Family Mniaceae was established by Schwägrichen (1830). It is an important cosmopolitan moss group with many species. However, the family's circumscription is controversial (Koponen 1981; Vitt 1984; Buck and Goffinet 2000; Frey and Stech 2009). The conflicts were mainly on the clades of Mielichhoferia, Pohlia, and related genera. These genera were transferred to Mniaceae from family Bryaceae and Mielichhoferiaceae (Buck and Goffinet 2000; Frey and Stech 2009). And these changes were supported by studies based on molecular data (Cox et al. 2014; Guerra et al. 2011; Niu et al. 2018). Thus, Mniaceae became the largest family of order Bryales. The relationship between Mniaceae's genera, such as Mnium, Mielichhoferia, and Pohlia, is unclear and needs further study. The chloroplast genome study of Mnium marginatum will be helpful to reflect the fact of this relationship.

In this study, the complete chloroplast genome of M. marginatum was sequenced and described. Only one chloroplast genome of family Mniaceae, Pohlia cruda (Zhang et al. 2019), was reported before this work. This study will be helpful for further studies of Mniaceae.

Genomic DNA of M. marginatum was extracted from dry leaves by a modified CTAB method (Li et al. 2013). Specimen collected from Xinjiang, China (Haxionggu Forest Park, Urumqi: 87.996’E, 43.832’N) by Jiancheng Zhao, and deposited in HBN (the herbarium of Hebei Normal University). The collection number of the specimen is Z16823. With a paired-end (PE 150) genomic library acquired by the sequencing platform of Illumina HiSeq (by Nuohexhiyuan Biotech Company, Beijing), the complete chloroplast genome of M. marginatum was assembled with Geneious (Kearey et al. 2012). The sequence was annotated in DOGMA (Wyman et al. 2004) and edited in Sequin version 15.50 (www.ncbi.nlm.nih.gov/Sequin/).

The complete chloroplast DNA sequence of M. marginatum (GenBank accession No. MT897999) is 124,935 bp in length. The two inverted repeat regions (IRs) are 9,910 bp long and separated by a large single-copy (LSC) region of 86,572 bp and a small single-copy region of 18,543 bp. Based on the chloroplast genome data of 11 bryophytes downloaded from GenBank and one acquired in this study, phylogenetic trees were constructed.
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Disclosure statement

No potential competing interest was reported by the authors.

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Data availability statement

The genome sequence data that support the findings of this study are openly available in GenBank of NCBI at https://www.ncbi.nlm.nih.gov under the accession no. MT897999.

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Figure 1. The ML tree is based on 12 chloroplast genome sequences of bryophytes. Numbers on the branches are bootstrap values.
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