The complete chloroplast genome of *Campsis grandiflora* (Bignoniaceae)

Jongsun PARK1,2* and Hong XI1,2

1InfoBoss Inc., Seoul 07766, Korea  
2InfoBoss Research Center, Seoul 07766, Korea

**ABSTRACT:** *Campsis grandiflora* (Thunb.) K. Schum is an ornamental species with various useful biological effects. The chloroplast genome of *C. grandiflora* isolated in Korea is 154,293 bp long (GC ratio: 38.1%) and has four subregions: 84,121 bp of large single-copy (36.2%) and 18,521 bp of small single-copy (30.0%) regions are separated by 24,332 bp of inverted repeat (42.9%) regions including 132 genes (87 protein-coding genes, eight rRNAs, and 37 tRNAs). One single-nucleotide polymorphism and five insertion and deletion (INDEL) regions (40-bp in total) were identified, indicating a low level of intraspecific variation in the chloroplast genome. All five INDEL regions were linked to the repetitive sequences. Seventy-two normal simple sequence repeats (SSRs) and 47 extended SSRs were identified to develop molecular markers. The phylogenetic trees of 29 representative Bignoniaceae chloroplast genomes indicate that the tribe-level phylogenetic relationship is congruent with the findings of previous studies.

**Keywords:** *Campsis grandiflora*, ornamental plant, chloroplast genome, simple sequence repeats, intraspecific variations, Bignoniaceae

**RECEIVED** 27 February 2022; **REVISED** 26 September 2022; **ACCEPTED** 28 September 2022

**INTRODUCTION**

Genus *Campsis* Lour. consists of only two species, *Campsis grandiflora* (Thunb.) distributed in East Asia and *Campsis radicans* (L.) Bureau found in North America (Wen and Jansen, 1995). Because of its disjunct distribution, this genus was considered as a material to understand their evolutionary history, resulting that both species was estimated to be diversified at 24.4 million years ago (Wen and Jansen, 1995). *Campsis grandiflora* has been utilized as an ornamental species because of their trumpet shape flowers (Jia et al., 2012). Moreover, *C. grandiflora* was known to have various biological effects (Yu et al., 2015; Oku et al., 2019), such as anti-oxidative and anti-inflammatory (Cui et al., 2006), and useful phytocompounds (Jia et al., 2012; Kim et al., 2012; Han et al., 2012) including triterpenoids (Kim et al., 2005). To understand intraspecific variations of *C. grandiflora* chloroplast genome together with the previously published chloroplast genome isolated in China (Chen et al., 2022), we completed the chloroplast genome of *C. grandiflora* isolated in Korea.

**MATERIALS AND METHODS**

**Plant material**

The sample was collected on Gangseo postal office, Seoul, Korea (37.56175N, 126.840624E). A specimen was deposited at the InfoBoss Cyber Herbarium (IN) under the voucher number, IB-01065. No permission is required for the collection.

**DNA extraction and chloroplast genome determination**

Total DNA was extracted from the fresh leaves using a DNeasy Plant Mini Kit (Qiagen, Hilden, Germany). The sequencing library was constructed using an Illumina TruSeq Nano DNA Library Preparation Kit (Illumina, San Diego, CA, USA) following the manufacturer’s recommendations with approximately 350-bp DNA fragments. 4.15-Gbp raw sequences were obtained using NovaSeq6000 at Macrogen Inc., Korea, and were filtered by Trimmomatic v0.33 (Bolger et al., 2014). The chloroplast genome was *de novo* assembled with Velvet v1.2.10 (Zerbino and Birney, 2008), and gaps
were closed using GapCloser v1.12 (Zhao et al., 2011). The genome sequence was confirmed by aligning all raw reads against the assembled genome using BWA v0.7.17 and SAMtools v1.9 (Li et al., 2009; Li, 2013). All processes were conducted in the Genome Information System (http://geis.infoboss.co.kr) utilized in previous studies (Kim et al., 2019e, 2020; Park et al., 2019c; Park and Xi, 2021). Geneious Prime v2020.2.4 (Biomatters Ltd., Auckland, New Zealand) was used for annotation based on the *Tecomaria capensis* chloroplast genome (GenBank accession number: NC_037462) (Fonseca and Lohmann, 2018). A circular map of *C. grandiflora* chloroplast genome was drawn using OGDRAW v1.31 (Greiner et al., 2019). Large single-copy (LSC), small single-copy (SSC), and inverted repeat (IR) regions were determined by bl2seq (Tatusova and Madden, 1999).

### Identification of intraspecific variations

Single nucleotide polymorphisms (SNPs) and insertions and deletions (INDELs) were identified from the pair-wise sequence alignment of the two *C. grandiflora* chloroplast genomes conducted by MAFFT 7.450 (Katoh and Standley, 2013) with ‘Find variations/SNPs’ implemented in Geneious Prime 2020.2.4 (Biomatters Ltd.), which has been used in the previous studies investigating intraspecific variations on organelle genomes (Kim et al., 2021a; Oh et al., 2021; Suh et al., 2021). INDEL region was defined as the continuous INDELs.

### Identification and comparative analysis of simple sequence repeats

Simple sequence repeats (SSRs) were identified on the chloroplast genome sequence using the pipeline of the SSR database (SSRDB; http://ssrdb.infoboss.co.kr/) which has been utilized in several organelle genomic studies (Lee et al., 2020; Choi et al., 2021; Park et al., 2021d, 2022). The SSR is conventionally recognized as the nucleotide array composed of repeats with one or up to six base pair units. For example, monoSSR refers an array of nucleotide repeats containing a particular base and hexaSSR an array of nucleotide repeats containing six base pair unit. The overall length of SSR is mostly over 10 base pairs. In this study, we tried to classify SSR with more criteria which has been applied in previous analyses (Gandhi et al., 2010; Chen et al., 2015; Cheng et al., 2016; Shukla et al., 2018; Jeon and Kim, 2019; Li et al., 2019). The criteria applied are (1) ‘normal SSR’ as a conventional definition from monoSSR to hexaSSR, (2) ‘extended SSR’ referring from heptaSSR (repeats of 7 bp unit) to decaSSR (repeats of 10 bp unit), and (3) ‘potential SSR’ referring specific cases with only 2 units in pentaSSR and hexaSSR. These criteria have been applied and provided better understanding of SSR patterns in previous analyses in chloroplast genomes of *Dysphania* species (Kim et al., 2019d), *Arabidopsis thaliana* (Park et al., 2020c), *Chenopodium album* (Park et al., 2021b), *Diarthron linifolium* (Kim et al., 2021b), and mitochondrial genome of *Rosa rugosa* (Park et al., 2020d).

### Phylogenetic analysis

Twenty-nine representative Bignoniaceae chloroplast genomes including two *C. grandiflora* chloroplast genomes and one outgroup species, *Paulownia tomentosa* (Yi and Kim, 2016), were used for calculating multiple sequence alignments of 60 conserved genes by MAFFT v7.450 (Katoh and Standley, 2013) for constructing phylogenetic trees. We used MEGA X (Kumar et al., 2018) to construct maximum likelihood (ML) and neighbor-joining (NJ) and MrBayes v3.2.6 (Ronquist et al., 2012) to carry out Bayesian inference (BI). A heuristic search was used with nearest-neighbor interchange branch swapping, the Tamura-Nei model, and uniform rates among sites to construct ML and NJ phylogenetic trees with default values for other options. To estimate the node confidences bootstrap analyses with 1,000 and 10,000 bootstrap pseudoreplicates were conducted for ML and NJ trees, respectively. For the BI analysis, the GTR (general time reversible) model with gamma rates was used as a molecular model and Markov-Chain Monte Carlo algorithm was employed for 1,000,000 generations with four chains running simultaneously. To build the consensus tree of BI, we sampled trees every 200 generations after removing 100,000 generations as a ‘burn-in’.

### RESULTS AND DISCUSSION

The chloroplast genome of *C. grandiflora* (GenBank accession number: OM279807) is 154,293 bp (GC ratio: 38.1%) and has four subregions: 85,078 bp of LSC region (36.2%) and 18,577 bp of SSC region (33.0%) regions are separated by 25,319 bp of IR region (43.2%) (Fig. 1). Its length is shorter than that of the previous chloroplast genome by 10 bp (154,303 bp; GenBank accession number: MW430049). It contains 132 genes (87 protein-coding genes [PCGs], eight ribosomal RNAs [rRNAs], and 37 transfer RNAs [tRNAs]; 19 genes (eight PCGs, four rRNAs, and seven tRNAs) are duplicated in IR regions (Fig. 1). Structural variation between *C. grandiflora* and *T. capensis* was identified using Mauve v1.1.3 (Darling et al., 2004) in LSC region: the region between 48,536 bp and 73,124 bp in *C. grandiflora* chloroplast genome was inverted against that of *T. capensis*. 

