Analysis of the complete organellar genomes of *Palmaria decipiens* (Palmariales, Rhodophyta) from Antarctica confirms its taxonomic placement in the genus *Palmaria*

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**ABSTRACT**

*Palmaria decipiens* (Reinsch) R.W.Ricker is a ecologically important red seaweed restricted to high latitudes of the southern hemisphere. Here, we contribute to the bioinformatics and evolutionary systematics of the Palmariales by performing high throughput sequencing analysis on a specimen of *P. decipiens* from the western Antarctic Peninsula. The *P. decipiens* mitogenome is 26,645 base pairs (bp) in length and contains 49 genes (GenBank accession MN967053) and the plastid genome is 193,007 bp and contains 245 genes (GenBank accession MN967052). The mitogenome and plastid genome of *P. decipiens* are similar to *P. palmata* from Japan in pairwise genetic distances (93.71% and 98.14%, respectively), and *P. palmata* from the Maine, USA (87.45% and 94.57%, respectively). The genomes of *P. decipiens* showed high gene synteny with *P. palmata*, however several tRNA differences are documented. Organellar genome content and phylogenetic analyses of *P. decipiens* supports its placement in the genus *Palmaria*.

*Palmaria decipiens* is a dominant marine red algal ecosystem species that occurs in the intertidal and subtidal, where it provides habitat, nourishment and shelter for many marine organisms (Becker et al. 2011). It is characterized as having reddish to purple, unbranched blades, that extend up to 70 cm long and have a lubricious glossy surface (Ricker 1987; Becker et al. 2011). To better understand the taxonomy of *Palmaria* and *P. decipiens*, the complete mitogenome and plastid genome of *P. decipiens* from Yelcho Chilean station, Doumer Island, Antarctic Peninsula (64°52’41″S, 63°35’51″W) were characterized.

DNA was extracted from *P. decipiens* (Specimen Voucher-MS0000004 in HIP, see Thiers 2016) using the NucleoSpin Plant II Kit (Macherey-Nagel, Düren, Germany) following the manufacturer’s instructions. The 150 bp PE Illumina library construction and sequencing was performed by myGenomics, LLC (Alpharetta, Georgia, USA). The genomes were assembled using default de novo settings in MEGAHIT (Li et al. 2016) and Geneious Prime to close the gaps (Biomersitters, Ltd, Auckland, New Zealand). The genes were annotated manually using blastx, NCBI ORFFinder, tRNAscan-SE 1.21 (Schattner et al. 2005), and RNAMmer (Lagesen et al. 2007). The *P. decipiens* plastid genome was aligned to other plastomes using MAFFT (Katoh and Standley 2013). The phylogenetic analysis was executed with RAxML-NG (Kozlov et al. 2019) using the GTR + gamma model and 1000 bootstraps. The tree was visualized with TreeDyn 198.3 at Phylogeny.fr (Dereeper et al. 2008).

The mitogenome of *P. decipiens* is 26,645 bp in length and contains 49 genes. It is A + T-rich (67.0%) and includes 23 tRNA, 5 ribosomal proteins, 2 rRNA (rrl, rrs), and 19 other genes involved in mitochondrial function. The plastid genome of *P. decipiens* is 193,007 bp and contains 245 genes. It is also A + T biased (65.2%) and includes 45 ribosomal proteins, 33 tRNA, 32 photosystem I and II, 30 ycf, 12 cytochrome b/f complex, 8 ATP synthase, 4 RNA polymerase, 6 rRNA, and 75 other genes. The mitogenome of *P. decipiens* differs from *P. palmata* from Japan contains trnD and trnH (Kumagai et al. 2019). The plastid genome of *P. decipiens* from Japan contains trnI gene, but like *P. palmata* lacks the trnl gene, and *P. palmata* from Japan contains trnE gene (Costa et al. 2016; Kumagai et al. 2019). Pairwise genetic distances of the mitogenome and plastid genome of *P. decipiens* and *P. palmata* from Japan are more similar in mitogenome (93.71%) and plastid genome (98.14%) sequence than *P. decipiens* is to *P. palmata* from the Maine, USA (87.45% and 94.57%, respectively).
respectively). These organellar data support the existence of three distinct entities: *P. palmata* from the Atlantic; *P. ‘palmata’* from Japan; and *P. decipiens* from Antarctica.

Phylogenetic analysis of the plastid genome of *P. decipiens* positions it in a clade with *P. palmata* from Japan and the USA (Figure 1). This evolutionary relationship is similar to the most recent analyses in which the Palmariales is closely allied with the Acrochaetiales, Balbianiales, and Nemaliales (Costa et al. 2016; Yang et al. 2016; Saunders et al. 2018).

**Disclosure statement**

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