are indicated at the nodes.

DISCUSSION

The complete chloroplast genome of *Inula grandis* exhibited the typical quadripartite structure characteristic of most angiosperm plastomes, comprising a large single-copy region, a small single-copy region, and two inverted-repeat regions [6, 15]. The plastome was 151,160 bp in length and contained 87 protein-coding genes, 36 tRNA genes, and eight rRNA genes. Its overall structure, gene content, and GC content were generally consistent with previously reported chloroplast genomes of *Inula*, *Carpesium*, and other members of Asteraceae [24, 30].

The plastome sizes of the examined accessions ranged from 150,754 to 152,592 bp, indicating a relatively conserved genome organization. The observed differences in total plastome length were associated with variation in the lengths of the LSC, SSC, and IR regions. Small expansions and contractions of IR regions are commonly observed in angiosperm chloroplast genomes and may contribute to differences in plastome size among closely related taxa [6, 15, 24, 30].

The LSC/IRb and IRa/LSC junctions were comparatively conserved among the examined plastomes. At the LSC/IRb junction, *rps19* was located near the end of the LSC region, whereas *rpl2* was positioned within IRb. At the IRa/LSC junction, *rpl2* occurred within IRa, while *trnH-GUG* and *psbA* were located within or close to the adjacent LSC region. Similar conservation of the LSC/IR junctions has been reported in comparative plastome studies of *Carpesium* and *Inula* [24, 30].

In contrast, greater variation was observed at the IRb/SSC and SSC/IRa junctions. The position of *ndhF* relative to the IRb/SSC junction differed among the examined accessions, and both the length and position of the truncated *ycf1* copy varied. At the SSC/IRa junction, *ycf1* extended from the SSC region into IRa in several plastomes. Variation in the positions of *ndhF* and *ycf1* at IR/SSC junctions has also been reported in other Asteraceae plastomes and represents a common source of structural variation among closely related taxa [24, 30].

Nevertheless, minor differences in IR boundaries should be interpreted cautiously. Alternative orientations of the SSC region, differences in genome assembly, and inconsistencies in annotation may affect the apparent positions of genes near plastome junctions. Consequently, small differences in IR boundaries should not be regarded as taxonomically diagnostic without standardized genome orientation, consistent annotation, and broader taxonomic sampling.

Sliding-window analysis showed that nucleotide diversity was unevenly distributed across the aligned chloroplast genomes. Most plastome regions were relatively conserved, whereas several localized regions showed increased nucleotide variation. The highest π value was detected in the region associated with *rpl32*. Additional variable regions occurred around *rps16*–

psbK, *rpoB*, *trnS-CGA*–*trnT-GGU*, and *ndhA-ycf1*. Comparable studies have also shown that non-coding and intergenic plastome regions frequently contain higher levels of nucleotide variation than conserved coding regions [24, 30].

The highly variable regions identified in this study may provide candidate loci for phylogenetic analyses, population-level studies, and DNA barcoding [5, 22, 30]. However, these regions should not yet be regarded as validated molecular markers. Their discriminatory efficiency must be evaluated using multiple individuals per species, broader geographical sampling, and comparisons with established plastid and nuclear markers. A region that is variable among the accessions examined here may not necessarily provide reliable species-level discrimination across the entire distribution ranges of the sampled taxa.

The maximum-likelihood analysis placed *Inula grandis* as sister to a lineage containing most of the sampled *Carpesium* accessions. This result indicates a close plastome relationship between *I. grandis* and the sampled representatives of *Carpesium*. However, it does not provide sufficient evidence for transferring *I. grandis* to *Carpesium*. Chloroplast genomes generally represent a single, uniparentally inherited genomic compartment, and plastome relationships may differ from the evolutionary history inferred from nuclear data because of processes such as hybridization, introgression, and plastid capture [9, 14].

Several accessions assigned to the same species were recovered as sister pairs. This pattern was observed in *Carpesium cernuum*, *C. faberi*, *C. lipskyi*, *Inula linariifolia*, *I. racemosa*, *I. helianthus-aquatilis*, and *Pentanema britannicum*. These results indicate relatively consistent plastome relationships among the corresponding accessions.

In contrast, accessions identified as *Inula japonica* occupied different positions in the phylogenetic tree. The accession MN974527 was recovered close to the two accessions of *I. linariifolia*, whereas NC_063729 and MW115528 formed a separate pair near *P. britannicum*. The separation of accessions assigned to the same species may be related to specimen misidentification, differences in taxonomic treatment, assembly or annotation errors, introgression, plastid capture, or genuine intraspecific plastome variation. Examination of authenticated voucher specimens and original sequence data will be required to distinguish among these possible explanations.

