

Table S1. Matrix of pairwise genetic distance (F_{ST}) below diagonal for samples of *Z. marina*. Values in brackets are from the reduced data set ($n = 10$ shoots per sample for a total of 110) and those in red indicate differentiation patterns that differ from the full data set ($n = 293$). Within site comparisons are shaded in grey; within year comparisons are underlined. Bolded values are significant ($p < 0.05$). *Indicates the second sample within a given year.

	NC1 2007	NC1 2008	NC1 2016	NC1 2017	NC1 2017b*	NC2 2007	NC2 2008	NC2 2016	NC2 2016b*	NC2 2017
NC1 2008	-0.007 (-0.007)	----								
NC1 2016	0.046 (0.038)	0.062 (0.055)	----							
NC1 2017	0.041 (0.033)	0.051 (0.046)	0.005 (-0.015)	----						
NC1 2017b*	0.032 (0.023)	0.057 (0.042)	0.016 (0.006)	<u>0.023</u> (0.019)	----					
NC2 2007	0.059 (0.059)	0.093 (0.093)	0.087 (0.069)	0.097 (0.092)	0.057 (0.062)	----				
NC2 2008	0.023 (0.023)	0.039 (0.039)	0.067 (0.050)	0.076 (0.064)	0.041 (0.053)	-0.006 (-0.006)	----			
NC2 2016	0.048 (0.041)	0.077 (0.070)	0.013 (0.003)	0.034 (0.022)	0.013 (0.013)	0.056 (0.051)	0.041 (0.036)	----		
NC2 2016b*	0.034 (0.008)	0.039 (0.040)	0.007 (-0.013)	0.008 (-0.005)	0.017 (0.004)	0.076 (0.068)	0.053 (0.028)	<u>0.010</u> (0.013)	----	
NC2 2017	0.033 (0.066)	0.053 (0.088)	0.007 (0.007)	0.019 (0.017)	0.011 (0.045)	0.067 (0.089)	0.040 (0.059)	0.001 (0.003)	0.004 (0.026)	----
NC2 2017b*	0.027 (0.035)	0.059 (0.077)	0.031 (0.003)	0.041 (0.013)	0.013 (0.017)	0.039 (0.054)	0.016 (0.033)	0.009 (0.018)	0.006 (-0.009)	<u>0.017</u> (0.016)

Table S2. Comparison of kinship values between the full (n=293) and reduced data set (n = 10 shoots per sample for a total of 110). Values from the reduced data set are in brackets. Observations include: mean kinship within samples (k), and the proportion of kinship observations that were greater than chance for: full siblings, half siblings, quarter siblings and unrelated individuals.

	NC1 2007	NC2 2007	NC1 2008	NC2 2008	NC1 2016	NC2 2016	NC2 2016b*	NC1 2017	NC2 2017	NC1 2017b*	NC2 2017b*
Mean k	0.067	0.069	0.097	0.048	0.013	0.011	0.002	0.015	0.031	0.014	0.005
	(0.067)	(0.069)	(0.097)	(0.059)	(0.001)	(-0.014)	(-0.019)	(0.017)	(0.019)	(0.014)	(0.042)
Full sibling	0.00	1.82	8.18	2.22	1.36	-0.27	1.00	0.79	1.59	5.14	8.82
	(0.00)	(1.82)	(8.18)	(2.22)	(-5.45)	(-1.82)	(1.82)	(0.00)	(7.27)	(0.00)	(12.73)
Half sibling	8.89	25.45	23.64	15.56	2.64	0.89	4.33	7.62	-0.26	2.75	0.00
	(8.89)	(25.45)	(23.64)	(15.56)	(-1.82)	(1.82)	(5.45)	(1.82)	(1.82)	(5.45)	(7.27)
Quarter sib	17.78	0.00	14.24	-13.33	4.59	2.84	2.00	2.54	0.00	-2.48	-2.21
	(17.78)	(0.00)	(14.24)	(-13.33)	(3.64)	(-5.45)	(0.00)	(7.27)	(7.27)	(9.09)	(-7.27)
Unrelated	2.22	-9.09	-10.30	4.44	-5.36	1.15	-15.67	4.13	2.12	-6.03	-9.56
	(2.22)	(-9.09)	(-10.30)	(4.44)	(3.64)	(-5.45)	(-10.91)	(9.09)	(-3.640)	(-7.27)	(-12.73)



Figure S1. STRUCTURE clustering results obtained at $K=2$ for (a) the full dataset ($n = 293$) and (b) the reduced dataset ($n = 110$). Each individual is represented by a thin bar corresponding to the sum of assignment probabilities to the K cluster. Black bars separate samples.

