Supplementary Materials

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Concatenated (*rbc*L and nrSSU) data set: Outgroups from Yang et al. (2020)
125 taxa with 4 partitions and 3304 total sites

Partition	No. of Sites	Unique sites	Informative sites	Invariant sites
rbcL codon1	489	149	48	416
rbcL codon2	489	102	5	466
rbcL codon3	489	456	379	68
SSU	1837	741	385	1251

Best-fit model according to BIC:
rbcL codon1	GTR+F+I+G4
rbcL codon2	F81+F+I
rbcL codon3	TVM+F+I+G4
SSU	GTR+F+I+G4

Maximum Log-likelihood of the tree: -30218.4689

Concatenated (*rbc*L and nrSSU) data set: Outgroups "Bangia 3" from Sutherland et al. (2011)
121 taxa with 4 partitions and 3322 total sites

Partition	No. of Sites	Unique sites	Informative sites	Invariant sites
rbcL codon1	489	143	44	423
rbcL codon2	489	98	3	472
rbcL codon3	489	441	356	85
SSU	1855	605	305	1406

Best-fit model according to BIC:
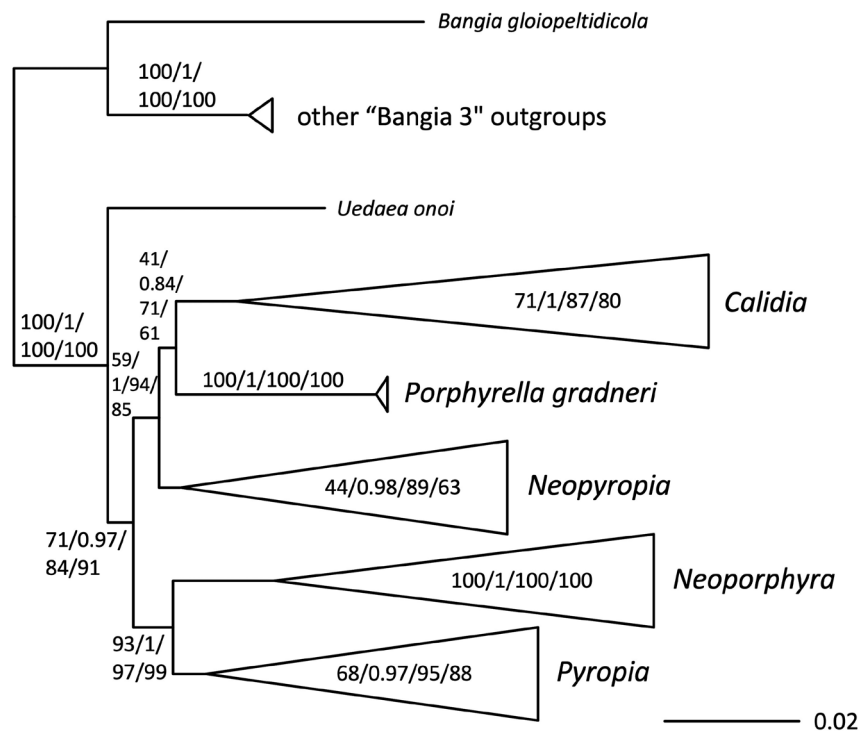|	
rbcL codon1	TIM+F+I+G4
rbcL codon2	F81+F+I
rbcL codon3	GTR+F+I+G4
SSU	SYM+I+G4

Maximum Log-likelihood of the tree: -25625.0053

MrBayes 3.2 commands
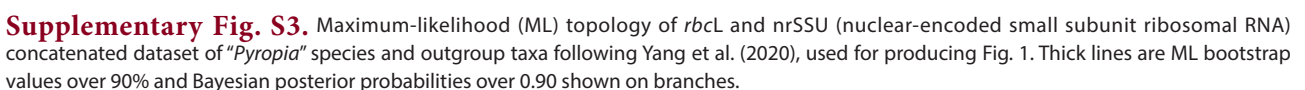**Partition**
charset rbclcodon1 = 1-xxxx\3;
charset rbclcodon2 = 2-xxxx\3;
charset rbclcodon3 = 3-xxxx\3;
charset SSU = xxxx-xxxx;
partition allpart = 4: rbclcodon1, rbclcodon2, rbclcodon3, SSU; set partition = allpart;

lset applyto=(all) nst=6 rates=invgamma ngammacat=4; prset applyto=(all) ratepr=variable;
unlink statefreq=(all) revmat=(all) shape=(all) pinvar=(all);
mcmcp ngen=3000000 nruns=2 nchains=4 samplefreq=1000 printfreq=1000
savebrlens=yes;
sumt nruns=2 contype=allcompat filename=3gene burnin=300;

Supplementary Fig S1. Output data from the two dataset analysis, including variation in partitions, models selected per partition and -Log likelihood scores of maximum-likelihood tree, for the two different analyses. Bayesian parameters for MrBayes analysis are also shown.

Supplementary Fig. S2. Cartoon of maximum-likelihood topology of *rbc*L and nrSSU (nuclear-encoded small subunit ribosomal RNA) concatenated dataset of "*Pyropia*" species with 'Bangia 3' used as an outgroup, following Sutherland et al. (2011). Values on generic and inter-generic branches are displayed on branches or in triangles: non-parametric bootstrap % / Bayesian posterior probabilities / approximate likelihood-ratio test % / Ultrafast bootstrap %.

Supplementary Fig. S3. Maximum-likelihood (ML) topology of *rbc*L and nrSSU (nuclear-encoded small subunit ribosomal RNA) concatenated dataset of "*Pyropia*" species and outgroup taxa following Yang et al. (2020), used for producing Fig. 1. Thick lines are ML bootstrap values over 90% and Bayesian posterior probabilities over 0.90 shown on branches.

REFERENCES

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Yang, L. -E., Deng, Y. -Y., Xu, G. -P, Russell, S., Lu, Q. -Q. & Brodie, J. 2020. Redefining *Pyropia* (Bangiales, Rhodophyta): four new genera, resurrection of *Porphyrella* and description of *Calidia pseudolobata* sp. nov. from China. J. Phycol. 56:862–879.