---

**2022 PARK and Xi: Chloroplast genome of Campsis grandiflora** 157
This phenomenon also occurred between two *Incarvillea* chloroplast genomes in the same family (Ma et al., 2019; Wu et al., 2021), congruent to the previous study (Chen et al., 2022). It suggests that inversion events in LSC occurred in Bignoniaceae in comparison to the other families, such as Amaranthaceae (Park et al., 2021b) and Oleaceae (Park et al., 2019f).

Interspecific variations between the two *C. grandiflora* chloroplast genomes were investigated. In total, one SNP and five INDEL regions (40 bp in total). One SNP was located between *trnC* and *petN*. The 20-bp deletion, which is the longest INDEL, was found in 3' end of *ycf1*, which expanded two more amino acids (Fig. 2A). Another 15-bp INDEL region was located in the first intron of *accD*, presenting the three-time repeat in the chloroplast genome assembled in this study while two-time repeat in the previous chloroplast genome (Fig. 2B). One-bp deletion was found in the intergenic region between *trnK* and *rps16*, exhibiting difference of monoSSR (Fig. 2C). The two INDEL regions were found in 16S rRNA in the IR region (Fig. 2D), showing that two-time repeat of CAT was destroyed in the chloroplast genome assembled in this study by this 2-bp deletion (Fig. 2D). Interestingly, all INDEL regions were linked to the repetitive sequences and proportion of INDEL regions related to SSRs (20%) was low. Numbers of intraspecific variations of *C. grandiflora* are relatively lower than those identified...

**Fig. 1.** Circular map of *Campsis grandiflora* complete chloroplast genome. The genes located outside of the circle are transcribed clockwise, while those located inside are transcribed counterclockwise. The dark gray plot in the inner circle corresponds to GC content. Large single-copy (LSC), small single-copy (SSC), and inverted repeat (IR) are indicated with LSC, SSC, and IR (IRA and IRB), respectively.
Fig. 2. Intraspecific variations identified from the two *Campsis grandiflora* chloroplast genomes. A–D. Consensus sequences were displayed with different background colors of each base. Insertions and deletions were presented as orange-colored boxes. Yellow and red arrows indicate protein-coding genes (PCGs) and rRNAs, respectively. Amino acid sequences in PCG were displayed below the nucleotide sequences. Blue arrows and lines indicate repetitive sequences found in insertions and deletions. E. X-axis means the number of single nucleotide polymorphism (SNPs) and Y-axis indicates insertion and deletion (INDEL) coverage (bp). Blue-colored circle indicates the number of intraspecific variations identified in *C. grandiflora* chloroplast genomes. Orange, gray, and yellow-colored circles presented those identified between Chinese and Korean isolates, Chinese and Chinese isolates, and Korean and Korean isolates, respectively.

Table 1. List of numbers of intraspecific variations in the chloroplast genomes identified from the samples isolated from Korea and China.

| Family                | Species name         | Source (accession number) | Target (accession number) | No. of SNPs | INDEL length (bp) | Reference                                      |
|-----------------------|----------------------|---------------------------|---------------------------|-------------|-------------------|------------------------------------------------|
| Selaginellaceae       | *Selaginella tamariscina* | Korean isolate (MN894555) | Chinese isolate (NC_041646) | 1,223       | 1,635             | Park et al. (2020a), Xu et al. (2018)          |
| Rosaceae              | *Hagenia abyssinica*  | Chinese isolate (KX008604) | Chinese isolate (KY420026) | 82          | 262               | Gichira et al. (2017), Zhang et al. (2017)     |
| **Sanguisorba officinalis** | Chinese isolate (NC_044694) | Korean isolate (MZ145058) | 85 | 301 |
|                       | Sanguisorba officinalis | Chinese isolate (NC_044694) | Korean isolate (MK696193) | 75          | 290               | Meng et al. (2018)                            |
|                       | Sanguisorba officinalis | Korean isolate (MZ145058) | Korean isolate (MK696193) | 10          | 105               |                                                 |
| Sanguisorba tenuifolia | Chinese isolate (NC_044692) | Chinese isolate (NC_042223) | 27 | 138 |
|                       | Sanguisorba tenuifolia | Chinese isolate (NC_044692) | Korean isolate (MK696194) | 91          | 338               | Meng et al. (2018), Park et al. (2018)        |
|                       | Sanguisorba tenuifolia | Chinese isolate (NC_042223) | Korean isolate (MK696194) | 89          | 344               |                                                 |
| Sanguisorba stipulata | Korean isolate (MZ145059) | Korean isolate (MK696195) | 78 | 367 |
| Sanguisorba stipulata | Chinese isolate (NC_044693) | Chinese isolate (KY419920) | 45 | 478 |
| Sanguisorba stipulata | Chinese isolate (NC_044693) | Chinese isolate (KY419920) | 45 | 478 | Meng et al. (2018), Zhang et al. (2017)      |
Table 1. Continued.

| Family           | Species name         | Source                 | Target                  | No. of SNPs | INDEL length (bp) | Reference                  |
|------------------|----------------------|------------------------|-------------------------|-------------|-------------------|----------------------------|
| Amaranthaceae    | Chenopodium album    | Korean isolate (MW446246) | Korean isolate (MW446245) | 28          | 19                | Hong et al. (2017), Park et al. (2021b) |
|                  |                      | Korean isolate (MW446246) | Korean isolate (MW446243) | 2           | 2                 |                            |
|                  |                      | Korean isolate (MW446246) | Korean isolate (MW446241) | 27          | 315               |                            |
|                  |                      | Korean isolate (MW446246) | Korean isolate (MW446242) | 21          | 18                |                            |
|                  |                      | Korean isolate (MW446246) | Korean isolate (MW446244) | 14          | 33                |                            |
|                  |                      | Korean isolate (MW446246) | Korean isolate (NC_034950) | 17          | 36                |                            |
|                  |                      | Korean isolate (MW446245) | Korean isolate (MW446243) | 30          | 35                |                            |
|                  |                      | Korean isolate (MW446245) | Korean isolate (MW446241) | 0           | 298               |                            |
|                  |                      | Korean isolate (MW446245) | Korean isolate (MW446242) | 21          | 15                |                            |
|                  |                      | Korean isolate (MW446245) | Korean isolate (MW446244) | 30          | 40                |                            |
|                  |                      | Korean isolate (MW446245) | Korean isolate (NC_034950) | 33          | 37                |                            |
|                  |                      | Korean isolate (MW446243) | Korean isolate (MW446241) | 29          | 331               |                            |
|                  |                      | Korean isolate (MW446243) | Korean isolate (MW446242) | 23          | 34                |                            |
|                  |                      | Korean isolate (MW446243) | Korean isolate (MW446244) | 16          | 49                |                            |
|                  |                      | Korean isolate (MW446243) | Korean isolate (NC_034950) | 19          | 52                |                            |
|                  |                      | Korean isolate (MW446241) | Korean isolate (MW446242) | 21          | 309               |                            |
|                  |                      | Korean isolate (MW446241) | Korean isolate (MW446244) | 30          | 336               |                            |
|                  |                      | Korean isolate (MW446241) | Korean isolate (NC_034950) | 33          | 333               |                            |
|                  |                      | Korean isolate (MW446242) | Korean isolate (MW446244) | 23          | 39                |                            |
|                  |                      | Korean isolate (MW446242) | Korean isolate (NC_034950) | 26          | 36                |                            |
|                  |                      | Korean isolate (MW446244) | Korean isolate (NC_034950) | 18          | 57                |                            |
| Dysphania pumilio|                      | Korean isolate (MI936550) | Korean isolate (MK541016) | 25          | 2                 | Kim et al. (2019b), Park and Kim (2019) |
| Suaeda japonica  |                      | Korean isolate (MK764271) | Korean isolate (MK558824) | 3           | 3                 | Kim et al. (2019g), Kang et al. (2020) |
| Magnoliaceae     | Magnolia kobus       | Korean isolate (NC_023237) | Korean isolate (MN894553) | 50          | 63                | Cai et al. (2006), Kwon et al. (2019b) |
|                  | Liriodendron tulipifera | Korean isolate (MK477550) | Chinese isolate (NC_008326) | 12          | 0                 |                            |
| Family        | Species name         | Source                  | Target                  | No. of SNPs | INDEL length (bp) | Reference                                                                 |
|--------------|----------------------|-------------------------|-------------------------|-------------|-------------------|--------------------------------------------------------------------------|
| Theaceae     | Camellia japonica    | Korean isolate (MK353210) | Korean isolate (MK353211) | 25          | 2                 | Kim et al. (2017), Kwon et al. (2019a), Li et al. (2019), Min et al. (2019b) |
|              |                      | Korean isolate (MK353210) | Korean isolate (KU951523) | 25          | 2                 |                                                                          |
|              |                      | Korean isolate (MK353211) | Korean isolate (KU951523) | 25          | 0                 |                                                                          |
|              |                      | Chinese isolate (MW602996) | Korean isolate (MK353210) | 8           | 36                |                                                                          |
|              |                      | Chinese isolate (MW602996) | Korean isolate (MK353211) | 8           | 38                |                                                                          |
|              |                      | Chinese isolate (MW602996) | Korean isolate (KU951523) | 33          | 38                |                                                                          |
|              |                      | Chinese isolate (NC_036830) | Korean isolate (MK353210) | 78          | 644               |                                                                          |
|              |                      | Chinese isolate (NC_036830) | Korean isolate (MK353211) | 78          | 645               |                                                                          |
|              |                      | Chinese isolate (NC_036830) | Korean isolate (KU951523) | 103         | 645               |                                                                          |
|              |                      | Chinese isolate (NC_036830) | Chinese isolate (MW602996) | 80          | 671               |                                                                          |
| Fagaceae     | Fagus multinervis    | Korean isolate (OM373199) | Korean isolate (MZ962344) | 4           | 1                 | Park and Oh (2020), Park et al. (2019a), Yang et al. (2020), Park et al. (unpubl. data) |
|              |                      | Korean isolate (OM373199) | Korean isolate (MK518070) | 1           | 2                 |                                                                          |
|              |                      | Korean isolate (OM373199) | Korean isolate (MN894556) | 1           | 0                 |                                                                          |
|              |                      | Korean isolate (OM373199) | Korean isolate (MT762296) | 1           | 2                 |                                                                          |
|              |                      | Korean isolate (MZ962344) | Korean isolate (MK518070) | 3           | 3                 |                                                                          |
|              |                      | Korean isolate (MZ962344) | Korean isolate (MN894556) | 5           | 1                 |                                                                          |
|              |                      | Korean isolate (MZ962344) | Korean isolate (MT762296) | 3           | 3                 |                                                                          |
|              |                      | Korean isolate (MK518070) | Korean isolate (MT762296) | 0           | 0                 |                                                                          |
|              |                      | Korean isolate (MK518070) | Korean isolate (MN894556) | 2           | 2                 |                                                                          |
|              |                      | Korean isolate (MN894556) | Korean isolate (MT762296) | 2           | 2                 |                                                                          |
|              |                      | Korean isolate (NC_053352) | Korean isolate (MT762295) | 1           | 32                | Yang et al. (2020), Park et al. (unpubl. data)                          |
| Caryophyllace | Pseudostellaria     | Korean isolate (MK120981) | Korean isolate (MK309611) | 84          | 175               | Kim et al. (2019c, 2019d)                                               |
| Salicaceae   | Salix koriyanagi    | Korean isolate (MK541017) | Korean isolate (MK120982) | 0           | 0                 | Kim et al. (2019a), Park et al. (2019d)                                  |
| Rosaceae     | Pyrus ussuriensis   | Korean isolate (MK507863) | Korean isolate (MK172841) | 121         | 781               | Cho et al. (2019), Gil et al. (2019)                                     |
Table 1. Continued.