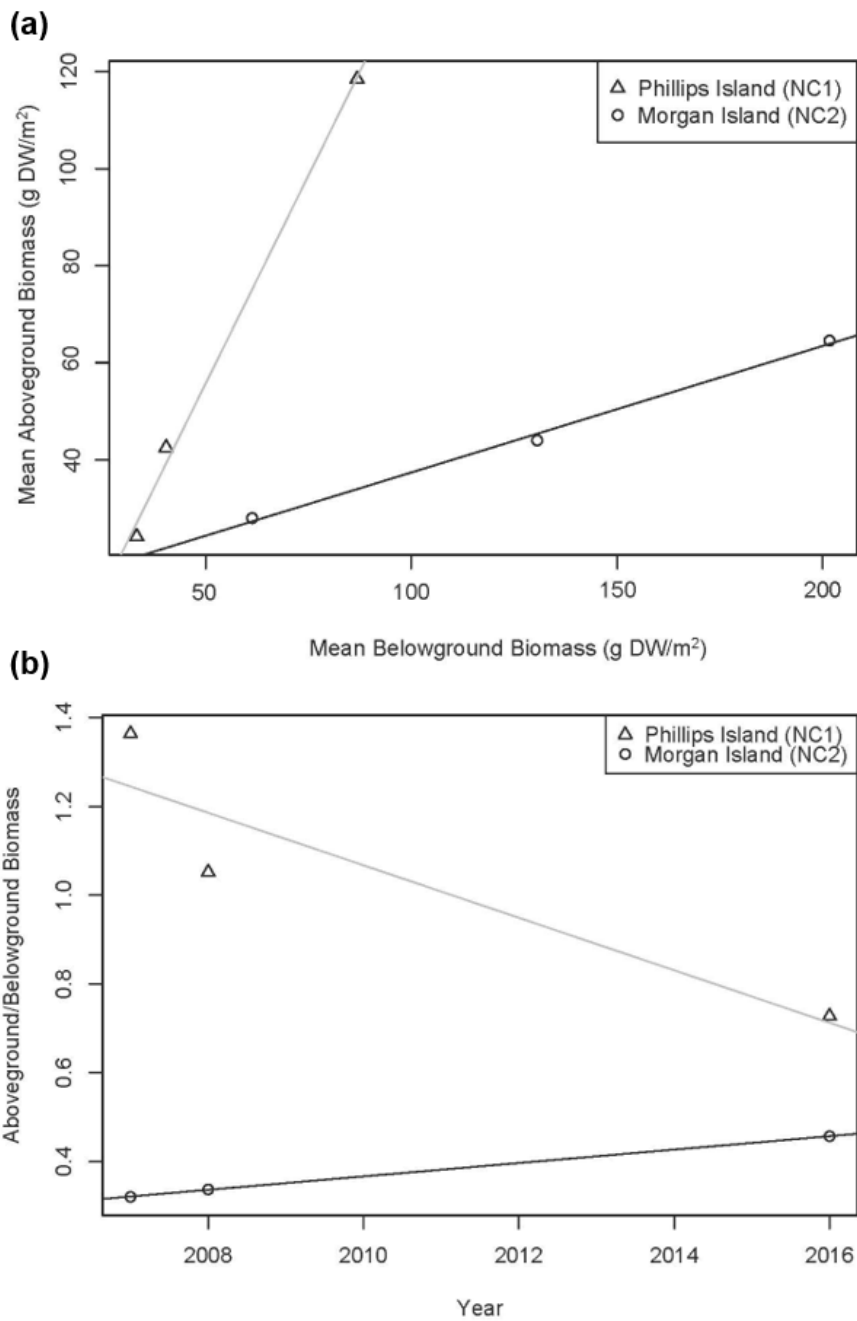


Figure S2. (a) Relationship between mean above-ground and mean below-ground biomass at each site; (b) AG/BG ratio over time at each site.