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PLASTOME REPORT

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The complete chloroplast genome assembly of *Solidago altissima* (Lineaus, 1753) (Astereae; Asteraceae)

Eun Su Kang, Dong Chan Son and Sang-Chul Kim

Forest Biodiversity Division, Korea National Arboretum, Gyeonggi-do, Republic of Korea

ABSTRACT

This study aims to report the complete chloroplast genome of *Solidago altissima* L., a globally recognized invasive plant. The complete genome length of *S. altissima* is 152,961 bp; *S. altissima* has a typical quadripartite structure (including a large single copy of 84,829 bp, a small single copy of 18,084 bp, and two inverted repeat regions of 25,024 bp), which is commonly found in angiosperms. The genome contains 129 genes, consisting of 85 coding sequences, 36 tRNA genes, and 8 rRNA genes. To understand the phylogenetic relationship between *S. altissima* and its related species, maximum likelihood analysis was performed. The results revealed that *S. altissima* is closely related to *Symphyotrichum subulatum*. The findings of the present study could provide fundamental data for the future phylogenetic and evolutionary studies, while also research on species invasion and resolving complexity of *S. altissima*.

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Plastome; coding sequences; Asteraceae; Astereae; phylogenetic relationship

Introduction

Solidago altissima (Linnaeus 1753), commonly known as goldenrod, is a perennial species belonging to the *Triplinervae* subsection of *Solidago* (Astereae, Asteraceae) (Sakata et al. 2015; Semple and Beck 2021), and is globally recognized as an invasive plant. It is estimated to possess exceptional competitive advantages in ecosystems, owing to its abundant reproductive capacity and production of allelopathic substances (Sakata et al. 2015; Verloove et al. 2017; Kato-Noguchi and Kato 2022). This species demonstrates strong invasiveness in both disturbed areas and natural ecosystems, such as grasslands, meadows, and forest edges (Sakata et al. 2015). Several countries have designated *S. altissima* as an invasive species that requires management to control its unbridled spread (Park et al. 2020), and various studies are being performed to understand the spread and invasion patterns of this species.

The chloroplast genome plays a crucial role in various molecular approaches. Analysis of chloroplast genome sequences is necessary to identify morphologically indistinct species and offer insights into the relationships and evolutionary patterns of taxa (Nock et al. 2011; Li et al. 2015; Daniell et al. 2016; Li et al. 2016). Furthermore, it has been applied in recent studies on species invasion (Dowell et al. 2016; Wood et al. 2016; Hinsinger and Strijk 2017; Meyer et al. 2017). To explore the genetic diversity of populations, studies were performed wherein SNP and SSR markers were developed using chloroplast genome information (Dowell et al. 2016; Wood et al. 2016; Hinsinger and Strijk 2017; Meyer et al. 2017). These studies can assist in deducing the origin and introduction pathways of species and identifying their genetic invasions within the ecosystem. The findings of these studies can provide insights into the invasion processes of invasive species and ultimately contribute to the advancement of research on species invasion and biodiversity conservation.

For the aforementioned studies on *S. altissima*, a complete chloroplast genome of this species can be considered necessary; but, it has not been reported. Therefore, the present study aimed to analyze and report the chloroplast genome sequence of this species. The results could serve as foundational information for future studies, not only on the phylogenetics and evolutionary aspects of the *Solidago* genus but also on the invasion and conservation of species.

Materials and methods

Solidago altissima was identified and collected in Orasam-dong, Jeju-si, Jeju-do, South Korea (N33.464583 E126.513666) in September 2021 by Seong Gwon Lee, the director of the Jeju Ecotourism Society (Figure 1). The specimens were deposited at the Herbarium of Korea National Arboretum (KH) (http://www.nature.go.kr, Dong Chan Son, e-mail: sdclym@korea.kr, voucher number: KHB1644521) (Figure S1). Dried leaves (100 mg) were used for DNA extraction, which was performed using a DNeasy Plant Mini Kit (Qiagen, Hilden, Germany), as per the provided protocol. The extracted DNA