| Family      | Species name                  | Source                      | Target                      | No. of SNPs | INDEL length (bp) | Reference                                      |
|-------------|--------------------------------|-----------------------------|-----------------------------|-------------|-------------------|------------------------------------------------|
| Asteraceae  | Artemisia fukudo              | Korean isolate (NC_044156)  | Korean isolate (MG951488)  | 7           | 12                | Lee et al. (2016), Min et al. (2019c),          |
|             |                                | Korean isolate (NC_046789)  |                             |             |                   | Park et al. (unpubl. data), Zhang et al. (2019) |
|             | Erigeron canadensis           | Korean isolate (MT806101)   | Chinese isolate (NC_046789)| 103         | 208               | Park et al. (unpubl. data), Zhang et al. (2019) |
|             | Chrysanthemum zawadskii       | Korean isolate (MW539687)   | Chinese isolate (MG799556) | 110         | 251               | Baeck et al. (2021), Hongmei et al. (2021)     |
| Orchidaceae | Goodyera schlechtendaliana    | Korean isolate (MK144665)   | Korean isolate (MK134679)  | 200         | 511               | Niu et al. (2017), Oh et al. (2019a, 2019b)    |
|             |                                | Chinese isolate (NC_029364) | Korean isolate (MK144665)  | 842         | 1,779             | Park et al. (unpubl. data), Zhang et al. (2019) |
|             |                                | Chinese isolate (NC_029364) | Korean isolate (MK134679)  | 740         | 1,470             | Park et al. (unpubl. data), Zhang et al. (2019) |
|             |                                | Chinese isolate (LC085346)  | Chinese isolate (NC_029364)| 514         | 2,133             | Park et al. (unpubl. data), Zhang et al. (2019) |
|             |                                | Chinese isolate (LC085346)  | Korean isolate (MK144665)  | 700         | 1,366             | Park et al. (unpubl. data), Zhang et al. (2019) |
|             |                                | Chinese isolate (LC085346)  | Korean isolate (MK134679)  | 597         | 1,065             | Park et al. (unpubl. data), Zhang et al. (2019) |
|             |                                | Chinese isolate (AB893949)  | Chinese isolate (LC085346) | 445         | 415               | Park et al. (unpubl. data), Zhang et al. (2019) |
|             |                                | Chinese isolate (AB893949)  | Chinese isolate (NC_029364)| 864         | 2,045             | Park et al. (unpubl. data), Zhang et al. (2019) |
|             |                                | Chinese isolate (AB893949)  | Korean isolate (MK144665)  | 282         | 1,060             | Park et al. (unpubl. data), Zhang et al. (2019) |
|             |                                | Chinese isolate (AB893949)  | Korean isolate (MK134679)  | 163         | 652               | Park et al. (unpubl. data), Zhang et al. (2019) |
|             | Gastrodia elata               | Korean isolate (MN026874)   | Korean isolate (MN296709)  | 324         | 630               | Kang et al. (2020), Park et al. (2020b),       |
|             |                                | Chinese isolate (NC_037409) | Korean isolate (MN026874)  | 493         | 651               | Yuan et al. (2018)                              |
|             |                                | Chinese isolate (NC_037409) | Korean isolate (MN296709)  | 457         | 671               |                                               |
| Oleaceae    | Abeliophyllum distichum        | Korean isolate (NC_031445)  | Korean isolate (MN127986)  | 93          | 57                | Min et al. (2019a), Park et al. (2019c, 2019f, |
|             |                                | Korean isolate (NC_031445)  | Korean isolate (MK616470)  | 93          | 64                | 2021c)                                         |
|             |                                | Korean isolate (NC_031445)  | Korean isolate (MF407183)  | 93          | 57                |                                               |
|             |                                | Korean isolate (NC_031445)  | Korean isolate (MN116559)  | 102         | 64                |                                               |
|             |                                | Korean isolate (NC_031445)  | Korean isolate (MW426545)  | 99          | 72                |                                               |
|             |                                | Korean isolate (MN127986)   | Korean isolate (MK616470)  | 0           | 0                 |                                               |
|             |                                | Korean isolate (MN127986)   | Korean isolate (MF407183)  | 0           | 1                 |                                               |
|             |                                | Korean isolate (MN127986)   | Korean isolate (MN116559)  | 9           | 12                |                                               |
between the samples between Korea and China (Fig. 2E, Table 1). This result seems to be incongruent to the previous studies that estimated their genetic diversities using the classical methods (He and Gu, 1990; Wu et al., 1990; Wen and Jansen, 1995). Therefore, additional *C. grandiflora* chloroplast genomes will be required to evaluate its genetic diversity.

