

1 Appendix S1

2 Declines in plant palatability from polar to tropical latitudes depend on herbivore
3 and plant identity

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20 Table S1. Three-way ANOVA on palatability (%T) of seaweed from tropical (Fiji), temperate
 21 (California) and polar (Antarctica) locations to generalist marine herbivores. “% Variance”
 22 indicates the proportion of the Mean Sums of Squares that is explained by a factor or interaction
 23 term.

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	df	Sum sq	Mean sq	F value	<i>p</i> -value	% Var
Zone	2	6437	3218	18.774	<0.001	0.22
Division	1	10	10	0.061	0.806	0.00
Herbivore	1	8185	8185	47.746	<0.001	0.57
Zone x division	2	1233	616	3.596	0.032	0.04
Zone x herbivore	2	2663	1331	7.766	0.001	0.09
Division x herbivore	1	110	110	0.642	0.425	0.01
Zone x division x herbivore	2	1431	716	4.175	0.019	0.05
Residuals	88	15085	171			0.01

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28 Table S2. Amplification and sequencing primers.

Seaweed Division	Primer	Direction	Sequence (5'-3')	Reference
Phaeophyta & Rhodophyta	F-566	Forward	CAG CAG CCG CGG TAA TTC C	Hadziavdic <i>et al.</i> 2014
Phaeophyta & Rhodophyta	R-1200	Reverse	CCC GTG TTG AGT CAA ATT AAG C	Hadziavdic <i>et al.</i> 2014
Phaeophyta	RbcL68F	Forward	TGC CWA AAT GGG RWA YTG GGA TGC	Draisma <i>et al.</i> 2001
Phaeophyta	RbcL496R	Reverse	ACG WCC AAA TKT RTC TAA TCT	Draisma <i>et al.</i> 2001
Rhodophyta	F-57	Forward	GTA ATT CCA TAT GCT AAA ATG GG	Hommersand <i>et al.</i> 1994
Rhodophyta	R-753	Reverse	GCT CTT TCA TAC ATA TCT TCC	Hommersand <i>et al.</i> 1994

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32 Table S3. Source of sequences used in the construction of phylogenetic trees.

Sequence Source		Species
18S	<i>rbcL</i>	
This study	This study	<i>Padina sp.</i> , <i>Adenocystis utricularis</i> , <i>Petalonia binghamiae</i> , <i>Hormophysa sp.</i> , <i>Silvetia compressa</i> , <i>Halidrys siliquosa</i> , <i>Sargassum sp.</i> , <i>Turbinaria sp.</i> , <i>Laminaria sp.</i> , <i>Macrocystis pyrifera</i> , <i>Egregia sp.</i> , <i>Eisenia sp.</i> , <i>Delisea pulchra</i> , <i>Bossiella sp.</i> , <i>Calliarthron sp.</i> , <i>Corallina vancouveriensis</i> , <i>Gelidium coulteri</i> , <i>Gelidium sp.</i> , <i>Cystoclonium obtusangulum</i> , <i>Chondracanthus canaliculatus</i> , <i>Gigartina skottsbergii</i> , <i>Iridaea sp.</i> , <i>Mazzaella leptorhynchos</i> , <i>Hypnea sp.</i> , <i>Peyssonnelia sp.</i> , <i>Phacelocarpus neurymenioides</i> , <i>Portieria sp.</i> , <i>Callophycus serratus</i> , <i>Gracilaria edulis</i> , <i>Tricleocarpa cylindrica</i> , <i>Tricleocarpa fragilis</i> , <i>Palmaria decipiens</i> , <i>Plocamium cartilagineum</i> , <i>Plocamium sp.</i>
NCBI	NCBI	<i>Amphiroa fragilissima</i> , <i>Dichotomaria marginata</i>
This study	NCBI	<i>Himantothallus grandifolius</i> , <i>Cystosphaera jacquinotii</i>
NA	This study	<i>Dictyota acutiloba</i> , <i>Dictyota sp.</i> , <i>Chnoospora implexa</i> , <i>Pelagophycus porra</i> , <i>Egregia menziesii</i> , <i>Ceramium sp.</i> , <i>Myriogramme smithii</i>
NA	NCBI	<i>Gymnogongrus turquetii</i>
No data		<i>Neurymenia fraxinifolia</i> , <i>Amphiroa crassa</i> , <i>Actinotrichia sp.</i> , <i>Galaxaura sp.</i>

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35 Table S4. Accession numbers and information for supplemental sequences used in the
 36 construction of phylogenies and in-house generated sequences.

