

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

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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 65,199 bp 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*.

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*Peltigera rufescens* is a species of lichen-forming fungi, belonging to the family Peltigeraceae (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 Franco 2000). In recent years, several studies have suggested that lichenized fungus 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 Haxiongou, 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](mailto: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 PilonSeS-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.

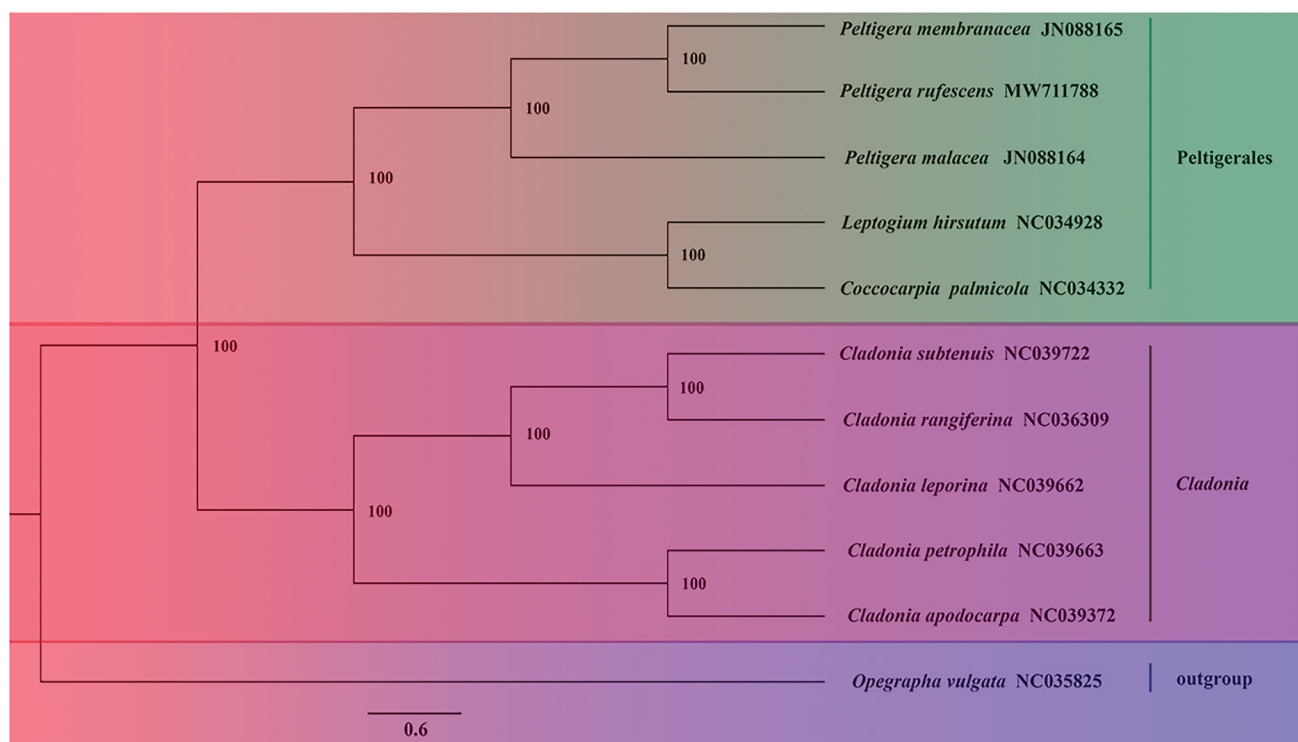
The total length of the mitochondrial genome of *P. rufescens* is 65,199 bp and CG content is 26.7%. The complete mitochondrial genome of *P. rufescens* contains 15 PCGs, 27 tRNAs, and 3 rRNAs. The genome presented here contained a conserved set of 15 PCGs (*cox1*, *cox2*, *cox3*, *nad1*, *nad2*, *nad3*, *nad4*, *nad4L*, *nad5*, *nad6*, *atp6*, *atp8*, *atp9*, *cytb*, 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*, *cytb*, *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).

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**Figure 1.** Phylogenetic analysis of *Peltigera rufescens*. A phylogenetic tree was constructed from the total length of the mitochondrial genomes of 11 species by using the Bayesian method, five species of *Cladonia* and five species of the order Peltigerales, *Opegrapha vulgata* is set as an outgroup, BI-PP = 100%.

## 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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