The complete chloroplast genome of a Chinese endemic poorly known species
Campylotropis grandifolia (Fabaceae)

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ABSTRACT
The first complete chloroplast genome of Campylotropis grandifolia Schindl. is reported and characterized in this study. The whole chloroplast genome was 153,213 bp in length with 128 genes, including 81 protein-coding genes, 39 tRNAs, and eight rRNAs. Maximum-likelihood (ML) phylogenetic analysis of 25 legume species strongly supported that Campylotropis is most closely related with Kummerowia and Lespedeza, which is consistent with previous studies.

In order to confirm the systematical position of C. grandifolia, a total of 24 legume chloroplast genomes were downloaded from GenBank and applied to construct the phylogenetic tree, where Lysiphyllum binatum (Blanco) de Wit was selected as the outgroup. Specially, we aligned these 25 cp genomes with MAFFT v.7.481 (Katoh and Standley 2013), eliminated the gaps with MEGA X (Kumar et al. 2018), and constructed maximum-likelihood (ML) tree with IQ-TREE v.1.6.12 (Nguyen et al. 2015) in K3Pu + F + R5 model (Figure 1). Our results showed that C. grandifolia is sister to the clade consisting of Kummerowia striata (Thunb.) Schindl. and Lespedeza bicolor Turcz., which is congruent with previous study using the combined cpDNA fragments data (Xu et al. 2012).

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

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Data availability statement
The genome sequence data that support the findings of this study are openly available in The DNA Data Bank of Japan (DDBJ; http://www.ddbj.nig.ac.jp) under the accession no. MZ918589. The associated BioProject and Bio-Sample numbers are PRJNA743046 and SAMN20688300, respectively.
Table 1. Base composition of chloroplast genome in *Campylotropis grandifolia*.

| Species                  | Genome length (bp) | GC content (%) |
|--------------------------|--------------------|----------------|
| *Campylotropis grandifolia* | 153213             | 35.0           |
|                          | 84739              | 30.4           |
|                          | 27678              | 33.3           |
|                          | 40796              | 42.8           |

| Species                  | Genome length (bp) | GC content (%) |
|--------------------------|--------------------|----------------|
| *Campylotropis grandifolia* | 302577             | 35.0           |
|                          | 157540             | 30.4           |
|                          | 170250             | 33.3           |
|                          | 54786              | 42.8           |

IR: inverted repeat; LSC: large single copy; SSC: small single copy.

Table 2. Genes present in chloroplast genome of *Campylotropis grandifolia*.

| Gene classification | Gene group | The name of the gene |
|---------------------|------------|---------------------|
| Photosystem I       | psaA, psaB, psaC, psaL, psaJ |                   |
| Photosystem II      | psbA, psbB, psbC, psbD, psbE, psbF, psbH, psbI, psbJ |                   |
| Cytochrome b/f complex | petA, petB, petD, petE, petG, petL, petN |                   |
| ATP synthase        | atpA, atpB, atpE, atpF, atpH, atpI |                   |
| NADH dehydrogenase  | ndhA, ndhB, ndhC, ndhD, ndhE, ndhF, ndhG, ndhH, ndhI |                   |
| Rubisco large subunit | rbcL |                   |
| Ribosomal proteins (LSU) | rps2, rps3, rps4, rps7, rps8, rps11, rps12, rps14, rps15 |                   |
| Ribosomal proteins (SSU) | rps16, rps18, rps19 |                   |
| Transfer RNAs       | trnA-UGC, trnC-GCA, trnD-GUC, trnE-UUC, trnF-GAA |                   |
| RNA polymerase      | rpoB |                   |
| Rubosomal RNAs      | rnr4.5, rrs5, rrm16, rrm23 |                   |
| Hypothetical chloroplast reading frames | ccsA, ccmE, ccmK, cipP, matK |                   |
| Hypothetical chloroplast reading frames | ycf1, ycf2, ycf3, ycf4 |                   |

Figure 1. The maximum-likelihood (ML) phylogenetic tree for 25 species of Fabaceae. Bold branches indicate nodes with 100 bootstrap support. The newly sequenced species, *Campylotropis grandifolia* in this study is marked in italic bold font.

References

Greiner S, Lehwark P, Bock R. 2019. OrganellarGenomeDRAW (OGDRAW) version 1.3.1: expanded toolkit for the graphical visualization of organellar genomes. Nucleic Acids Res. 47(W1): W59–W64.

Huang PH, Ohashi H, Iokawa Y. 2010. *Campylotropis*. In: Wu ZY, Raven PH, Hong DY, editors. Flora of China 10. Beijing and St. Louis: Science Press and Missouri Botanical Garden Press; p. 292–302.

Iokawa Y, Ohashi H. 2002a. A taxonomic study of *Campylotropis* (Leguminosae) I. J Jpn Bot. 77(4):179–222.

Iokawa Y, Ohashi H. 2002b. A taxonomic study of *Campylotropis* (Leguminosae) II. J Jpn Bot. 77(5):251–283.

Iokawa Y, Ohashi H. 2008. *Campylotropis* (Leguminosae) of China, an enumeration and distribution. J Jpn Bot. 83(1):36–59.

Jin J-J, Yu W-B, Yang J-B, Song Y, dePamphilis CW, Yi T-S, Li D-Z. 2020. GetOrganelle: a fast and versatile toolkit for accurate de novo assembly of organelle genomes. Genome Biol. 21(1):241.

Katoh K, Standley DM. 2013. MAFFT multiple sequence alignment software version 7: improvements in performance and usability. Mol Biol Evol. 30(4):772–780.

Kumar S, Stecher G, Li M, Knyaz C, Tamura K. 2018. MEGA X: Molecular Evolutionary Genetics Analysis across Computing Platforms. Mol Biol Evol. 35(1):74–79.

Liao M, Xu B. 2020. ACCRA: a software package for rapid and accurate, and flexible bath annotation of plastomes. Plant Methods. 15(1):1–12.

Xu B, Wu M, Gao X-F, Zhang L-B. 2012. Analysis of DNA sequences of six chloroplast and nuclear genes suggests incongruence, introgression, and incomplete lineage sorting in the evolution of *Lespedeza* (Fabaceae). Mol Phylogenet Evol. 62(1):346–358.