Species	Gene	Accession Number
<i>Amphiroa fragilissima</i>	18S	KM044027; U60744
<i>Dichotomaria marginata</i>	18S	GQ227517-18
<i>Amphiroa fragilissima</i>	rbcL	KM044022; U04039
<i>Dichotomaria marginata</i>	rbcL	KC134339; AB117630; KP238504; AY688022-23; AY688018-19; AY688017; KF752510-13; AB258440-46; KU360125; KU321676;
<i>Gymnogongrus turquetti</i>	rbcL	U04196; U22510; U27018-19
<i>Cystosphaera jaquinotii</i>	rbcL	EF990250
<i>Himantothallus grandifolius</i>	rbcL	GQ368320; AJ287850; HE866853; AJ287904
Multiple species	Both	KY987557- 639

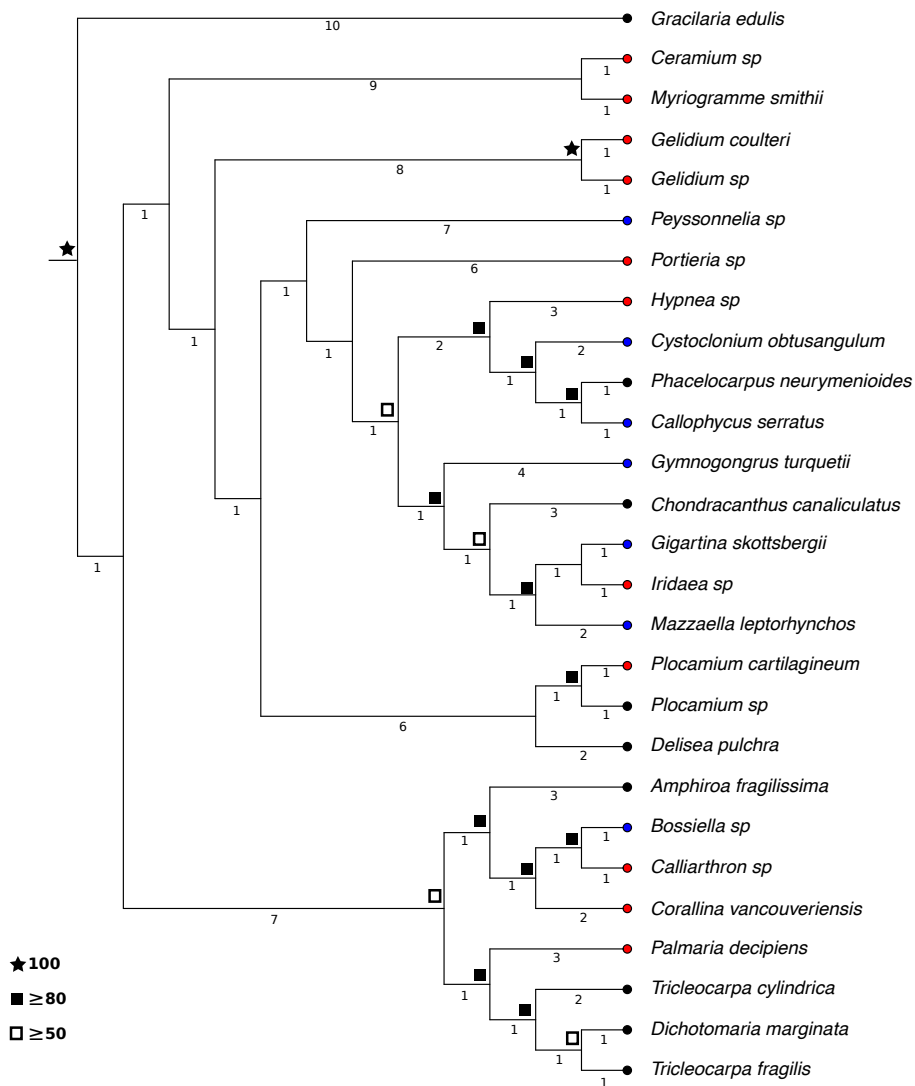
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40 Figure S1. Maximum Parsimony Phylogeny based on 18S and *rbcL* sequences with 10,000
 41 bootstrap replicates of a) Rhodophyta and b) Phaeophyta (strict consensus of 3 trees). Branch
 42 lengths are under their corresponding branch and bootstrap values are identified by symbol based
 43 on the legend. Seaweed origin is denoted by the colored circles (red = Fiji; black = CA, blue =
 44 Antarctica).