SSR has been utilized as useful molecular markers (Huang et al., 2015; Li et al., 2020a, 2020b). Seventy-two normal SSRs, 418 potential SSRs, and 47 extended SSRs were identified in both *C. grandiflora* chloroplast genomes (Table 2). Most of normal SSRs are monoSSRs (Fig. 3), which is similar to those of the other plant species (Kim et al., 2019f, 2021b; Park et al., 2020c, 2021b). Nine normal SSRs and 18 extended SSRs (22.68%) were identified in the genic regions of *matK*, *atpA*, *rpoC2*, *psbC*, *psaI*, *psbB*, *rpoA*, *rpl22*, *ycf2*,

| Family      | Species name         | Source          | Target           | No. of SNPs | INDEL length (bp) | Reference                                      |
|-------------|----------------------|-----------------|------------------|-------------|-------------------|------------------------------------------------|
| Oleaceae    | *Abeliophyllum distichum* | Korean isolate (MN127986) | Korean isolate (MW426545) | 6 | 20 | Min et al. (2019a), Park et al. (2019c, 2019f, 2021c) |
|             |                      | Korean isolate (MK616470) | Korean isolate (MF407183) | 0 | 1 |                                              |
|             |                      | Korean isolate (MK616470) | Korean isolate (MN116559) | 9 | 11 |                                              |
|             |                      | Korean isolate (MK616470) | Korean isolate (MW426545) | 6 | 19 |                                              |
|             |                      | Korean isolate (MF407183) | Korean isolate (MN116559) | 9 | 11 |                                              |
|             |                      | Korean isolate (MF407183) | Korean isolate (MW426545) | 6 | 21 |                                              |
|             |                      | Korean isolate (MN116559) | Korean isolate (MW426545) | 7 | 23 |                                              |
| Adoxaceae   | *Viburnum erosum*    | Korean isolate (MN641480) | Korean isolate (MN218778) | 16 | 50 | Choi et al. (2020), Park et al. (2019b)     |
| Brasicaceae | *Arabidopsis thaliana* | Korean isolate (MK353213) | Chinese isolate (MK380719) | 10 | 33 | Park et al. (2020c)                         |
| Ranunculaceae| *Aconitum coreanum*  | Korean isolate (NC_031421) | Korean isolate (KU318669) | 29 | 61 | Kim et al. (2019b), Park et al. (2017)     |
|             |                      | Korean isolate (NC_031421) | Korean isolate (MN400660) | 5 | 52 |                                              |
|             |                      | Korean isolate (MN400660) | Korean isolate (KU318669) | 19 | 92 |                                              |
| Thymelaeaceae| *Daphne genkwa*      | Korean isolate (MT754180) | Korean isolate (Unpub) | 59 | 404 | Yoo et al. (2021)                           |
|             |                      | Korean isolate (MT754180) | Chinese isolate (NC_045891) | 69 | 772 |                                              |
|             |                      | Korean isolate (Unpub) | Chinese isolate (NC_045891) | 85 | 543 |                                              |
| Campanulaceae| *Campanula takesimana* | Korean isolate (MW013763) | Korean isolate (NC_026203) | 33 | 662 | Cheon et al. (2016), Park et al. (2021a) |
| Poaceae     | *Zoysia japonica*    | Korean isolate (MW690657) | Korean isolate (NC_036827) | 68 | 50 | Lee and Park (2021)                         |
|             | *Zoysia macrostachya* | Korean isolate (MZ233426) | Korean isolate (NC_042189) | 29 | 18 | Cheon et al. (2021), Oh et al. (2021)       |
| Staphyleaceae| *Euscaphis japonica* | Chinese isolate (MN159078) | Korean isolate (NC_052922) | 424 | 809 | Oh and Park (2020), Xiang et al. (2019)    |

Table 1. Continued.
Table 2. List of normal SSRs and extended SSRs identified in the C. grandiflora chloroplast genomes isolated in Korea.

| No. | Name      | SSRType | Type       | Start | End  | Unit sequence | Repeat No. | Gene   | Position |
|-----|------------|---------|------------|-------|------|---------------|------------|--------|----------|
| 1   | cO0000001 | ExtendedSSR | OctaSSR   | 2551  | 2566 | ATAATTGG      | 2          | matK   | Genic    |
| 2   | cM0000001 | SSR      | MonoSSR   | 4417  | 4427 | A             | 11         | -      | -        |
| 3   | cM0000002 | SSR      | MonoSSR   | 4729  | 4739 | G             | 11         | -      | -        |
| 4   | cM0000003 | SSR      | MonoSSR   | 4807  | 4817 | T             | 11         | -      | -        |
| 5   | cM0000004 | SSR      | MonoSSR   | 5226  | 5235 | T             | 10         | rps16  | Intrinsic |
| 6   | cM0000005 | SSR      | MonoSSR   | 5249  | 5258 | A             | 10         | rps16  | Intrinsic |
| 7   | cO0000002 | ExtendedSSR | OctaSSR   | 6472  | 6487 | AAATAGAT      | 2          | -      | -        |
| 8   | cM0000006 | SSR      | MonoSSR   | 6513  | 6522 | T             | 10         | -      | -        |
| 9   | cD0000001 | SSR      | DiSSR     | 7299  | 7310 | AT            | 6          | -      | -        |
| 10  | cM0000007 | SSR      | MonoSSR   | 8095  | 8105 | T             | 11         | -      | -        |
| 11  | cHe000001 | ExtendedSSR | HeptaSSR  | 8479  | 8492 | AATGTAA       | 2          | -      | -        |
| 12  | cD0000002 | SSR      | DiSSR     | 8530  | 8539 | TA            | 5          | -      | -        |
| 13  | cM0000008 | SSR      | MonoSSR   | 8698  | 8709 | T             | 12         | -      | -        |
| 14  | cM0000009 | SSR      | MonoSSR   | 9087  | 9096 | A             | 10         | trnS-CGA | Intrinsic |
| 15  | cM0000010 | SSR      | MonoSSR   | 9287  | 9298 | A             | 12         | trnS-CGA | Intrinsic |
| 16  | cO0000003 | ExtendedSSR | OctaSSR   | 10230 | 10245 | TACGTAAG     | 2          | atpA   | Genic    |
| 17  | cTe0000001 | SSR      | TetraSSR  | 11104 | 11115 | GTCT         | 3          | atpA   | Genic    |
| 18  | cM0000011 | SSR      | MonoSSR   | 12359 | 12371 | T             | 13         | atpF   | Intrinsic |
| 19  | cN0000001 | ExtendedSSR | NonaSSR  | 13024 | 13041 | TCTTTTTTA    | 2          | -      | -        |
| 20  | cM0000012 | SSR      | MonoSSR   | 13054 | 13063 | T             | 10         | -      | -        |
| 21  | cHe0000003 | ExtendedSSR | HeptaSSR  | 14205 | 14218 | ATTTATT      | 2          | -      | -        |
| 22  | cHe0000004 | ExtendedSSR | HeptaSSR  | 14480 | 14493 | ATTTTTT      | 2          | -      | -        |
| 23  | cM0000013 | SSR      | MonoSSR   | 16315 | 16327 | T             | 13         | -      | -        |
| 24  | cP0000031 | SSR      | PentaSSR  | 16455 | 16469 | CAAAT        | 3          | -      | -        |
| 25  | cHe0000005 | ExtendedSSR | OctaSSR   | 17159 | 17172 | CAACCTCT     | 2          | rpoC2  | Genic    |
| 26  | cM0000014 | SSR      | MonoSSR   | 18522 | 18532 | T             | 11         | rpoC2  | Genic    |
| 27  | cD0000003 | SSR      | DiSSR     | 19907 | 19916 | AT            | 5          | rpoC2  | Genic    |
| 28  | cHe0000006 | ExtendedSSR | HeptaSSR  | 27420 | 27433 | TGTATAA      | 2          | -      | -        |
| 29  | cHe0000007 | ExtendedSSR | HeptaSSR  | 27459 | 27472 | TGTATAA      | 2          | -      | -        |
| 30  | cM0000015 | SSR      | MonoSSR   | 30555 | 30567 | A             | 13         | -      | -        |
| 31  | cHe0000008 | ExtendedSSR | HeptaSSR  | 30733 | 30746 | AAAGAAA      | 2          | -      | -        |
| 32  | cHe0000009 | ExtendedSSR | HeptaSSR  | 30834 | 30847 | TATGGGA      | 2          | -      | -        |
| 33  | cTe0000001 | SSR      | TriSSR    | 35063 | 35074 | TTC           | 4          | psbC   | Genic    |
| 34  | cM0000016 | SSR      | MonoSSR   | 35277 | 35291 | T             | 15         | -      | -        |
| 35  | cO0000004 | ExtendedSSR | OctaSSR   | 35310 | 35325 | TCGATTTT     | 2          | -      | -        |
| 36  | cM0000017 | SSR      | MonoSSR   | 35664 | 35673 | A             | 10         | -      | -        |
| 37  | cM0000018 | SSR      | MonoSSR   | 36062 | 36072 | C             | 11         | -      | -        |
| 38  | cM0000019 | SSR      | MonoSSR   | 36073 | 36084 | A             | 12         | -      | -        |
| 39  | cM0000020 | SSR      | MonoSSR   | 36178 | 36187 | A             | 10         | -      | -        |
| 40  | cHe0000011 | ExtendedSSR | HeptaSSR  | 42112 | 42125 | TTAATAT      | 2          | -      | -        |
| 41  | cM0000021 | SSR      | MonoSSR   | 42252 | 42261 | A             | 10         | -      | -        |
| 42  | cTe0000002 | SSR      | TetraSSR  | 42470 | 42481 | TAAA         | 3          | -      | -        |
| 43  | cM0000022 | SSR      | MonoSSR   | 43350 | 43361 | T             | 12         | ycf3   | Intrinsic |
### Table 2. Continued.

