

## Characterization of the complete chloroplast genome of *Carex myosuroides* Villars, 1779 (Cyperaceae)

Hong-Yan Chen<sup>a</sup>, Xiao-Fei Xia<sup>b</sup>, Zhe Pan<sup>c</sup> and Yu Ning<sup>d</sup>

<sup>a</sup>Beijing Botanical Garden, Beijing, China; <sup>b</sup>Department of Specimens, Beijing Museum of Nature History, Beijing, China; <sup>c</sup>Sichuan Academy of Environmental Policy and Planning, Chengdu, China; <sup>d</sup>Institute of Wetland Research, Chinese Academy of Forestry Research, Beijing, China

### ABSTRACT

*Carex myosuroides* Villars, 1779 is a typical alpine sedge with both ecological and agricultural value. The work reported here is the first complete chloroplast genome of this species. The chloroplast genome, with a total size of 185,609 bp, consists of two inverted repeats (IRs, 38,374 bp) separated by a large single-copy (LSC, 99,911 bp) region, and a small single-copy (SSC, 8950 bp) region. The overall genome GC content is 34.12%. The genome contains 125 genes, consisting of 82 protein-coding genes, 35 tRNA genes, and eight rRNA genes. Phylogenetic analysis supports the taxonomic treatment of incorporating genus *Kobresia* to a broader circumscription of *Carex*. Our work could be helpful to future research on Cyperaceae.

### ARTICLE HISTORY

Received 1 November 2021  
Accepted 23 February 2022

### KEYWORDS

*Carex myosuroides*;  
Cyperaceae; complete  
chloroplast genome; alpine

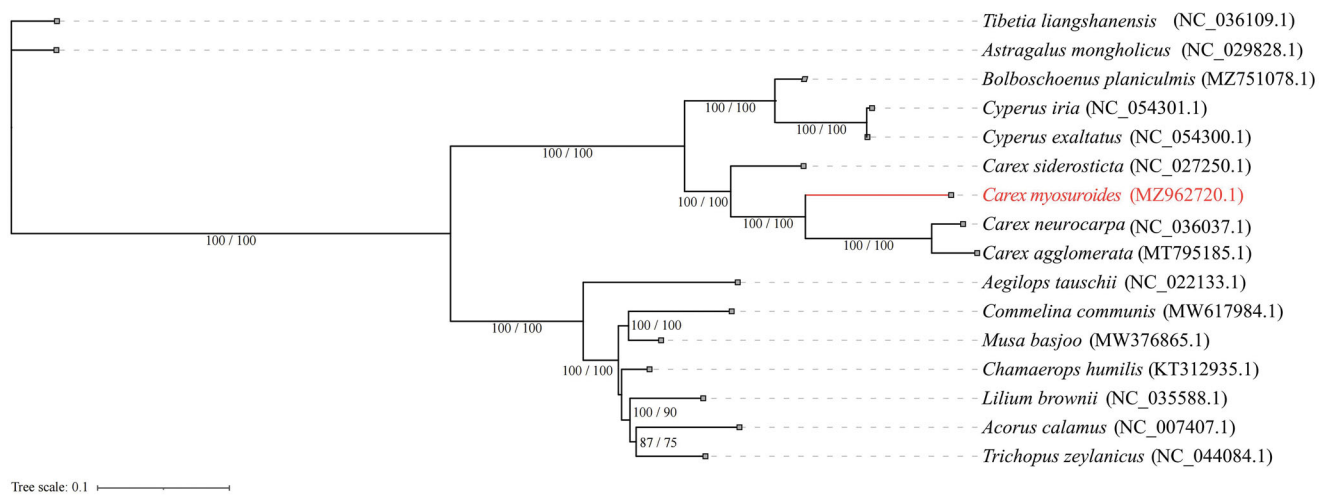
*Carex myosuroides* Villars, 1779, formerly known as *Kobresia myosuroides* (Villars) Foiri, 1896 (Zhang and Noltie 2010), is a typical sedge in alpine environment. It is the only known sedge to harbor associations with ectomycorrhizal fungi, establishing an effective way of transferring amino acid-nitrogen from the soil solution (Lipson et al. 1999). Thus, it usually appears as the main species in high-altitude vegetation, especially in highland meadow. It is reported that this species also contributes a notable part to the feeding of livestock in Qinghai-Tibet Plateau (Miehe et al. 2019). As alpine ecosystems commonly are considered to be more prone to challenges brought up by climate change, the integrity and vigor of alpine dominant species is of vital importance (Li et al. 2020). However, molecular information to date is limited for alpine sedges. Our work here presents the first annotated full-length assembly of the chloroplast of *C. myosuroides*, which could be helpful to future research on Cyperaceae.