A) Rhodophyta

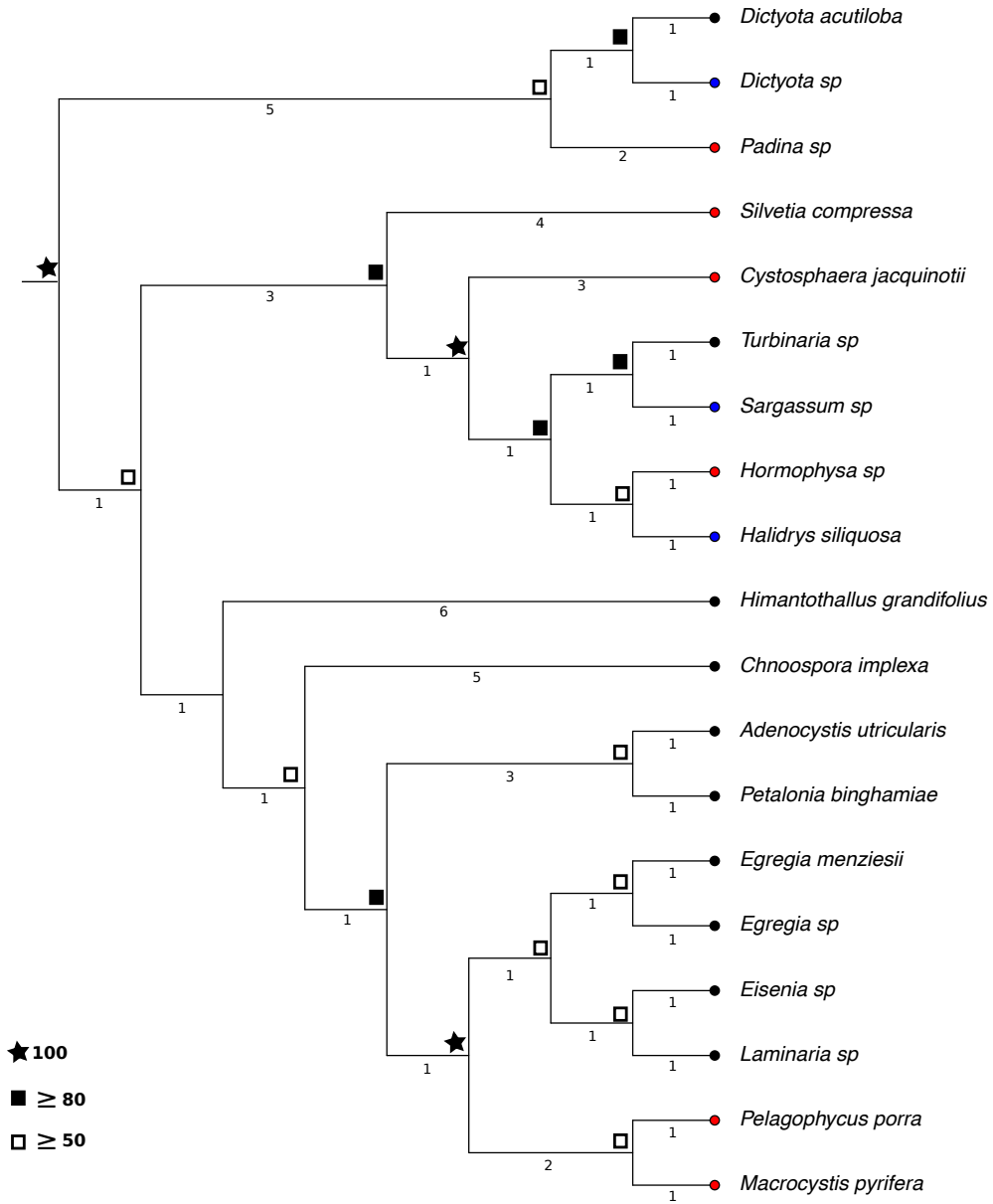


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B) Phaeophyta



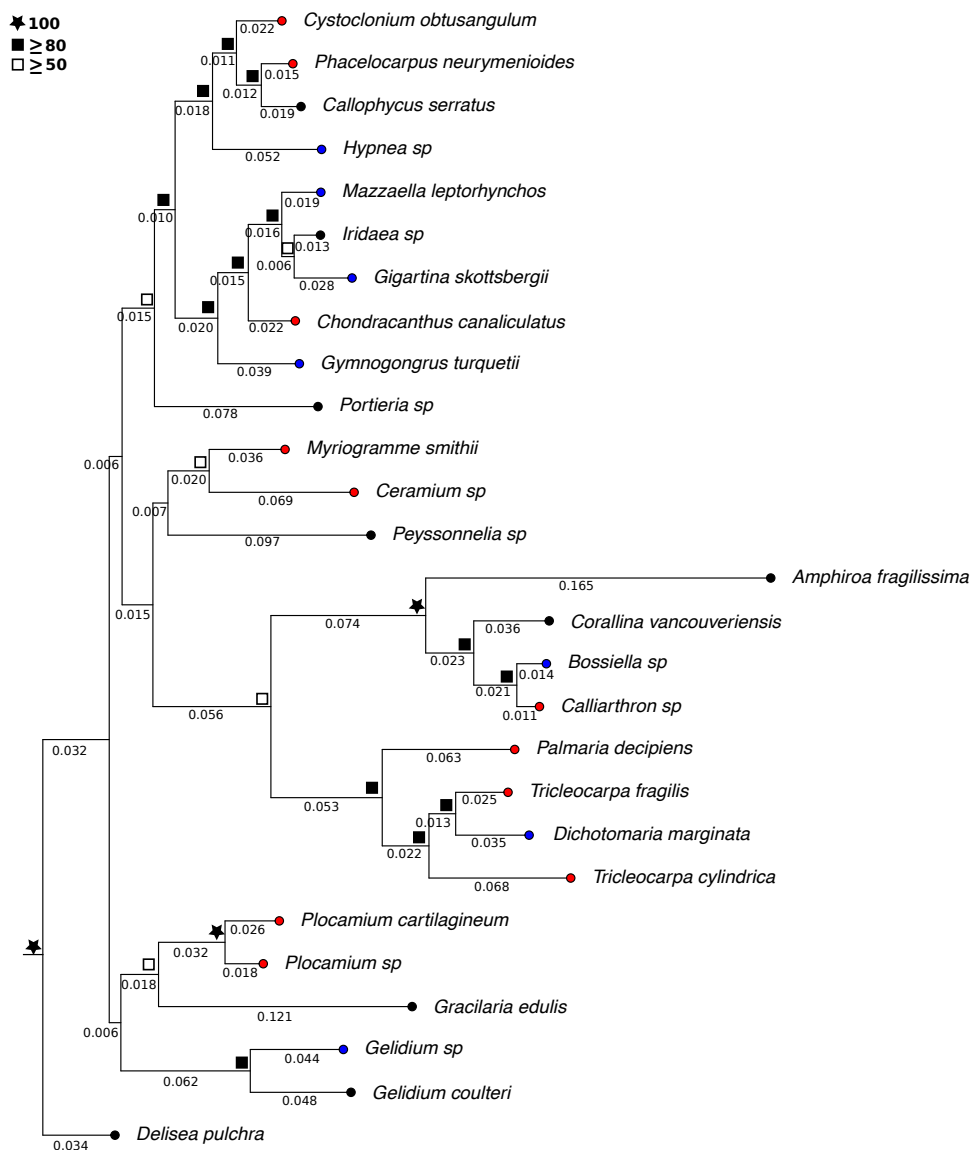
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51 Figure S2. Maximum Likelihood Phylogeny based on 18S and *rbcL* sequences with 10,000
 52 bootstrap replicates of a) Rhodophyta and b) Phaeophyta. Branch lengths are under their
 53 corresponding branch and bootstrap values are identified by symbol based on the legend.
 54 Seaweed origin is denoted by the colored circles (red = Fiji; black = CA, blue = Antarctica).
 55 Unlabeled Phaeophyta branches have lengths of 1.3e-06.

