

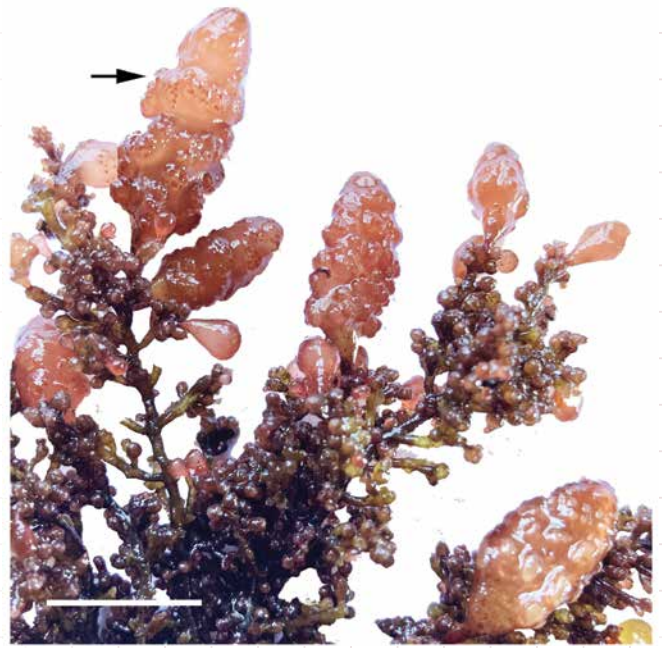
# MICRO-INTERNSHIP

## Transfer of the marine red alga *Erythrocytis saccata* (Rhodomelaceae, Rhodophyta) to the tribe Streblodcladieae inferred from organellar genome analysis

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*Erythrocytis saccata* growing epiphytically on *Laurencia pacifica* from Stillwater Cove, Pebble Beach, California, USA (UC 2085026). The arrow indicates the specimen analyzed in this study. White bar = 2 cm.

*Erythrocytis saccata* is a hemiparasitic marine red alga that grows on the branch apices of species classified in the tribe Laurenciaeae. Molecular evidence shows that the majority of red algal parasites are closely related evolutionarily to their hosts, however, very little is known about the phylogenetics of hemiparasitic red algae. To determine its genomic structure and genetic relationship to related host species and other Rhodomelaceae, high-throughput sequencing analysis was performed on a specimen from Pebble, Beach, California, USA. Assembly of the Illumina sequencing reads yielded the complete mitogenome and plastid genome. The mitogenome is 24,975 bp in length and contains 45 genes.

The plastid genome is 165,292 bp and contains 224 genes. Comparison of organellar genome structure and content to other Rhodomelaceae revealed a high-level of gene synteny. Phylogenetic analysis of *E. saccata* resolved it in a fully supported clade sister to the genera *Carradoriella* and *Leptosiphonia*, and embedded in the tribe *Streblodcladieae*. These genetic results support the transfer of *E. saccata* to the *Streblodcladieae* and represent the first complete organellar genomes of a red algal hemiparasite.

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