Mitochondrial genome from the lichenized fungus *Peltigera rufescens* (Weiss) Humb, 1793 (Ascomycota: Peltigeraeaceae)

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**ABSTRACT**

Known colloquially as ‘dog-lichens’ or ‘pelt-lichens’, most species of *Peltigera* grow on soil and mosses. Some species contribute a significant amount of nitrogen to the environment and have been used as traditional medicines. We analyzed the complete mitochondrial genome of *P. rufescens*, which is a circular genome 65,199bp in size and its CG content is 26.7%. It contains 15 protein-coding genes (PCGs), 27 transport RNAs (tRNAs), and 3 ribosomal RNAs (rRNAs). Also, the *atp9* gene is present in the genome. We used the complete mitochondrial genome to construct a phylogenetic tree by the Bayesian method, which was consistent with the phylogenetic relationship published for *P. membranacea* which is closely related to *P. rufescens*.

*Peltigera rufescens* is a species of lichen-forming fungi, belonging to the family Peltigeraeaceae (Ascomycota), which is a widely distributed species around the world (Eriksson and Winka 1998). The thallus of *P. rufescens* is gray to brown, usually with a heavy tomentum on the upper surface (hence the name dog-lichens). The lower surface has distinctly raised veins, the apothecia is commonly dark red-brown, saddle-shaped, and on upright lobes (Miadlikowska and Francois 2000). In recent years, several studies have suggested that lichenized fungi can be used as a possible food supplement and as an easily available natural source of medicines. Studies have shown that *P. rufescens* extracts have antioxidant, anti-inflammatory, and antigenotoxic effects. It has an important application for the protection of human lymphocytes from the genotoxic damages induced by agricultural chemicals hazardous to people (Tanas et al. 2010; Aydin and Tuerkez 2011; Türkez et al. 2012). Therefore, *P. rufescens* has an important practical research significance.

The sample of *P. rufescens* was collected from Haxionggou, in Xinjiang Province (87°59.846’N, 43°48.783’E). This voucher specimen was deposited in the Herbarium of College of Life Science and Technology at Xinjiang University in Urumchi, China (https://mail.163.com/, for more information about this voucher please contact Reyim MAMUT, email: arman99@163.com) under the voucher number 201899269A. DNA was extracted using the NEBNext®UltraTM DNA Library Prep Kit for Illumina (NEB, USA) Kit. The sequence was performed in Novaseq PE150. The whole library was prepared by terminal repair, adding A tail, adding sequencing connector, purification, PCR amplification, and other steps. After the library construction was completed, the library was initially quantified using Qubit 2.0 and diluted to 2 ng/µL. Using readfq to capture all data for QC (Quality control). Sequence splicing used SPAdes (http://bioinf.spbau.ru/SPAdes/), then used Gapcloser and Gapfiller for scaffold gap, and finally used PrInSeS-G for sequences correction. The mitochondrial genome was annotated by GeSeq and Geneious (Kearse et al. 2012; Tillich et al. 2017), and the whole genome sequence data was deposited in GenBank under the accession number MW711788.

The total length of the mitochondrial genome of *P. rufescens* is 65,199bp and CG content is 26.7%. The complete mitochondrial genome of *P. rufescens* contains 15 PCGs, 27 tRNAs, and 3 rRNAs. The genome presented here contained a conserved set of 15 PCGs (cox1, cox2, cox3, nad1, nad2, nad3, nad4, nad4L, nad5, nad6, atp6, atp8, atp9, cyt b, and rps3), which are arranged in the same order as in *P. membranacea*. In some lichen lineages, the *atp9* gene is lost (Pogoda et al. 2018), such as *Usnea* (Lan and Huang 2020). However, the *atp9* gene is present in *P. rufescens*, and introns invade five different genes: four PCGs (cox1, cyt b, nad4L, and nad5), one site in rRNA (rnl), we predicted a total of 11 introns I, including intron IA (6), intron IB (1), intron IC (2), and intron ID (1).

We used 11 complete mitochondrial genomes to conduct a phylogenetic analysis of *Peltigera rufescens*, using MrBayes v3.2 (Huelsenbeck and Ronquist 2001). The phylogenetic tree is divided into two clades, *Cladonia* clade and Peltigerales clade, *Opegrapha vulgata* is set as an outgroup. The phylogenetic tree indicated that *P. rufescens* is closely related to *P. membranacea* (Figure 1).
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 GenBank of NCBI at https://www.ncbi.nlm.nih.gov under the accession no. MW711788. The associated BioProject, SRA, and BioSample numbers are PRJNA656065, SRR14561385, and SAMN19223377 respectively.

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