The samples were collected at Dongling mountain, Beijing, China (GPS: E115°30'11", N 40°3'7"). Fresh leaves were collected and wrapped in drikold, then transferred to be stored at –80 °C lab environment. The relevant specimen was deposited at the herbarium of Beijing Museum of Nature History (<http://www.bmnh.org.cn/en/>) under the voucher number BJM0271944 (contact [xiaxiaofei@bmnh.org.cn](mailto:xiaxiaofei@bmnh.org.cn)). The total genomic DNA was extracted using DP305-3 plant genomic DNA Kit (Tiangen, Beijing, China) according to the standard protocol. The sequencing platform was Illumina NovaSeq 6000. Totally, 19,595,642 high-quality clean reads (PE 150) were generated. Aligning, assembly and annotation

were conducted by bowtie2 (v2.2.4) (Langmead and Salzberg 2012), SPAdes (v3.10.1) (Bankevich et al. 2012), SSPACE (v2.0) (Boetzer et al. 2011), and Gapfiller (v2.1.1) (Nadalín et al. 2012). The assembled and annotated chloroplast genome sequence has been submitted to GenBank under the accession number MZ962720.1.

The plastome of *C. myosuroides* is a circular DNA molecule with a length of 185,609 bp. Although this genome size is notably higher than the average genome size of monocots (0.144 M) presented by Mohanta et al. (2020), it is comparable to several published *Carex* chloroplast genomes (~0.187 M), indicating further investigation is needed for a likely unique evolution trajectory of the sedge group. The full plastome consists of a large single-copy (LSC) region of 99,911 bp, small single-copy (SSC) region of 8950 bp and two inverted repeats (IRs) of 38,374 bp by each. The overall GC content of *C. myosuroides* chloroplast genome was 34.12%, similar to the average level of 36.82% (Mohanta et al. 2020), with corresponding GC values of the LSC, SSC, and IR regions for 32.01%, 26.96%, and 37.69%, respectively. The chloroplast genome of *C. myosuroides* comprises 125 genes, including 82 protein-coding genes, eight ribosomal RNA (rRNA) genes, and 35 transfer RNA (tRNA) genes.

We constructed a maximum likelihood tree to explore the evolutionary position of *C. myosuroides* (Figure 1). In total, 16 complete chloroplast genomes were used to build the phylogeny. Two species from Fabaceae were used as the outgroup (*Astragalus mongholicus* Bunge, 1868 and *Tibetia liangshanensis* Li, Pei Chun, 1981). The sequences were



**Figure 1.** Phylogenetic relationships among 16 complete chloroplast genomes. Branch scores are given as (SH-aLRT value/ultrafast bootstrap value). The analyzed species are shown with the corresponding GenBank accession numbers in parentheses.

aligned using the default settings in MAFFT v7 (Kato et al. 2019). The phylogenetic analyses were conducted using IQTREE v1.6.7 (Nguyen et al. 2015). The fitted model was TVM + F + R3, with branch support tested by SH-aLRT (1000 replicates) and ultrafast bootstrap (1000 replicates). Branches were labeled if their SH-aLRT score >85% and ultrafast bootstrap support >75%. Based on the current sampling extent, our result presents a phylogeny with most internal relationships well supported. This result is also in accordance with the taxonomic treatment of incorporating genus *Kobresia* to a broader circumscription of *Carex* (Global Carex Group 2015). Our work could be helpful to further researches in Cyperaceae.