| No. | Name         | SSRType      | Type   | Start  | End    | Unit sequence | Repeat No. | Gene   | Position    |
|-----|--------------|--------------|--------|--------|--------|---------------|------------|--------|-------------|
| 44  | cO00000005   | ExtendedSSR  | OctaSSR| 44658  | 44673  | ATCCCTAAT     | 2          | -      | -           |
| 45  | cM0000023    | SSR          | MonoSSR| 45132  | 45146  | A             | 15         | -      | -           |
| 46  | cM0000024    | SSR          | MonoSSR| 46347  | 46359  | T             | 13         | -      | -           |
| 47  | cD0000004    | SSR          | DiSSR  | 46520  | 46533  | TA            | 7          | -      | -           |
| 48  | cH00000012   | ExtendedSSR  | HeptaSSR| 46676  | 46689  | AAAAAT        | 2          | -      | -           |
| 49  | cM0000025    | SSR          | MonoSSR| 46996  | 47007  | T             | 12         | -      | -           |
| 50  | cH00000013   | ExtendedSSR  | HeptaSSR| 47052  | 47065  | TATATT        | 2          | -      | -           |
| 51  | cM0000026    | SSR          | MonoSSR| 47199  | 47212  | A             | 14         | -      | -           |
| 52  | cH00000014   | ExtendedSSR  | HeptaSSR| 47362  | 47375  | TCCCTATA      | 2          | -      | -           |
| 53  | cM0000027    | SSR          | MonoSSR| 47393  | 47402  | T             | 10         | -      | -           |
| 54  | cM0000028    | SSR          | MonoSSR| 47671  | 47681  | A             | 11         | trnL-UAA| Intronic    |
| 55  | cH00000015   | ExtendedSSR  | HeptaSSR| 47801  | 47814  | ATATCAAG      | 2          | trnL-UAA| Intronic    |
| 56  | cH00000016   | ExtendedSSR  | HeptaSSR| 48224  | 48237  | AATTAAG       | 2          | -      | -           |
| 57  | cN0000006    | ExtendedSSR  | NonaSSR| 48587  | 48604  | ATGATAAG      | 2          | -      | -           |
| 58  | cN0000007    | ExtendedSSR  | NonaSSR| 48643  | 48660  | AAAGTGTAAG    | 2          | -      | -           |
| 59  | cM0000029    | SSR          | MonoSSR| 50718  | 50730  | A             | 13         | -      | -           |
| 60  | cH00000017   | ExtendedSSR  | HeptaSSR| 51214  | 51227  | ATTAGTT       | 2          | -      | -           |
| 61  | cOe0000004   | ExtendedSSR  | DecaSSR| 51678  | 51697  | TATAGAAAG     | 2          | -      | -           |
| 62  | cM0000030    | SSR          | MonoSSR| 51739  | 51748  | T             | 10         | -      | -           |
| 63  | cTe0000003   | SSR          | TetraSSR| 52184  | 52195  | GTTT          | 3          | -      | -           |
| 64  | cO0000006    | ExtendedSSR  | OctaSSR| 53336  | 53351  | ATATATAA      | 2          | -      | -           |
| 65  | cM0000031    | SSR          | MonoSSR| 54063  | 54073  | A             | 11         | -      | -           |
| 66  | cM0000032    | SSR          | MonoSSR| 56504  | 56514  | A             | 11         | -      | -           |
| 67  | cO0000007    | ExtendedSSR  | OctaSSR| 59209  | 59224  | TATCAAA       | 2          | -      | -           |
| 68  | cM0000033    | SSR          | MonoSSR| 59479  | 59489  | A             | 11         | -      | -           |
| 69  | cTe0000004   | SSR          | TetraSSR| 59496  | 59507  | TTTC          | 3          | -      | -           |
| 70  | cM0000034    | SSR          | MonoSSR| 59697  | 59709  | A             | 13         | -      | -           |
| 71  | cO0000008    | ExtendedSSR  | OctaSSR| 60779  | 60794  | ATAAAGAAAG    | 2          | psal    | Genic       |
| 72  | cTe0000005   | SSR          | TetraSSR| 63789  | 63800  | TTTA          | 3          | -      | -           |
| 73  | cM0000035    | SSR          | MonoSSR| 66657  | 66666  | A             | 10         | atpB    | Genic       |
| 74  | cOe0000005   | ExtendedSSR  | DecaSSR| 68648  | 68667  | AAAATCAAATA   | 2          | -      | -           |
| 75  | cM0000036    | SSR          | MonoSSR| 70334  | 70344  | A             | 11         | -      | -           |
| 76  | cM0000037    | SSR          | MonoSSR| 70396  | 70405  | A             | 10         | -      | -           |
| 77  | cM0000038    | SSR          | MonoSSR| 72938  | 72949  | A             | 12         | -      | -           |
| 78  | cH00000021   | ExtendedSSR  | HeptaSSR| 72980  | 72993  | ATTTAAG       | 2          | -      | -           |
| 79  | cTe0000006   | SSR          | TetraSSR| 73132  | 73143  | AAAG          | 3          | -      | -           |
| 80  | cH00000022   | ExtendedSSR  | HeptaSSR| 73526  | 73539  | CTGGTGG       | 2          | psbB    | Genic       |
| 81  | cH00000023   | ExtendedSSR  | HeptaSSR| 73990  | 74003  | GGCCTGG       | 2          | psbB    | Genic       |
| 82  | cM0000039    | SSR          | MonoSSR| 75085  | 75094  | C             | 10         | -      | -           |
| 83  | cM0000040    | SSR          | MonoSSR| 75096  | 75108  | A             | 13         | -      | -           |
| 84  | cM0000041    | SSR          | MonoSSR| 76129  | 76140  | A             | 12         | -      | -           |
| 85  | cO0000011    | ExtendedSSR  | OctaSSR| 77589  | 77604  | ATACAGAA      | 2          | petD    | Intronic    |
| 86  | cM0000042    | SSR          | MonoSSR| 79112  | 79125  | T             | 14         | rpoA    | Genic       |
Table 2. Continued.

| No. | Name          | SSRType  | Type     | Start | End   | Unit sequence | Repeat No. | Gene  | Position |
|-----|---------------|----------|----------|-------|-------|---------------|------------|--------|----------|
| 87  | cN0000009     | ExtendedSSR | NonaSSR  | 79940 | 79957 | TTTCCTTTTG    | 2          | -      | -        |
| 88  | cM00000043    | SSR       | MonoSSR  | 81025 | 81035 | T             | 11         | -      | -        |
| 89  | cM00000044    | SSR       | MonoSSR  | 81538 | 81550 | T             | 13         | -      | -        |
| 90  | cM00000045    | SSR       | MonoSSR  | 82710 | 82725 | T             | 16         | rpl16  | Intronic |
| 91  | cM00000046    | SSR       | MonoSSR  | 82788 | 82800 | A             | 13         | rpl16  | Intronic |
| 92  | cO00000012    | ExtendedSSR | OctaSSR | 83219 | 83234 | TTTCCTTC     | 2          | rpl16  | Intronic |
| 93  | cHe00000026   | ExtendedSSR | HeptaSSR | 84484 | 84497 | TTACTAA      | 2          | rpl22  | Genic    |
| 94  | cM00000047    | SSR       | MonoSSR  | 85098 | 85107 | T             | 10         | -      | -        |
| 95  | cN00000010    | ExtendedSSR | NonaSSR  | 89648 | 89665 | GGAACATT      | 2          | ycf2   | Genic    |
| 96  | cN00000011    | ExtendedSSR | NonaSSR  | 92241 | 92258 | GATAATT       | 2          | ycf2   | Genic    |
| 97  | cN00000012    | ExtendedSSR | NonaSSR  | 92285 | 92302 | TATTGATGC     | 2          | ycf2   | Genic    |
| 98  | cHe00000027   | ExtendedSSR | HeptaSSR | 92995 | 93008 | ACTTGGA      | 2          | ycf2   | Genic    |
| 99  | cM00000048    | SSR       | MonoSSR  | 112535| 112544 | A             | 10         | ycf1   | Genic    |
| 100 | cM00000049    | SSR       | MonoSSR  | 113091| 113102 | A             | 12         | ycf1   | Genic    |
| 101 | cTe0000007    | SSR       | TetraSSR | 115405| 115416 | GATT          | 3          | -      | -        |
| 102 | cM00000050    | SSR       | MonoSSR  | 118228| 118239 | T             | 12         | ndhA   | Intronic |
| 103 | cM00000051    | SSR       | MonoSSR  | 118287| 118296 | A             | 10         | ndhA   | Intronic |
| 104 | cM00000052    | SSR       | MonoSSR  | 118446| 118455 | T             | 10         | ndhA   | Intronic |
| 105 | cHe00000030   | ExtendedSSR | HeptaSSR | 119608| 119621 | ATGGAA        | 2          | ndhI   | Genic    |
| 106 | cTe0000008    | SSR       | TetraSSR | 120108| 120119 | TTTCA         | 3          | -      | -        |
| 107 | cHe00000031   | ExtendedSSR | HeptaSSR | 120362| 120375 | TATTCTCA      | 2          | ndhG   | Genic    |
| 108 | cM00000053    | SSR       | MonoSSR  | 121803| 121816 | T             | 14         | -      | -        |
| 109 | cN00000013    | ExtendedSSR | NonaSSR  | 122187| 122204 | CTACTTTAG     | 2          | ndhD   | Genic    |
| 110 | cTe0000009    | SSR       | TetraSSR | 123187| 123198 | TATT          | 3          | ndhD   | Genic    |
| 111 | cM00000054    | SSR       | MonoSSR  | 125479| 125488 | T             | 10         | -      | -        |
| 112 | cM00000055    | SSR       | MonoSSR  | 125903| 125915 | A             | 13         | -      | -        |
| 113 | cHe00000032   | ExtendedSSR | HeptaSSR | 126066| 126079 | TTNTTTTA      | 2          | -      | -        |
| 114 | cM00000056    | SSR       | MonoSSR  | 128639| 128648 | A             | 10         | -      | -        |
| 115 | cHe00000034   | ExtendedSSR | HeptaSSR | 146362| 146375 | GTTCCAA       | 2          | ycf2   | Genic    |
| 116 | cN00000014    | ExtendedSSR | NonaSSR  | 147070| 147087 | GCATCATGA     | 2          | ycf2   | Genic    |
| 117 | cN00000015    | ExtendedSSR | NonaSSR  | 147110| 147127 | TATCATCAA     | 2          | ycf2   | Genic    |
| 118 | cN00000016    | ExtendedSSR | NonaSSR  | 149707| 149724 | AAATGTTCC     | 2          | ycf2   | Genic    |
| 119 | cM00000057    | SSR       | MonoSSR  | 154265| 154274 | A             | 10         | -      | -        |