CONTACT Sang-Chul Kim majin01@korea.kr Forest Biodiversity Division, Korea National Arboretum, Gyeonggi-do, Republic of Korea

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Figure 1. Photographs of *solidago altissima*. (A) *Solidago altissima* usually grows along roadsides or in open areas in South Korea, and in their habitats, abundant individuals occupy vast areas; (B) the whole plants grow up to heights of 50–250 cm; (C) the capitula are arranged in paniculiform synflorescences, attached on one side, with their branches curved downward; (D) the flowers are yellow, and bloom from September to October in South Korea. The photographs were taken by Seong Gwon Lee in Jeju-si, Jeju-do, South Korea, and we obtained permission for their use in this study.

was filtered through a 2% agarose gel to obtain high-purity gDNA, which was subsequently sequenced on an Illumina MiSeq platform with a 301 bp insert size. A total of 6,376,768 reads were acquired and used for *de novo* plastome assembly using the GetOrganelle v1.7.7.0 toolkit (Jin et al. 2018), and the read coverage depth of the generated genome was validated using the Draw_SequencingDepth.py script provided by Ni et al. (2023). The chloroplast genome was annotated using GeSeq (Tillich et al. 2017) and finally compared, validated, and corrected in Geneious v.8.0.5 with reference to *Symphyotrichum subulatum* (MN541093) from NCBI (https://www.ncbi.nlm.nih.gov). The map of the genome was drawn using CPGView (http://www.1kmpg.cn/cpgview).

To investigate the phylogenetic relationships between *S. altissima* and its related species, maximum liklihood (ML) analysis was conducted using coding sequences (CDS). To perform the analysis, selected nine species from the Astereae tribe, which includes *S. altissima*, and two outgroup species (*Eclipta* spp.) from the Heliantheae tribe. The chloroplast genome data for these species were downloaded from the NCBI database. In total, 79 CDS were concatenated and aligned with MAFFT using Geneious v.8.0.5 (https://www.geneious.com). Subsequently, the analysis model was tested using Phylosuite v.1.2.2, and ML analysis was performed using IQ-tree v.2.1.3, with model GTR + F + I + G4 and 1000 bootstrap replicates. The results were visualized using FigTree v.1.4.4 (http://tree.bio.ed.ac.uk/software/figtree).

Results

The length of the complete chloroplast genome is 152,961 bp, with a GC content of 39.0% (Figure 2), and the average value of the genome coverage depth is 185.29 X (Figure S2). The complete chloroplast genome data of *S. altissima* have been submitted to the NCBI (accession number PP108063).

The genome has a typical quadripartite structure, with two inverted repeat (IR) regions separating the large single