## Acknowledgements

**Ethical statement:** This study was approved by the Committee of Beijing Museum of Nature History. All the procedures of the field and lab work are in accordance with the local/international guidelines. No protected/endangered species was involved.

## Authors contributions

H-Y Chen and X-F Xia conceived and designed the experiment. Y Ning and X-F Xia collected the specimen. Z Pan carried out the extraction and sequencing. Y Ning analyzed the data and made the figure. H-Y Chen and X-F Xia contributed to writing and editing the manuscript. Y Ning and Z Pan revised the manuscript.

## Disclosure statement

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

## Funding

This work was supported by the Fundamental Research Funds of CAF under Grant [CAFYBB2020SY042] and National Natural Science Foundation of China under Grant [NSFC31800348].

## Data availability statement

The data that support the findings of this study are openly available in the GenBank database at <https://www.ncbi.nlm.nih.gov/>, under accession number [MZ962720.1]. The associated BioProject, SRA, and BioSample numbers are PRJNA772905, SRR 16494724, and SAMN 22419664, respectively.

## References

- Bankevich A, Nurk S, Antipov D, Gurevich AA, Dvorkin M, Kulikov AS, Lesin VM, Nikolenko SI, Pham S, Pribelski AD, et al. 2012. SPAdes: a new genome assembly algorithm and its applications to single-cell sequencing. *J Comput Biol.* 19(5):455–477.
- Boetzer M, Henkel CV, Jansen HJ, Butler D, Pirovano W. 2011. Scaffolding pre-assembled contigs using SSPACE. *Bioinformatics.* 27(4):578–579.
- Global Carex Group. 2015. Making *Carex* monophyletic (Cyperaceae, tribe Cariceae): a new broader circumscription. *Bot J Linn Soc.* 179(1):1–42.
- Kato K, Rozewicki J, Yamada KD. 2019. MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. *Brief Bioinform.* 20(4):1160–1166.
- Langmead B, Salzberg SL. 2012. Fast gapped-read alignment with Bowtie 2. *Nat Methods.* 9(4):357–359.
- Li M, Zhang X, He Y, Niu B, Wu J. 2020. Assessment of the vulnerability of alpine grasslands on the Qinghai-Tibetan Plateau. *Peer J.* 8:e8513.
- Lipson DA, Schadt CW, Schmidt SK, Monson RK. 1999. Ectomycorrhizal transfer of amino acid-nitrogen to the alpine sedge *Kobresia myosuroides*. *New Phytol.* 142(1):163–167.
- Miehe G, Schleuss P-M, Seeber E, Babel W, Biermann T, Braendle M, Chen F, Coners H, Foken T, Gerken T, et al. 2019. The *Kobresia pygmaea* ecosystem of the Tibetan highlands – origin, functioning and degradation of the world's largest pastoral alpine ecosystem: *Kobresia* pastures of Tibet. *Sci Total Environ.* 648:754–771.
- Mohanta TK, Mishra AK, Khan A, Hashem A, Abd\_Allah EF, Al-Harrasi A. 2020. Gene loss and evolution of the plastome. *Genes.* 11(10):1133.
- Nadalin F, Vezzi F, Policriti A. 2012. GapFiller: a de novo assembly approach to fill the gap within paired reads. *BMC Bioinformatics.* 13: 1–16.
- Nguyen L, Schmidt HA, Von Haeseler A, Minh BQ. 2015. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. *Mol Biol Evol.* 32(1):268–274.
- Zhang SR, Noltie HJ. 2010. *Kobresia Willdenow*. In: Wu ZY, Raven PH, editors. *Flora of China*. Vol. 23. St. Louis: Missouri Botanical Garden Press; p. 269–285.