Diagram

Description automatically generatedFigure S1. Maximum-likelihood phylogeny (−log Ln = -4204.8994) of *psb*Asequences of *Tethysphytum antarcticum* and related sequences from GenBank. Model used for codons (First = TNe+I+G4; second = F81+F+I+G4; third = TPM3u+F+I+G4). *Corallinapetra novaezelandiae* used as outgroup

Shape

Description automatically generated with medium confidence

Figure S2. Maximum-likelihood phylogeny (−log Ln = -5128.7249) of *psb*Asequences of *Ballia* sp.and related sequences from GenBank. Model used for codons (First = TNe+I+G4; second = JC+I+G4; third = TVM+F+G4). *Euthora cristata* used as outgroup.

Shape

Description automatically generated with medium confidence

Figure S3. Maximum-likelihood phylogeny (−log Ln = -2469.9688) of *rbc*Lsequences of *Palmaria decipiens* and related sequences from GenBank. Model used for codons (First = TN+F+G4; second = JC+I+G4; third = HKY+F+G4). *Rhodophysema georgei* used as outgroup.

Shape

Description automatically generated with low confidence

Figure S4. Maximum-likelihood phylogeny (−log Ln = -13281.8477) of *rbc*Lsequences of Dumontiaceaeand related sequences from GenBank. Model used for codons (First = TIM+F+I+G4; second = TVMe+I+G4; third = TIM2+F+I+G4). *Stylonema alsidii* and *Tsunamia transpacifica* used as outgroups.

Shape

Description automatically generated with medium confidence

Figure S5. Maximum-likelihood phylogeny (−log Ln = -6040.8960) of *rbc*Lsequences of *Iridaea* sp. and related sequences from GenBank. Model used for codons (First = TN+F+I+G4; second = F81+F+I+G4; third = HKY+F+G4). *Phyllophora crispa* and *Dumontia contorta* used as outgroups.

Shape

Description automatically generated with low confidence

Figure S6. Maximum-likelihood phylogeny (−log Ln = -7152.9271) of *rbc*L sequences of *Phyllophora antarctica* and related sequences from GenBank. Model used for codons (First = TN+F+I+G4; second = TVM+F+I+G4; third = K3Pu+F+I+G4). *Mazzaella japonica* and *M. rosea* used as outgroups.

Shape

Description automatically generated with low confidence

Figure S7. Maximum-likelihood phylogeny (−log Ln = -5658.2997) of *rbc*Lsequences of *Plocamium* sp.and related sequences from GenBank. Model used for codons (First = TN+F+I+G4; second = K3P+I+G4; third = TN+F+G4). *Rhodophyllis membranacea* and *R. multipartita* used as outgroup.