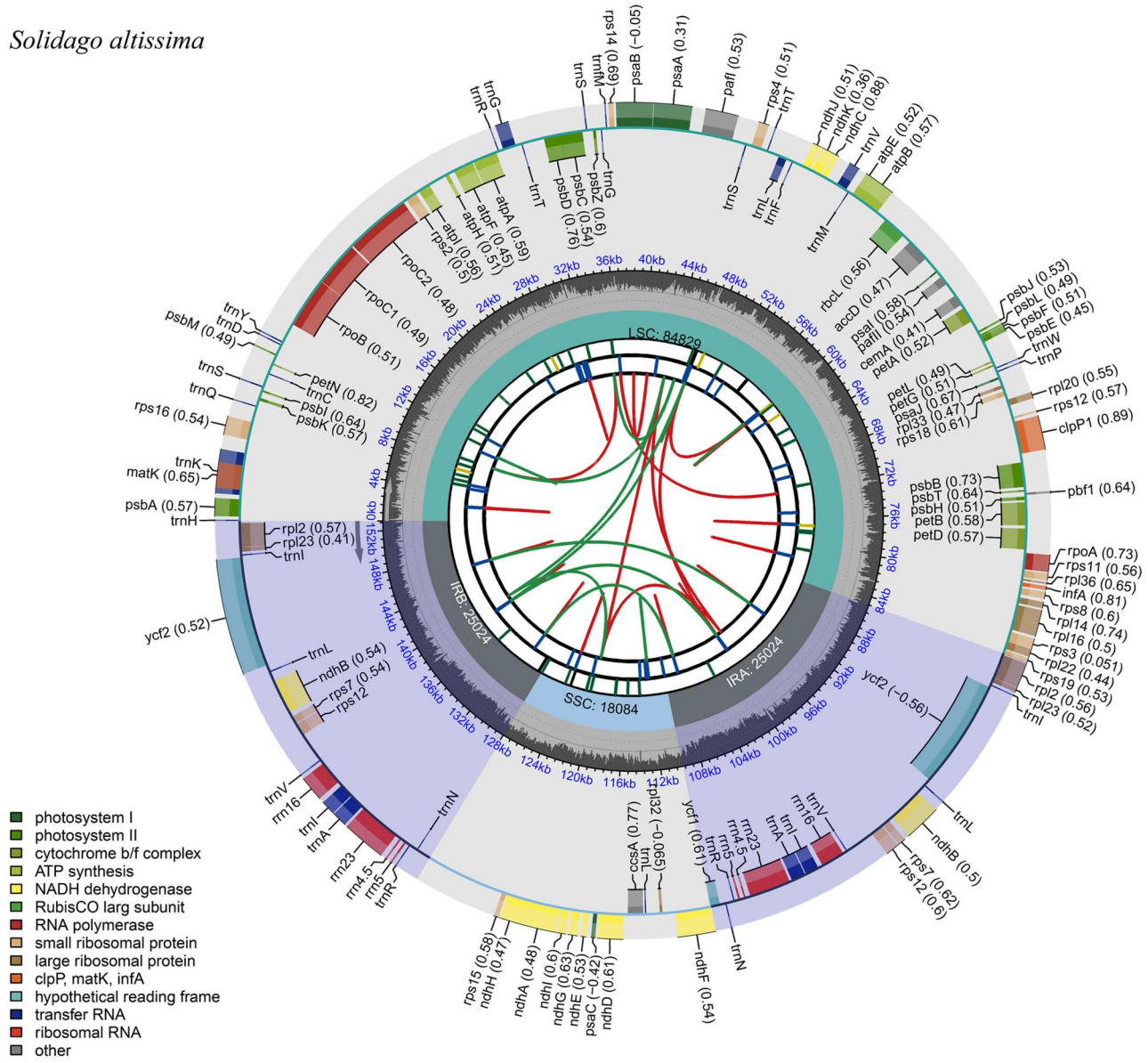

Figure 2. Circular map of *Solidago altissima*. The complete chloroplast genome was generated using. The map consists of six tracks. From the center to the outer, the first track shows dispersed repeats connected by red and green arcs indicating the direction (forward and reverse, respectively). The second track shows long tandem repeats as blue bands, and the third track shows short tandem repeats or microsatellites as green bands. The fourth track represents the GC content along the plastome. The sixth track represents the genes as colored boxes, the inner boxes present clockwise transcription, and the outer boxes present counterclockwise transcribed genes. The numbers within parentheses following gene names represent optional codon usage bias.

copy (LSC) and small single copy (SSC) regions. The length of each segment was as follows: LSC, 84,829 bp; SSC, 18,084 bp; and IR, 25,024 bp. The genome contains 129 genes, including 85 CDS genes, 36 tRNA genes, and eight rRNA genes. Among these, there are 17 genes in the IR region, including six CDS genes (*ndhB*, *rpl2*, *rpl23*, *rps7*, *rps12*, and *ycf2*), seven tRNA genes (*trnA-UGC*, *trnI-CAU*, *trnI-GAU*, *trnL-CAA*, *trnN-GUU*, *trnR-ACG*, and *trnV-GAC*), and four rRNA genes (*rrn4.5*, *rrn5*, *rrn16*, and *rrn23*). There are 11 cis-splicing genes: nine genes (*atpF*, *ndhA*, *ndhB*, *petB*, *petD*, *rpl2*, *rpl16*, *rpoC1*, and *rps16*) have a single intron each and two genes (*clpP1* and *pafI*,) have two introns each (Figure S3). The trans-splicing gene (*rps12*) spans from the 5′ end in the LSC region to the 3′ end in the IR region (Figure S4).

