

The complete mitogenome of the rockweed *Fucus distichus* (Fuaceae, Phaeophyceae)

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ABSTRACT

The rockweed *F. distichus* is one of the most common intertidal seaweeds in the northern hemisphere. The systematics of *F. distichus* however remains open to discussion. Here, we contribute to the bioinformatics and systematics of *F. distichus* by deciphering its complete mitogenome. The *F. distichus* mitogenome is 36,400 bp in length, contains 67 genes, and has a gene content, organization, and sequence that are similar to the generitype, *F. vesiculosus*. These data support the continued recognition of *F. distichus* as a polymorphic entity with a broad distribution and high degree of ecological diversity.

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Fucus L. is one of the three original genera proposed by Linnaeus (1753) to accommodate macroscopic marine algae. Since then more than 1000 names have been assigned to the genus (Guiry & Guiry 2017), but nearly all have been reclassified. Based on genetic analyses, three or four species are recognized: *F. distichus* L., *F. serratus* L., *F. spiralis* L., and *F. vesiculosus* L. (Serrao et al. 1999; Coyer et al. 2006; Kucera & Saunders 2008; Coyer et al. 2011; Laughinghouse et al. 2015). This classification remains problematic however, as exemplified by *F. distichus*, which displays a high degree of morphological, ecological, geographical, and reproductive variation (Gardner 1922; Kucera & Saunders 2008; Coyer et al. 2011; Laughinghouse et al. 2015). Herein, we characterize the mitogenome of *F. distichus* to clarify its systematics.

Fucus distichus (Voucher- UC 2050487) was collected from Coos Bay, Oregon (43°21'30.3", -124°18'32.2") and its DNA isolated following Lindstrom et al. (2011). The 76 bp paired-end library construction and sequencing was performed by

myGenomics, LLC (Alpharetta, GA,) yielding 22,040,820 reads. The mitogenome was assembled using the default *de novo* settings in CLC Genomics Workbench 9.5 (©2016 CLC bio, a QIAGEN Company, Waltham, MA) and annotated using blastx and NCBI ORF-finder. The mitogenome was aligned to other Phaeophyceae with MAFFT (Katoh & Standley 2013). The RaxML analysis was executed using complete mitogenome sequences at Trex-online (Boc & Makarenkov 2012) with the GTR + gamma model and 1000 fast bootstraps, then visualized with TreeDyn 198.3 at Phylogeny.fr (Dereeper et al. 2008).

The *F. distichus* mitogenome (GenBank KY678904) is 36,400 bp in length and contains *cob* and *tatC*, 3 rRNA, 3 open reading frames, 3 ATP synthase, 3 *cox*, 6 *rpl*, 10 NADH, 11 *rps*, and 26 tRNA genes (*trnL* occurs in triplicate and *trnI*, *trnM*, *trnS*, *trnY* in duplicate). Gene content, organization, and length are nearly identical to *F. vesiculosus* (36,392 bp) (Oudot-Le Secq et al. 2006). The genetic distance between

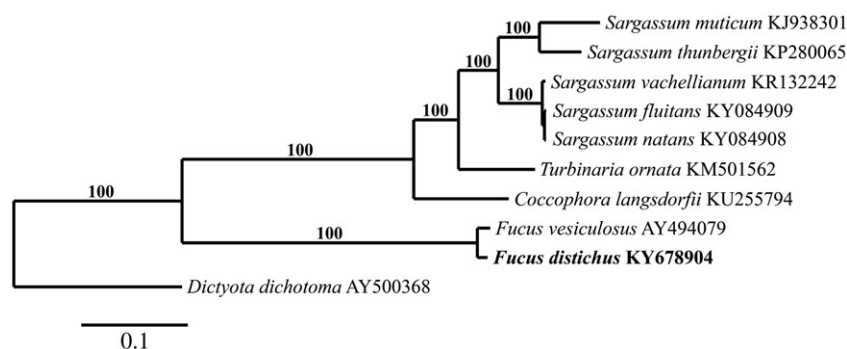




Figure 1. Maximum-likelihood phylogram of *F. distichus* (bold letters) and related Phaeophyceae mitogenomes. Numbers along branches are RaxML bootstrap supports based on 1000 reps. The legend below represents the scale for nucleotide substitutions.

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these two species is 2.0%. Phylogenetic analysis of *F. distichus* supports this close relationship, positioning it in a clade with *F. vesiculosus* (Figure 1). Sequence analysis of *F. distichus* from Oregon identifies it as haplotype *ic6* (Coyer et al. 2011) from Japan and Alaska, USA. Its *cox1* sequence was also an exact match to a specimen from British Columbia, Canada (GenBank EU646633), and only differed by 1 bp from *F. distichus* from Nova Scotia, Canada (GenBank EU646647), Nordland, Norway (GenBank LN877838), and California, USA (GenBank KM254965).

Disclosure statement

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