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A) Rhodophyta



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B) Phaeophyta

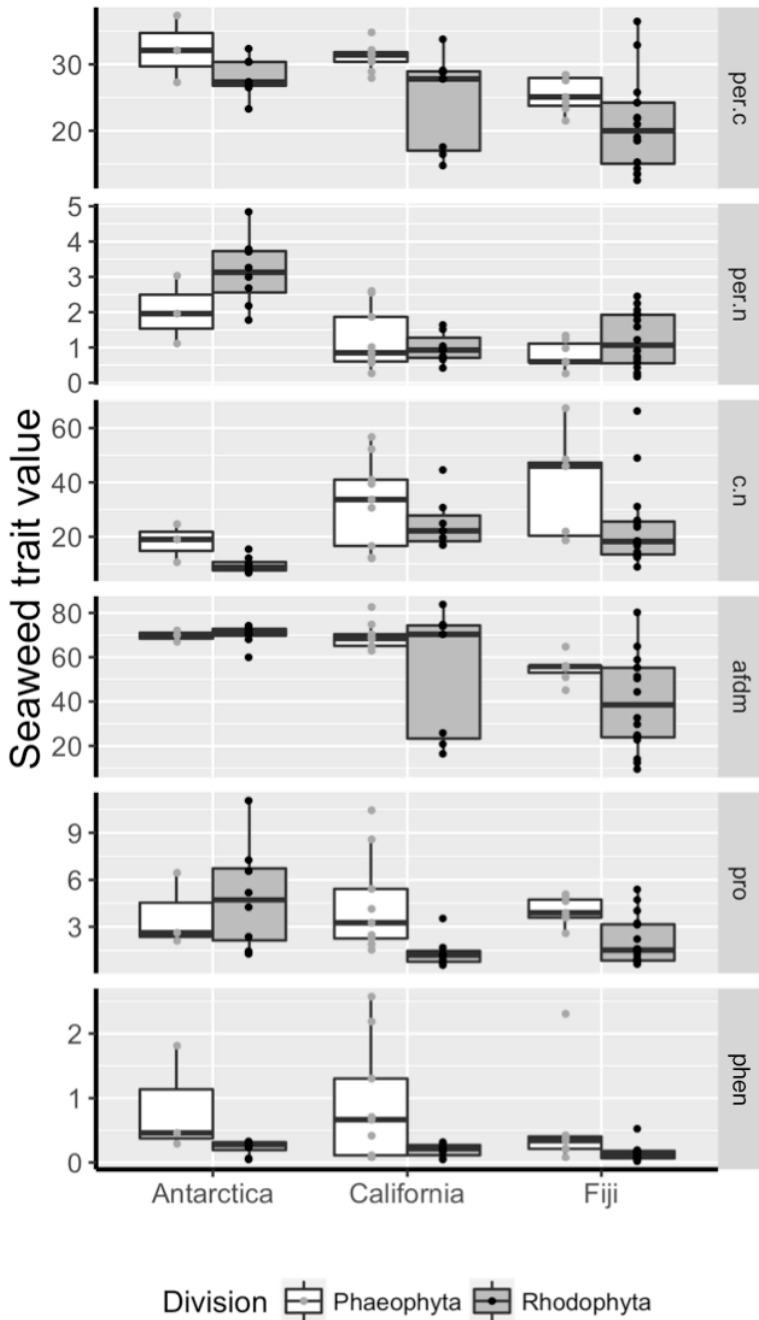
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63 Figure S3. Seaweed traits plotted across collection sites. Per.n and per.c represent percent
 64 nitrogen and carbon while c.n represents the carbon to nitrogen ratio. Percent ash-free dry mass
 65 (afdm), percent protein (pro) and percent phenolics (phen) are also represented. All traits were
 66 calculated as percentage per gram dry mass using lyophilized tissue.



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69 Figure S4. Palatability of Rhodophyta seaweeds (fleshy species only) to urchins depends on both
 70 organic content and collection site. Calcified seaweeds excluded were *Tricleocarpa cylindrica*,
 71 *T. fragilis*, *Amphiroa crassa*, *A. fragilissima*, *Galaxaura sp.*, *Dichotomaria marginata*,
 72 *Actinotrichia sp.*, *Peyssonnelia sp.*, *Bossiella sp.*, *Calliarthron sp.*, and *Corallina*
 73 *vancouveriensis*. Top panel regresses palatability against AFDM (percent ash-free dry mass per
 74 unit dry mass) ($F_{1,18} = 6.1$, adj. $r^2 = 0.210$, $p=0.024$) while the bottom panel shows the boxplot
 75 of their residuals against collection site ($F_{2,17} = 2.8$, $p = 0.092$). Point size in top panel indicates
 76 average latitudinal distribution of genus.

