



Supplementary FIGURE S1 Comparison of the performance of niche models that differed the betamultiplier (2 to 10 with increments of 0.5). Model-performance was estimated by the area under the receiver operating characteristic estimated from test data (AUC.Test) (Fielding and Bell, 1997). Each model with a certain beta-multiplier started with 13 variables and was simplified in a stepwise fashion by removing those variables with low contribution-scores (<5%) and high correlation with other variables (correlation coefficients >0.7 or <-0.7). The number of variables in each model is encoded both by color and size. The model of highest performance (based on AICc (Akaike, 1974), not AUC.Test) is marked in red.



Supplementary FIGURE S2 Comparison of the performance of niche models that differed in the beta-multiplier (2 to 10 with increments of 0.5). Model-performance was estimated by the sample-size-adjusted Akaike information criterion (AICc) (Akaike, 1974). AICc values could not be calculated where the number of model parameters exceeded the number of occurrence sites. Each model with a certain beta multiplier started with 13 variables and was simplified in a stepwise fashion by removing those variables with low contribution-scores (<5%) and high correlation with other variables (correlation coefficients >0.7 or <-0.7). The number of variables in each model is encoded both by color and size. The model of highest performance (lowest AICc) is marked in red.

Reference:

Akaike, H. (1974). A new look at the statistical model identification. *IEEE Trans. Autom. Control.* 19:716–723.

Fielding, A.H. and Bell, J.F. (1997). A review of methods for the assessment of prediction errors in conservation presence/absence models. *Environ. Conserv.* 24(1), 38–49. https://doi.org/10.1017/S0376892997000088



Supplementary FIGURE S3 Rooted ML/NJ trees inferred from mtDNA *cox*3. Bootstrap values higher than 0.5/0/5 are shown. The triangles represent the localities of each haplotype.



Supplementary FIGURE S4 Response curves of the three environmental variables that were chosen for distribution modelling. The curves show how the mean (red line) logistic probability of presence of *Sargassum horneri* depend on each variable over 15 replicate models; the range of two standard deviations are represented as blue shade. The scale of each variable is shaped by a buffer of 17.5 km from the coastline in our study area. MaxSST: LTA of maximum sea surface temperature; MinSSS: LTA of minimum surface sea salinity.



Supplementary FIGURE S5 Posterior probability distributions for the relative divergence timescales estimated between lineages of *Sargassum horneri*.



Supplementary FIGURE S6 Pairwise mismatch distributions and neutrality tests (Tajima's *D* and Fu's *F*s) for three lineages of *Sargassum horneri*. ***p < 0.05