Dichrocephala benthamii emerged as the earliest diverging species within the Astereae (Figure 3). Subsequently, *Aster* species, followed by *Lagenophora* species, formed successive branches in the ML tree. Later, *S. altissima* branched off, forming a closely related group with *Symphyotrichum subulatum*, and diverged from the *Erigeron* species group.

Discussion and conclusion

Solidago altissima, through aggressive spreading, has expanded its distribution range across most regions of the United States and the southern regions of Canada (Sakata et al. 2015; Verloove et al. 2017; Park et al. 2020; Kato-Noguchi and Kato 2022). Moreover, it displays invasiveness in introduced regions, including China, Japan, and South Korea (Sakata et al. 2015; Verloove et al. 2017; Park et al. 2020; Kato-Noguchi and Kato 2022). This invasive plant is also well-known for its morphological complexity (Sakata et al. 2015;

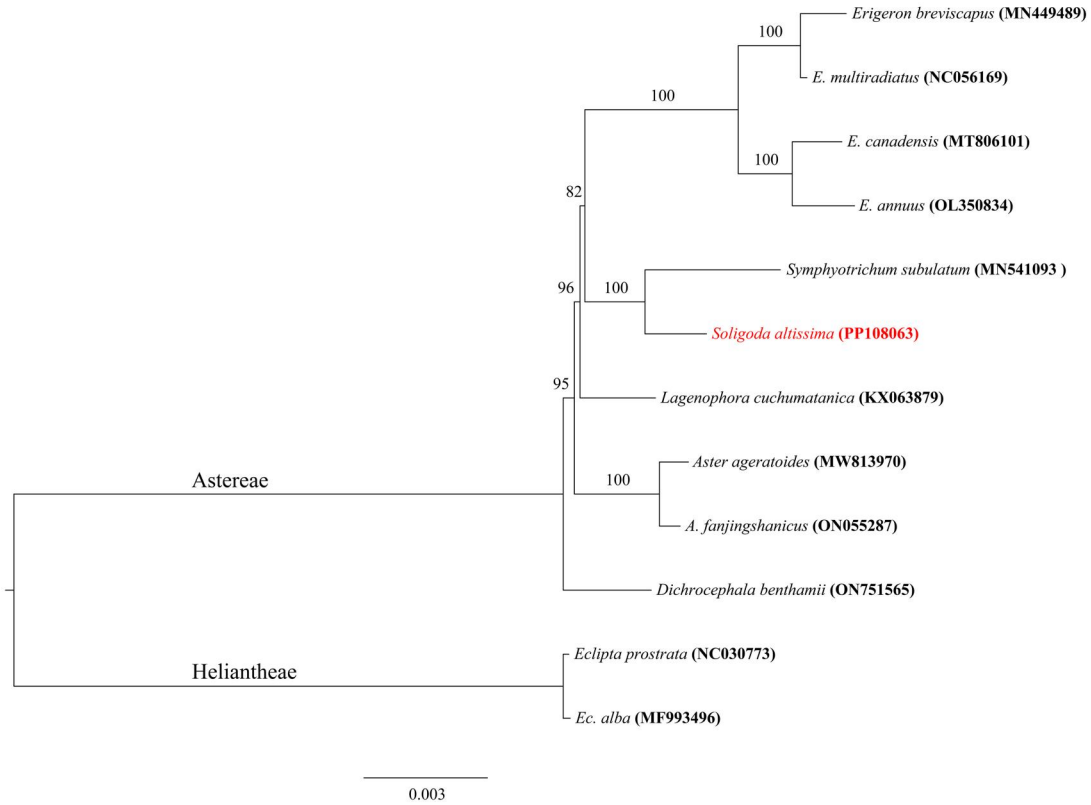

Figure 3. The maximum likelihood phylogenetic tree of ten species in Astereae tribe and, the outgroup, two species in Heliantheae tribe based on concatenated CDSs of chloroplast genomes. Numbers on the nodes indicated the bootstrap proportion. The following sequences were used: *Solidago altissima* PP108063 (present study), *Erigeron canadensis* MT806101 (Oh and Park 2023), *Dichrocephala benthamii* ON751565 (unpublished), *E. annuus* OL350834 (unpublished), *Aster ageratoides* MW813970 (unpublished), *Symphyotrichum subulatum* MN541093 (Hu 2020), *E. multiradiatus* NC056169 (Li et al. 2019), *E. breviscapus* MN449489 (Li et al. 2019), *Eclipta Alba* MF993496 (Kim et al. 2017), *Lagenophora cuchumatanica* KX063879 (Vargas et al. 2017), *Ec. prostrata* NC030773 (Park et al. 2016), *A. fanjingshanicus* ON055287 (Choi and Park 2015).

Verloove et al. 2017; Tian et al. 2023). This is due to diverse morphological variations depending on the environment and active intraspecific hybridization (Lopez Laphitz 2009; Sakata et al. 2015). Additionally, *S. altissima* exhibits differences, even in the polyploidy of individual, which are presumed to be associated with their micromorphological traits that contribute to their complexity (Sakata et al. 2015; Semple et al. 2015). Therefore, distinguishing *S. altissima* from other *Solidago* species poses challenges, especially considering the ongoing debate about whether it should be regarded as the same species as *S. canadensis* (Verloove et al. 2017, Tian et al. 2023).