The accessions deposited in GenBank as *Carpesium abrotanoides* also occupied different positions in the plastome tree. OM302256 was recovered within the lineage containing most other *Carpesium* accessions, whereas NC_063321 and MT663326 occurred in the second principal lineage together with several *Inula* accessions. Recent systematic research based on plastid, nuclear, morphological, and karyological evidence demonstrated that *Carpesium*, excluding *C. abrotanoides*, forms a monophyletic group and

established the genus *Cladocarpesium* for the latter species [18].

Accordingly, the sequences used in the present analysis may be referred to as “accessions deposited in GenBank as *Carpesium abrotanoides*” to preserve traceability to the database records. Their updated taxonomic treatment can be indicated in Supplementary Table S1 as *Cladocarpesium abrotanoides*. However, the markedly different positions of the three accessions cannot be explained by the nomenclatural change alone and require further verification of voucher identities and sequence data.

The sampled accessions assigned to *Inula* and *Carpesium* were not recovered as mutually exclusive genus-level plastome lineages. This result is consistent with earlier molecular studies that demonstrated complex relationships and difficult generic delimitation within the broader *Inula* complex [3, 9, 14, 18]. Nevertheless, the taxonomic sampling of the present analysis was limited and cannot provide a comprehensive test of the monophyly of either genus.

Only one species of *Pentanema*, represented by two accessions of *P. britannicum*, was included in the present dataset. Therefore, this analysis cannot determine whether *Pentanema* as a genus is monophyletic, paraphyletic, or polyphyletic. The placement of *P. britannicum* close to several *Inula* accessions should not be interpreted as evidence that *Pentanema* must be merged with *Inula*. Previous broader analyses using nuclear, plastid, morphological, and karyological evidence proposed a recircumscription of *Pentanema*, rather than its inclusion within *Inula* [14].

Formal taxonomic changes should not be proposed on the basis of the present plastome dataset alone. Reliable generic delimitation requires broader representation of species from *Inula*, *Carpesium*, *Pentanema*, and related genera, together with authenticated voucher specimens, nuclear sequence data, morphology, and, where relevant, cytological evidence [9, 14, 18]. Comparisons between nuclear and chloroplast phylogenies would also help identify possible cases of hybridization, introgression, or plastid capture.

In conclusion, the complete chloroplast genome of *I. grandis* provides a valuable genomic resource for comparative, phylogenetic, and molecular-marker studies. The plastome displayed a generally conserved structure, with the greatest boundary variation occurring at the IR/SSC junctions. Several highly variable regions were identified as potential candidate markers, although their effectiveness requires further validation.

The plastome phylogeny placed *I. grandis* close to most of the sampled *Carpesium* accessions and revealed inconsistencies between several GenBank taxon names and their chloroplast relationships. However, limited taxon sampling, reliance on a single genomic compartment, and the lack of independent verification of all voucher specimens prevent formal taxonomic conclusions. Future studies integrating broader species

and population sampling, nuclear genomic data, verified herbarium material, morphology, and cytology will provide a more reliable framework for understanding evolutionary relationships and generic boundaries within the *Inula* complex.

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Conflict of interest. There is no actual or potential conflict of interest in relation to this article.

Supplementary Table 1. NCBI accession numbers of the species of the genus *Inula* and outgroup.

No.	Species name	NCBI accession number
1.	<i>Limbarda crithmoides</i>	NC_066031
2.	<i>Inula grandis</i>	PQ389803
3.	<i>Carpesium abrotanoides</i>	OM302256
4.	<i>Carpesium abrotanoides</i>	NC_063321
5.	<i>Carpesium abrotanoides</i>	MT663326
6.	<i>Carpesium nepalense</i>	PV325052
7.	<i>Carpesium cernuum</i>	NC_066155
8.	<i>Carpesium cernuum</i>	OM302257
9.	<i>Carpesium faberi</i>	OM302258
10.	<i>Carpesium faberi</i>	NC_066156
11.	<i>Carpesium longifolium</i>	OQ555798
12.	<i>Carpesium lipskyi</i>	NC_080873
13.	<i>Carpesium lipskyi</i>	OR004472
14.	<i>Inula japonica</i>	MN974527
15.	<i>Inula japonica</i>	NC_063729
16.	<i>Inula japonica</i>	MW115528
17.	<i>Inula linariifolia</i>	MN954653
18.	<i>Inula linariifolia</i>	NC_063571
19.	<i>Inula racemosa</i>	NC_060313
20.	<i>Inula racemosa</i>	MT982395
21.	<i>Inula helianthus-aquaticus</i>	MW770455
22.	<i>Inula helianthus-aquaticus</i>	MW770456
23.	<i>Inula hupehensis</i>	MN418395
24.	<i>Pentanema britannicum</i>	NC_072347
25.	<i>Pentanema britannicum</i>	ON642333

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