



Next-generation sequencing yields the complete organellar genomes of kelp *Lessonia flavicans* (Lessoniaceae, Phaeophyceae) from the Sub-Antarctic ecoregion of Magallanes, Chile

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ABSTRACT

The genotype *Lessonia flavicans* Bory is an endemic and important kelp from Sub-Antarctic Magellanic ecoregion that shows affinity to extreme salinity, temperature, and photoperiod conditions. Genomic analysis of *L. flavicans* from Rinconada Bulnes, Punta Arenas, Chile, resulted in the assembly of its organellar genomes. The *L. flavicans* complete mitogenome is 37,226 base pairs (bp) in length and contains 66 genes (GenBank accession number MN561186), the complete plastid genome is 130,085 bp and has 173 genes (MN561187) and the data assembled 8205 bp of the nuclear ribosomal cistron (MN561188). The organellar genomes are similar in structure and content to *L. spicata* (Suhr) Santelices and other Laminariales.

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Lessonia flavicans is an intertidal to shallow subtidal kelp distributed in the Beagle Channel (Chile), Puerto Deseado (Argentina), and the Falkland Islands (Searles 1978; Mansilla et al. 2014). This species is characterized as having a stipe somewhat treelike cylindrical, branches compressed, blades oval-linear, somewhat denticulated, and yellowish (Searles 1978; Asensi and de Reviers 2009). *Lessonia flavicans* have major ecological roles in the structuring of benthic marine communities and are commercially exploited for the extraction of the phycocolloid alginates (Mansilla et al. 2014). This study characterized the complete organellar genomes of *L. flavicans* from Rinconada Bulnes, Punta Arenas, Chile to determine its genomic structure and genetic relationship as the genotype of the genus *Lessonia*.

DNA was extracted from *L. flavicans* (Specimen Voucher-LEMAS0005) using the NucleoSpin Plant II Kit (Macherey-Nagel, Düren, Germany) following the manufacturer's instructions. The 150 bp PE Illumina library construction and sequencing were performed by myGenomics, LLC (Alpharetta, GA). The genomes were assembled using default de novo settings in CLC Genomics Workbench version 12.0 (QIAGEN Bioinformatics, Redwood City, CA) and Geneious Prime to close gaps (Biomatters, Ltd, Auckland, New

Zealand). The genes were annotated manually using blastx, NCBI ORFfinder, and tRNAscan-SE version 1.21 (Schattner et al. 2005). The *L. flavicans* mitogenome was aligned to other mitogenomes using MAFFT (Katoh and Standley 2013). The phylogenetic analysis was executed with RAxML-NG (Kozlov et al. 2019) using the GTR + gamma model and 1,000 bootstraps. The tree was visualized with TreeDyn version 198.3 at Phylogeny.fr (Dereeper et al. 2008).

The mitogenome of *L. flavicans* is 37,226 bp in length and contains 66 genes. It is A + T rich (66.3%) and includes 25 tRNA (*trnK* and *trnS* occur in duplicate, *trnL* and *trnM* in triplicate), 17 ribosomal proteins, 3 rRNA (*rnl*, *rns*, and *rns5*), 3 orfs (*orf41*, *orf129*, and *orf378*), and 18 other genes involved in electron transport and oxidative phosphorylation. The plastid genome of *L. flavicans* is 130,085 bp and contains 173 genes. It is A + T biased (69.2%) and includes 45 ribosomal proteins, 27 tRNA (*trnA*, *trnG*, *trnI*, *trnR*, and *trnS* occur in duplicate, *trnM* occurs in triplicate), 27 photosystem I and II, 20 ycf, 8 cytochrome b/f complex, 8 ATP synthase, 4 RNA polymerase, 6 rRNA, and 28 other genes. The mitogenome and plastid genome of *L. flavicans* are similar in length, content, and organization to other Laminariales (Chen et al. 2019; Tineo et al. 2019; Zheng et al. 2019).

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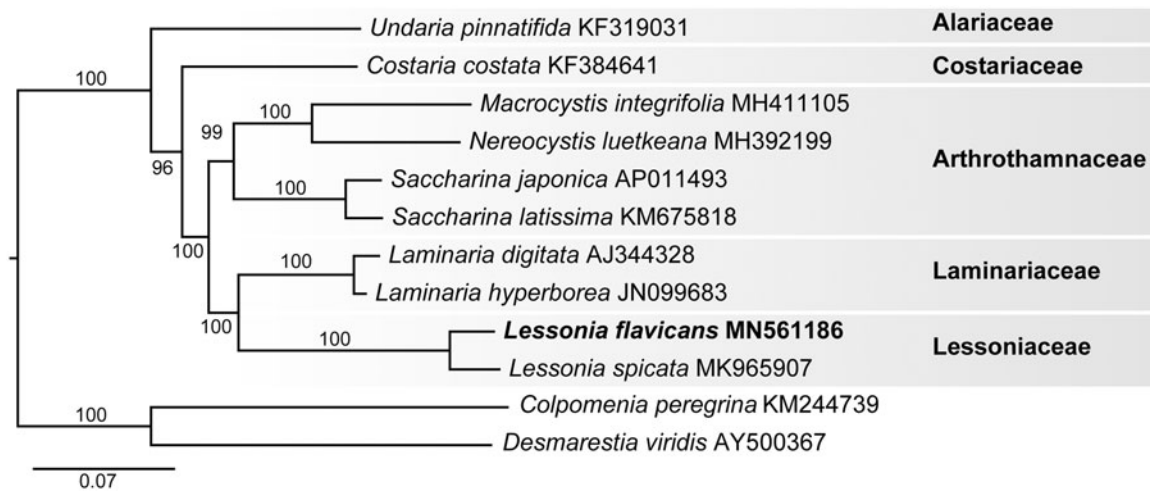


Figure 1. Maximum-likelihood phylogram of *Lessonia flavicans* (MN561186) and related Laminariales mitogenomes. Numbers along branches are RaxML bootstrap supports based on 1000 replicates. The legend below represents the scale for nucleotide substitutions.

Phylogenetic analysis of the *L. flavicans* mitogenome resolved it in a fully supported clade with *L. spicata* (Figure 1). The mitogenome of *L. flavicans* differed in pairwise distance from *L. spicata* by 3.8%. The plastid genome of *L. flavicans* differed from *L. spicata* by 1.4%. The evolutionary relationship of the generitype *L. flavicans* confirms that Lessoniaceae is closely allied with Laminariaceae (Tineo et al. 2019).

Disclosure statement

The authors report no conflicts of interest. The authors alone are responsible for the content and writing of this article.

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