

Supplementary Material

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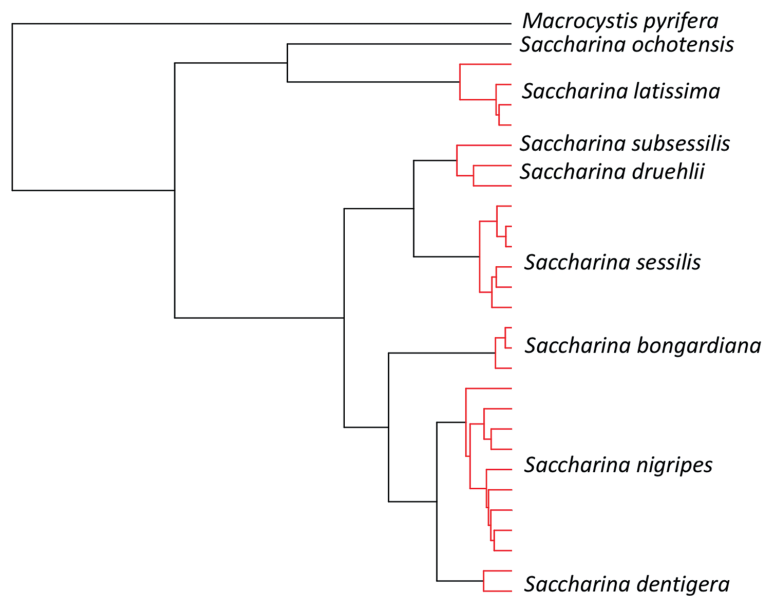
Supplementary Table S2. Genetic distance (internal transcribed spacer) between species of *Saccharina*

Species	Sample size ^a	Nearest neighbour (NN)	Distance to NN ^b	Max-intra difference ^b
<i>Saccharina subsessilis</i>	1	<i>S. nigripes</i>	0.8	NA
<i>S. druehlii</i>	5	<i>S. subsessilis</i> ^c	1.13	0
		<i>S. nigripes</i> ^c	1.20	-
<i>S. sessilis</i>	14	<i>S. nigripes</i>	2.23	1.11
<i>S. nigripes</i>	13	<i>S. subsessilis</i>	0.80	1.50
<i>Saccharina latissima</i> Global ^c	47	<i>S. nigripes</i>	6.47	0.88

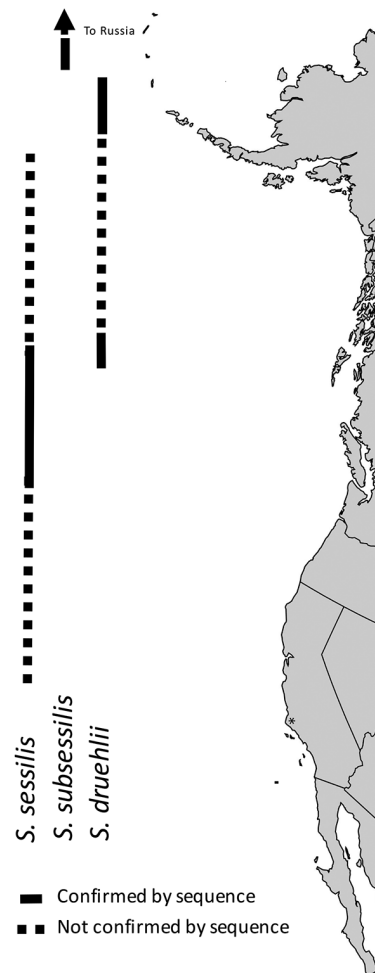
^aAll sequences from BOLD and this study.

^bExpressed as percent sequence divergence.

^cBoth neighbours shown due to similar distance.



Supplementary Fig. S1. Generalized Mixed Yule Coalescent analysis using CO1-5P gene tree. Ultrametric tree was constructed in BEAST using a HKY model of evolution and strict clock priors. Prior choice (relaxed clock, random local clock) did not influence the resulting topology or species clustering.



Supplementary Fig. S2. A map showing the known and putative distributions of *Saccharina sessilis*, *S. subsessilis*, and *S. druehlii*.