SSR, simple sequence repeat.

ycf1, ndhI, ndhG, and ndhD (Table 2) and 12 normal SSRs and three extended SSRs (12.61%) were found in the intronic regions of rps16, trnS-CGA, atpF, ycf3, trnL-UAA, petD, rps16, and ndhA (Table 2). Due to low number of intraspecific variations, only one monoSSR (cM0000002) displayed the differences of the number of repeats between the two chloroplast genomes. These SSRs will be useful to develop molecular makers because high genetic diversity of C. grandiflora was estimated in previous studies (He and Gu, 1990; Wu et al., 1990; Wen and Jansen, 1995).

Three phylogenetic trees showed that C. grandiflora was clustered with T. capensis/ Incarvillea with high supportive values (Fig. 4). In addition, trees presented that tribes covering more than one chloroplast genome, including Tecomeae, Catalpeae, Crescentiina, and Bignonieae, were well clustered with high supportive values (Fig. 4). It is congruent to previous phylogenetic studies, except for the Catalpeae and Oroxyllae clustered in one clade with week bootstrap values (Olmstead,
Fig. 3. Distribution of simple sequence repeats (SSRs) along with types identified from *Campsis grandiflora* chloroplast genome. X-axis presented SSR types of normal SSRs, potential SSRs, and extended SSRs. Y-axis indicates the number of SSRs.

Fig. 4. Phylogenetic trees of the 29 representative Bignoniaceae chloroplast genomes including two *Campsis grandiflora* chloroplast genomes. Phylogenetic tree was drawn based on the maximum likelihood phylogenetic tree. The numbers above the branches correspond to the bootstrap support values from the maximum likelihood and neighbor-joining methods, as well as posterior probability from the Bayesian inference.
et al., 2009). It may be caused by different coverage of samples between the two studies. Together with additional chloroplast genomes of Bignoniaceae, C. grandiflora chloroplast genome will help to understand evolutionary history of Bignoniaceae.

**ORCID:** Jongsun PARK http://orcid.org/0000-0003-0786-4701; Hong Xi https://orcid.org/0000-0003-0731-2210

**ACKNOWLEDGMENTS**

This study was supported by the InfoBoss Research Grant (IBG-0038).

**CONFLICTS OF INTEREST**

The authors declare that there are no conflicts of interest.

**LITERATURE CITED**

Baek, J., S. Park, J. Lee, J. Min, J. Park and G. W. Lee. 2021. The complete chloroplast genome of *Chrysanthemum zawadskii* Herbich (Asteraceae) isolated in Korea. Mitochondrial DNA Part B Resources 6: 1956–1958.

Bolger, A.M., Lohse, M. and B. Usadel. 2014. Trimmomatic: A flexible trimmer for Illumina sequence data. Bioinformatics 30: 2114–2120.

Cai, Z., C. Penaflor, J. V. Kuehl, J. Leebens-Mack, J. E. Carlson, C. W. dePamphilis, J. L. Boone and R. K. Jansen. 2006. Complete plastid genome sequences of *Drimys*, *Liriodendron*, and *Piper*: Implications for the phylogenetic relationships of magnoliids. BMC Evolutionary Biology 6: 77.

Chen, H., Z. Chen, Q. Du, M. Jiang, B. Wang and C. Liu. 2022. Complete chloroplast genome of *Campsis grandiflora* (Thunb.) schum and systematic and comparative analysis within the family Bignoniaceae. Molecular Biology Reports 49: 3085–3098.

Chen, J., Z. Hao, H. Xu, L. Yang, G. Liu, Y. Sheng, C. Zheng, W. Zheng, T. Cheng and J. Shi. 2015. The complete chloroplast genome sequence of the relict woody plant *Metasequoia glyptostroboides* Hu et Cheng. Frontiers in Plant Science 6: 447.

Cheng, J., Z. Zhao, B. Li, C. Qin, Z. Wu, D. L. Trejo-Saavedra, X. Luo, J. Cui, R. F. Rivera-Bustamante, S. Li and K. Hu. 2016. A comprehensive characterization of simple sequence repeats in pepper genomes provides valuable resources for marker development in *Capsicum*. Scientific Reports 6: 18919.

Cheon, K.-S., K.-A. Kim, S.-K. Jang and K.-O. Yoo. 2016. Complete chloroplast genome sequence of *Campanula takesimensa* (Campanulaceae), an endemic to Korea. Mitochondrial DNA Part A DNA Mapping, Sequencing, and Analysis 27: 2169–2171.

Cheon, S.-H., M.-A. Woo, S. Jo, Y.-K. Kim and K.-J. Kim. 2021. The chloroplast phylogenomics and systematics of *Zosyasia* (Poaceae). Plants 10: 1517.

Cho, M.-S., Y. Kim, S.-C. Kim and J. Park. 2019. The complete chloroplast genome of Korean *Pyrus ussuriensis* Maxim. (Rosaceae): A comparative analyses of the complete mitochondrial genomes of fungal endosymbionts in *Segatella furcifera*, white-backed planthoppers. International Journal of Genomics 2021: 6652508.

Choi, Y. G., N. Yun, J. Park, H. Xi, J. Min, Y. Kim and S.-H. Oh. 2020. The second complete chloroplast genome sequence of the *Viburnum erosum* (Adoxaceae) showed a low level of intra-species variations. Mitochondrial DNA Part B Resources 5: 271–272.

Cui, X.-Y., J.-H. Kim, X. Zhao, B.-Q. Chen, B.-C. Lee, H.-B. Pyo, Y.-P. Yun and Y.-H. Zhang. 2006. Antioxidative and acute anti-inflammatory effects of *Campsis grandiflora* flower. Journal of Ethnopharmacology 103: 223–228.

Darling, A. C. E., B. Mau, F. R. Blattner and N. T. Perna. 2004. MAUVE: Multiple alignment of conserved genomic sequence with rearrangements. Genome Research 14: 1394–1403.

Fonseca, L. H. M. and L. G. Lohmann. 2018. Combining high-throughput sequencing and targeted loci data to infer the phylogenies of the “Adeno-calymma-Neojobertia” clade (Bignoniaceae, Bignoniaceae). Molecular Phylogenetics and Evolution 123: 1–15.

Gandhi, S. G., P. Awasthi and Y. S. Bedi. 2010. Analysis of SSR dynamics in chloroplast genomes of Brassicaceae family. Bioinformation 5: 16–20.

