

Molecular Assisted Identification Reveals Hidden Red Algae Diversity from the Burica Peninsula, Pacific Panama

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Table S1. Data matrix dimensions and analysis parameters for phylogenetic analyses carried out in this study.

Taxon-locus	Maximum Likelihood					Bayesian ¹				
	# OTUs	# sites	Model	Algorithm ²	Bootstrap Replications	Model	Rate Variation	MCMC Generations	Subsample Frequency	Burnin
<i>Tricleocarpa rbcL</i> -3P	26	665	GTR CAT I	RBSBT	1000	GTR	invgamma	2 × 10 ⁶	2000	200,000
<i>T. cylindrica</i> COI-5P	14	577	GTR CAT I	RBSBT	1000	GTR	invgamma	2 × 10 ⁶	2000	200,000
Liagoraceae <i>rbcL</i> -3P	43	660	GTR CAT I	RHC-100	1000	GTR	invgamma	4 × 10 ⁶	4000	400,000
<i>G. floridanum-sclerophyllum complex</i> <i>rbcL</i> -3P	16	660	GTR CAT I	RHC-100	2000	GTR	invgamma	6 × 10 ⁶	6000	600,000
Gelidiellaceae <i>rbcL</i> -3P	20	688	GTR CAT I	RHC-100	2000	GTR	invgamma	4 × 10 ⁶	4000	400,000
<i>Hypnea rbcL</i> -3P	32	672	GTR CAT I	RHC-50	1000	GTR	invgamma	4 × 10 ⁶	4000	400,000
<i>Grateloupia s.l. rbcL</i> -3P	74	586	GTR CAT I	RHC-20	500	GTR	invgamma	4 × 10 ⁶	4000	400,000
<i>Ceratodictyon rbcL</i> -3P	20	694	GTR CAT I	RHC-100	2000	GTR	invgamma	4 × 10 ⁶	4000	400,000
<i>Gracilaria rbcL</i> -3P	44	683	GTR CAT I	RHC-100	2000	GTR	invgamma	4 × 10 ⁶	4000	400,000
Callithamnidae <i>rbcL</i> -3P	34	691	GTR CAT I	RHC-100	2000	GTR	Invgamma	6 × 10 ⁶	6000	600,000
<i>Centroceras rbcL</i> -3P	66	694	GTR CAT I	RHC-100	2000	GTR	invgamma	4 × 10 ⁶	4000	400,000
<i>Polysiphonia s.l. rbcL</i>	64	1467	GTR CAT I	RHC-25	1000	GTR	invgamma	4 × 10 ⁶	4000	400,000

¹ Bayesian analyses included two simultaneous MCMC runs of 3 heated and one cold chain. ²Algorithms used in RAxML analyses were Rapid hill-climbing (RHC), with the number of random starting trees, or Rapid Bootstrapping and search for best-scoring ML tree (RBSBT). When Rapid hill-climbing was used to generate the ML tree, this was followed by bootstrapping with the Rapid Bootstrapping algorithm.