In the present study, the chloroplast genome sequence of *S. altissima* was determined; the genome was identical to that of the 10 Astereae species used in the analysis in terms of structure, included genes, and gene order. According to the results of the ML analysis, *S. altissima* exhibits the closest phylogenetic relationship with *Symphyotrichum subulatum* among the Astereae species, a finding that is consistent with the results of Zhou et al. (2022).

Astereae is the second largest tribe of the Asteraceae, encompassing over 170 genera and more than 3000 species (Noyes and Rieseberg 1999). However, this study was conducted with a very limited number of species, only 10 Astereae species, and among them, there was only one *Solidago* species, *S. altissima*. Therefore, the results of the present study have limitations in providing precise insights into the relationships between *S. altissima* and related genera or species of Astereae. Therefore, further research on more species is needed. Nevertheless, the results of the present study could serve as foundational data for future phylogenetic and evolutionary studies on the *Solidago* genus, while also providing valuable information for research on species invasion and resolving the complexity of *S. altissima*.

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We sincerely appreciate Seong Kwon Lee for providing relevant photographs for this study.

Ethical approval

The materials used in this study were not listed on the IUCN Red List, and the collection area was not a protected area. We did not need specific permission to collect samples of this species from authorities.

Authors' contributions

E. S. Kang designed and wrote the paper, and created the figures. S.C. Kim and D.C. Son conducted the experiments and analyzed the data. The acquisition and management of funds for this research were carried out by D. C. Son. All authors contributed to this study and have read and agreed to the published version of the manuscript.

Disclosure statement

No potential conflict of interest was reported by the author(s).

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ORCID

Eun Su Kang http://orcid.org/0000-0003-3499-0869
Dong Chan Son http://orcid.org/0000-0002-6773-0580
Sang-Chul Kim http://orcid.org/0000-0003-0698-1500

Data availability statement

The complete chloroplast genome sequence data for *S. altissima* can be found in GenBank (https://www.ncbi.nlm.nih.gov/), and the accession numbers are no. PP108063. The associated Bio-Project, Bio-Sample, and SRA numbers are PRJNA1063455, SAMN39338333 and SRR27484778, respectively.

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