Gichira, A. W., Z. Li, J. K. Saina, Z. Long, G. Hu, R. W. Gituru, Q. Wang and J. Chen. 2017. The complete chloroplast genome sequence of an endemic monotypic genus *Hagenia* (Rosaceae): Structural comparative analysis, gene content and microsatellite detection. PeerJ 5: e2846.

Gil, H.-Y., Y. Kim, S.-H. Kim, J.-H. Jeon, Y. Kwon, S.-C. Kim and J. Park. 2019. The complete chloroplast genome of *Pyrus ussuriensis* Maxim. (Rosaceae). Mitochondrial DNA Part B Resources 4: 1000–1001.

Greiner, S., P. Lehwalk and R. Bock. 2019. OrganellarGenomeDRAW (OGDRAW) version 1.3.1: Expanded toolkit for the graphical visualization of organellar genomes. Nucleic Acids Research 47: W59–W64.

Han, X. H., J.-H. Oh, S. S. Hong, C. Lee, J. I. Park, M. K. Lee, B. Y. Hwang and M.-S. Lee. 2012. Novel iridoids from the flowers of *Campsis grandiflora*. Archives of Pharmacal Research...
The complete chloroplast genome of *Glycyrrhiza uralensis* Fisch. isolated in Korea (Fabaceae). Korean Journal of Plant Taxonomy 51: 353–362.

Kim, S.-H., C.-H. Cho, M. Yang and S.-C. Kim. 2017. The complete chloroplast genome sequence of the Japanese Camellia (*Camellia japonica* L.). Mitochondrial DNA Part B Resources 2: 583–584.

Kim, S.-T., S.-H. Oh and J. Park. 2021b. The complete chloroplast genome of *Diarthron linifolium* (Thymelaeaceae), a species found on a limestone outcrop in eastern Asia. Korean Journal of Plant Taxonomy 51: 345–352.

Kim, Y., Y. Chung and J. Park. 2019b. The complete chloroplast genome sequence of *Dysphania pumilio* (R. Br.) Mosyakin and Clemants (Amaranthaceae). Mitochondrial DNA Part B Resources 4: 403–404.

Kim, Y., Y. Chung and J. Park. 2020. The complete chloroplast genome of *Oxybasis glauca* (L.) S. Fuentes, Uotila and Borsch (Amaranthaceae) as the first chloroplast genome in genus *Oxybasis*. Mitochondrial DNA Part B Resources 5: 1410–1412.

Kim, Y., K.-I. Heo, S. Lee and J. Park. 2019c. The complete chloroplast genome sequence of *Pseudostellaria palibiniana* (Takeda) Ohwi (Caryophyllaceae). Mitochondrial DNA Part B Resources 4: 973–974.

Kim, Y., K.-I. Heo and J. Park. 2019d. The second complete chloroplast genome sequence of *Pseudostellaria palibiniana* (Takeda) Ohwi (Caryophyllaceae): Intraspecies variations based on geographical distribution. Mitochondrial DNA Part B Resources 4: 1310–1311.

Kim, Y., J. Min, W. Kwon, M. J. Song, S. Nam and J. Park. 2019e. The complete chloroplast genome sequence of the *Nymphaea capensis* Thunb. (Nymphaeaceae). Mitochondrial DNA Part B Resources 4: 401–402.

Kim, Y., J. Park and Y. Chung. 2019f. Comparative analysis of the chloroplast genome of *Dysphania ambrosioides* (L.) Mosyakin and Clemants understanding phylogenetic relationship in genus *Dysphania* R. Br. Korean Journal of Plant Resources 32: 644–668.

Kim, Y., J. Park and Y. Chung. 2019g. The complete chloroplast genome of *Stuza japonica* Makino (Amaranthaceae). Mitochondrial DNA Part B Resources 4: 1505–1507.

Kim, Y., Y. Yi, J. Min, H. Xi, D. Y. Kim, J. Son, J. Park and J.-I. Jeon. 2019h. The complete chloroplast genome of *Aconitum cavanum* (H. Lév.) Rapaics (Ranunculaceae). Mitochondrial DNA Part B Resources 4: 3404–3406.

Kumar, S., G. Stecher, M. Li, C. Knyaz and K. Tamura. 2018. MEGA X: Molecular evolutionary genetics analysis across computing platforms. Molecular Biology and Evolution 35: 1547–1549.
Kwon, W., Y. Kim and J. Park. 2019a. The complete mitochondrial genome of Korean Marchantia polymorpha subsp. ruderalis Bischl. and Boisselier: Inverted repeats on mitochondrial genome between Korean and Japanese isolates. Mitochondrial DNA Part B Resources 4: 769–770.

Kwon, W., J. Min, H. Xi and J. Park. 2019b. The complete chloroplast genome of Fissidens nobilis Griff. (Fissidentaceae, Bryophyta). Mitochondrial DNA Part B Resources 4: 2225–2226.

Lee, B. and J. Park. 2021. The complete chloroplast genome of Zoysia japonica Steud. isolated in Korea (Poaceae): Investigation of potential molecular markers on Z. japonica chloroplast genomes. Plant Biotechnology Reports 15: 707–715.

Lee, J., J. Park, H. Xi and J. Park. 2020. Comprehensive analyses of the complete mitochondrial genome of Ficus bifurcata (Cucurbitaceae: Cucurbitales). Journal of Insect Science 20: 10.

Lee, Y. S., J. Y. Park, J.-K. Kim, H. O. Lee, H.-S. Park, S.-C. Lee, J. H. Kang, T. J. Lee, S. H. Sung and T.-J. Yang. 2016. Complete chloroplast genome sequence of Artensia fukudo Makino (Asteraceae). Mitochondrial DNA Part B Resources 1: 376–377.

Li, B., F. Lin, P. Huang, W. Guo and Y. Zheng. 2020a. Development of nuclear SSR and chloroplast genome markers in diverse Liriodendron chinense germplasm based on low-coverage whole genome sequencing. Biological Research 53: 21.

Li, C., Y. Zheng and P. Huang. 2020b. Molecular markers from the chloroplast genome of rose provide a complementary tool for variety discrimination and profiling. Scientific Reports 10: 12188.

Li, H. 2013. Aligning sequence reads, clone sequences and assembly contigs with BWA-MEM. arXiv preprint at: https://arxiv.org/abs/1303.3997.

Li, W., C. Zhang, X. Guo, Q. Liu and K. Wang. 2019. Complete chloroplast genome of Camellia japonica genome structures, comparative and phylogenetic analysis. PLoS ONE 14: e0216645.

Ma, G-T., J.-G Yang, Y-F. Zhang and T.-X. Guan. 2019. Characterization of the complete chloroplast genome of Incarvillea arguta (Bignoniaceae). Mitochondrial DNA Part B Resources 4: 1603–1604.

Meng, X.-X., Y-F. Xian, L. Xiang, D. Zhang, Y.-H. Shi, M.-L. Wu, G-Q. Dong, S.-P. Ip, Z.-X. Lin and W. Sun. 2018. Complete chloroplast genomes from Sanguisorba: Identity and variation among four species. Molecules 23: 2137.

Min, J., Y. Kim, H. Xi, T. Jang, G. Kim, J. Park and J.-H. Park. 2019a. The complete chloroplast genome of a new candidate cultivar, Sang Jae, of Abietiophyllum distichum Nakai (Oleaceae): Initial step of A. distichum intraspecies variations atlas. Mitochondrial DNA Part B Resources 4: 3716–3718.

Min, J., W. Kwon, H. Xi and J. Park. 2019b. The complete chloroplast genome of Leucobryum juniperoidesum (brid.) C. Müll. (Leucobryaceae, Bryophyta). Mitochondrial DNA Part B Resources 4: 2962–2963.

Min, J., J. Park, Y. Kim and W. Kwon. 2019c. The complete chloroplast genome of Artenisia fukudo Makino (Asteraceae): Providing insight of intraspecies variations. Mitochondrial DNA Part B Resources 4: 1510–1512.

Niu, Z., Q. Xue, S. Zhu, J. Sun, W. Liu and X. Ding. 2017. The complete plastome sequences of four orchid species: Insights into the evolution of the Orchidaceae and the utility of plastomic mutational hotspots. Frontiers in Plant Science 8: 715.

Oh, S.-D., S.-K. Lee, D.-W. Yun, H.-J. Sun, H.-G. Kang, H.-Y. Lee, H. Xi, J. Park and B. Lee. 2021. The complete chloroplast genome of Zosysia macrostachya (Poaceae): Insights into intraspecific variations and species delimitation of the Zosysia species. Korean Journal of Plant Taxonomy 51: 326–331.

Oh, S.-H. and J. Park. 2020. The complete chloroplast genome of Eiscaphis japonica (Thunb.) Kanitz (Staphyleaceae) isolated in Korea. Mitochondrial DNA Part B Resources 5: 3769–3771.

Oh, S.-H., H.-J. Suh, J. Park, Y. Kim and S. Kim. 2019a. The complete chloroplast genome sequence of a morphotype of Goodyera schlechtendaliana (Orchidaceae) with the column appendages. Mitochondrial DNA Part B 4: 626–627.

Oh, S.-H., H. S. Suh, J. Park, Y. Kim and S. Kim. 2019b. The complete chloroplast genome sequence of Goodyera schlechtenthaliana in Korea (Orchidaceae). Mitochondrial DNA Part B Resources 4: 2692–2693.

Oki, H., E. Iwaoaka, M. Shinga, E. Yamamoto, M. Inuma and K. Ishiguro. 2019. Effect of the dried flowers of Campsis grandiflora on stagnant blood syndrome. Natural Product Communications 14: 1–5.

Olmstead, R. G., M. L. Zjhra, L. G. Lohmann, S. O. Grose and A. J. Eckert. 2009. A molecular phylogeny and classification of Bignoniaceae. American Journal of Botany 96: 1731–1743.

Park, I., W.-J. Kim, S. Yang, S.-M. Yeo, H. Li and B. C. Moon. 2017. The complete chloroplast genome sequence of Aconitum coreanum and Aconitum carmichaelii and comparative analysis with other Aconitum species. PLoS ONE 12: e0184257.

Park, I., S. Yang, W. J. Kim, P. Noh, H. O. Lee and B. C. Moon. 2018. Complete chloroplast genome of Sanguisorba × tenuifolia Fisch. ex Link. Mitochondrial DNA Part B Resources 3: 909–910.

Park, J.-S., D.-P. Jin, J.-W. Park and B.-H. Choi. 2019a. Complete chloroplast genome of Fagus multinervis, a beech species endemic to Ulleung Island in South Korea. Mitochondrial DNA Part B Resources 4: 1698–1699.
Park, J., Y. Bae, B.-Y. Kim, G.-H. Nam, J.-M. Park, B. Y. Lee, H.-J. Suh and S.-H. Oh. 2021a. The complete chloroplast genome of *Campanula tianshimensis* Nakai from Dokdos Island in Korea (Campanulaceae). Mitochondrial DNA Part B Resources 6: 135–137.

Park, J., Y. G. Choi, N. Yun, H. Xi, J. Min, Y. Kim and S.-H. Oh. 2019f. The complete chloroplast genome sequence of *Viburnum erosum* (Adoxaceae). Mitochondrial DNA Part B Resources 4: 3278–3279.

Park, J., K.-I. Heo, Y. Kim and W. Kwon. 2019c. The second complete chloroplast genome sequence of *Gastrodia elata* (Orchidaceae) represents high sequence variation in the species. Mitochondrial DNA Part B Resources 5: 517–519.

Park, J. and H. Xi. 2021. Investigation of nucleotide diversity based on 17 sea cucumber mitochondrial genomes and assessment of sea cucumber mitochondrial gene markers. Advances in Oceanography and Marine Biology 2: 2021.

Park, J., H. Xi and Y. Kim. 2020c. The complete chloroplast genome sequence of *Arabidopsis thaliana* isolated in Korea (Brassicaceae): An investigation of intraspecific variations of the chloroplast genome of *A. thaliana*. International Journal of Genomics 2020: 3236461.

Park, J., S. Park, T. Jang, G. Kim and J.-H. Park. 2021c. The complete chloroplast genome of *Abeliophyllum distichum* f. *lilacinum* Nakai (Oleaceae) from the Chungbuk Province, Korea. Mitochondrial DNA Part B Resources 6: 1754–1756.

Park, J., Y. Bae, B.-Y. Kim, G.-H. Nam, J.-M. Park, B. Y. Lee, H.-J. Suh, H.-J., J. Min, J. Park and S.-H. Oh. 2021. The complete chloroplast genome of *Abeliophyllum distichum* Nakai (Oleaceae), cultivar Ok Hwang 1ho: Insights of cultivar specific characteristics and comparative analyses of the complete chloroplast genome sequence of male individual of Korean endemic willow, *Salix koriyanagi* Kimura ex Goerz (Salicaceae). Mitochondrial DNA Part B Resources 5: 1654–1656.

Park, J., J. Min, Y. Kim and Y. Chung. 2021b. The comparative analyses of six complete chloroplast genomes of morphologically Diverse *Chenopodium album* L. (Amaranthaceae) collected in Korea. International Journal of Genomics 2021: 6643444.

Park, J., Y. Kim, H. Xi, W. Kwon, T. Jang, G. Kim and J.-H. Park. 2019f. The complete chloroplast genome of a new candidate cultivar, Dae Ryun, of *Abeliophyllum distichum* Nakai (Oleaceae). Mitochondrial DNA Part B Resources 4: 3713–3715.

Park, J. and S.-H. Oh. 2020. A second complete chloroplast genome sequence of *Fagus multivinerea* Nakai (Fagaceae): Intraspecific variations on chloroplast genome. Mitochondrial DNA Part B Resources 5: 1868–1869.
plast genome and its inference on the phylogenetic position of *Incarvillea sinensis* Lam. (Bignoniaceae). Mitochondrial DNA Part B Resources 6: 263–264.

Xiang, S., X.-D. Liu, W.-H. Sun, S.-R. Lan, Z.-J. Liu and S.-Q. Zou. 2019. The complete chloroplast genome sequence of *Euscaphis japonica* (Staphyleaceae). Mitochondrial DNA Part B Resources 4: 3484–3485.

Xu, Z., T. Xin, D. Bartels, Y. Li, W. Gu, H. Yao, S. Liu, H. Yu, X. Pu, J. Zhou, J. Xu, C. Xi, H. Lei, J. Song and S. Chen. 2018. Genome analysis of the ancient tracheophyte *Selaginella tamariscina* reveals evolutionary features relevant to the acquisition of desiccation tolerance. Molecular Plant 11: 983–994.

Yang, J., K. Takayama, J.-S. Youn, J.-H. Pak and S.-C. Kim. 2020. Plastome characterization and phylogenomics of East Asian beeches with a special emphasis on *Fagus multinervis* on Ulleung Island, Korea. Genes 11: 1338.

Yi, D.-K. and K.-J. Kim. 2016. Two complete chloroplast genome sequences of genus *Paulownia* (Paulowniaceae): *Paulownia coreana* and *P. tomentosa*. Mitochondrial DNA Part B Resources 1: 627–629.

Yoo, S.-C., S.-H. Oh and J. Park. 2021. Phylogenetic position of *Daphne genkwa* (Thymelaeaceae) inferred from complete chloroplast data. Korean Journal of Plant Taxonomy 51: 171–175.

Yu, H.-C., J. Wu, H.-X. Zhang, H.-S. Zhang, T.-T. Qiao, J.-X. Zhang, G.-L. Zhang, J. Sui, L.-W. Li, L.-R. Zhang and L.-X. Lv. 2015. Antidepressant-like and anti-oxidative efficacy of *Campsis grandiflora* flower. Journal of Pharmacy and Pharmacology 67: 1705–1715.

Yuan, Y., X. Jin, J. Liu, X. Zhao, J. Zhou, X. Wang, D. Wang, C. Lai, W. Xu, J. Huang, L. Zha, D. Lui, X. Ma, L. Wang, M. Zhou, Z. Jiang, H. Meng, H. Peng, Y. Liang, R. Li, C. Jiang, Y. Zhao, T. Nai, Y. Jin, Z. Zhan, J. Yang, W. Jiang and L. Huang. 2018. The *Gastrodia elata* genome provides insights into plant adaptation to heterotrophy. Nature Communications 9: 1615.

Zerbino, D.R. and E. Birney. 2008. Velvet: Algorithms for de novo short read assembly using de Bruijn graphs. Genome research 18: 821–829.

Zhang, S.-D., J.-J. Jin, S.-Y. Chen, M. W. Chase, D. E. Soltis, H.-T. Li, J.-B. Yang, D.-Z. Li and T.-S. Yi. 2017. Diversification of Rosaceae since the Late Cretaceous based on plastid phylogenomics. New Phytologist 214: 1355–1367.

Zhang, Z., X. Jiang, Y. Chen, P. Zhu, L. Li, Y. Zeng and T. Tang. 2019. Characterization of the complete chloroplast genome sequence of *Conyza canadensis* and its phylogenetic implications. Mitochondrial DNA Part B Resources 4: 2028–2030.

Zhao, Q.-Y., Y. Wang, Y.-M. Kong, D. Luo, X. Li and P. Hao. 2011. Optimizing de novo transcriptome assembly from short-read RNA-Seq data: A comparative study. BMC Bioinformatics 12(Suppl 14): S2.