

Invasion success of a habitat-forming marine invertebrate is limited by lower-than-expected dispersal ability

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Marine Ecology Progress Series 536: 221–227 (2015)

Supplementary Methods, Tables and Figures

Table S1. Priors specified for simulating the scenarios in Fig. 2.

Parameters (conditions)	Minimum	Maximum
N1	10	10000
N2	10	10000
N3	10	10000
N4	10	10000
N5	10	10000
N6	10	10000
t1	10	400
db (db < t1)	1	10
N6b	1	100
t2 (t2 > t1)	10	400
N5b	1	100
t3 (t3 > t2)	10	400
N4b	1	100
t4 (t4 > t3)	10	400
N3b	1	100
t5 (t5 > t4)	10	400
N2b	1	100

N = effective population size; Nb = effective population size during a bottleneck; t = timing of a colonisation event (the maximum of 400 represents the onset of European settlement); db duration of genetic bottlenecks.

Numbers after N and t correspond to those in Fig. 1.

Model checking (the ability of a specific scenario to produce data sets similar to the observed data set) was performed by simulating 1000 data sets. The similarity of data sets was assessed using the same summary statistics specified earlier. A significant difference ($p < 0.05$) was found in one out of 36 cases, namely for $(\delta\mu)^2$ for populations 5 and 6, suggesting that scenario 1 explains the observed data set sufficiently well (Cornuet et al. 2010).

Table S2. Observed (H_o) and expected (H_e) heterozygosity calculated for each locus and site.

Locus		Site					
		1	2	3	4	5	6
<i>Pysp02</i>	H_o	0.35	0.57	0.65	0.52	0.62	0.46
	H_e	0.40	0.46	0.47	0.48	0.48	0.48
<i>Pysp12</i>	H_o	0.39	0.33	0.41	0.61	0.70	0.74
	H_e	0.34	0.36	0.41	0.45	0.55	0.56
<i>Pysp13</i>	H_o	0.16	0.27	0.12	0.09	0.14	0.13
	H_e	0.21	0.23	0.12	0.08	0.13	0.12
<i>Pysp15</i>	H_o	0.00	0.00	0.04	0.04	0.05	0.03
	H_e	0.00	0.00	0.04	0.04	0.05	0.03
<i>Pysp19</i>	H_o	0.10	0.37	0.31	0.26	0.24	0.33
	H_e	0.09	0.30	0.29	0.26	0.24	0.40
<i>Pysp25</i>	H_o	0.13	0.30	0.20	0.22	0.14	0.41
	H_e	0.18	0.43	0.18	0.23	0.21	0.36
<i>Pysp26</i>	H_o	0.10	0.27	0.12	0.07	0.14	0.15
	H_e	0.15	0.23	0.12	0.06	0.13	0.14

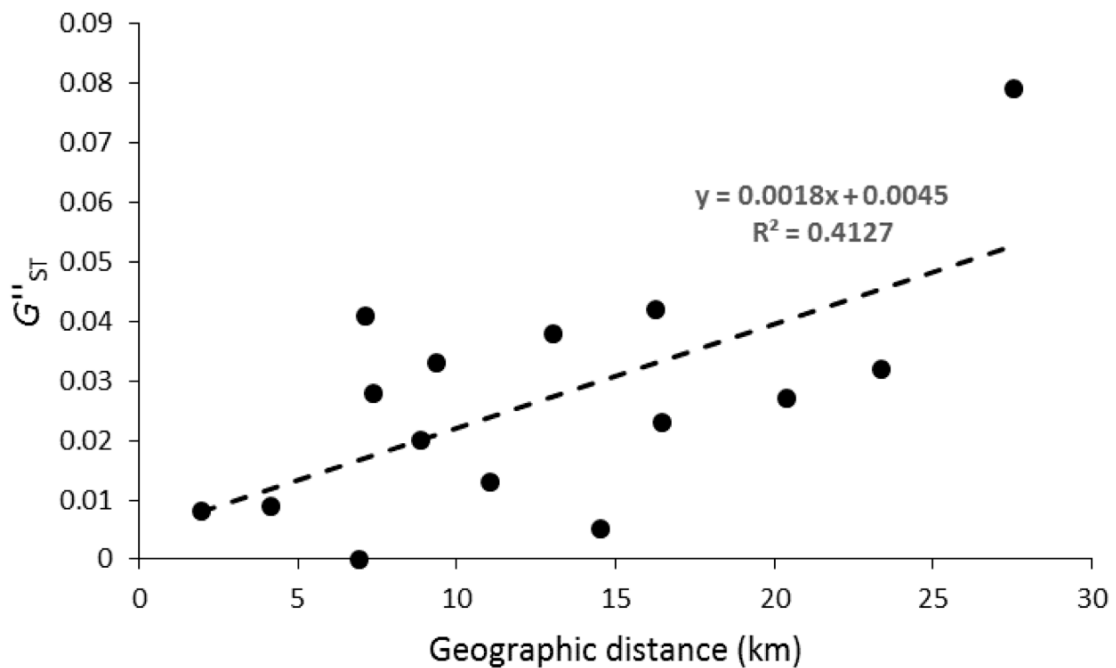


Fig. S1. A regression plot of geographic vs. genetic distance for pairs of sites in the Adelaide metropolitan area settled by *Pyura doppelgangera*.

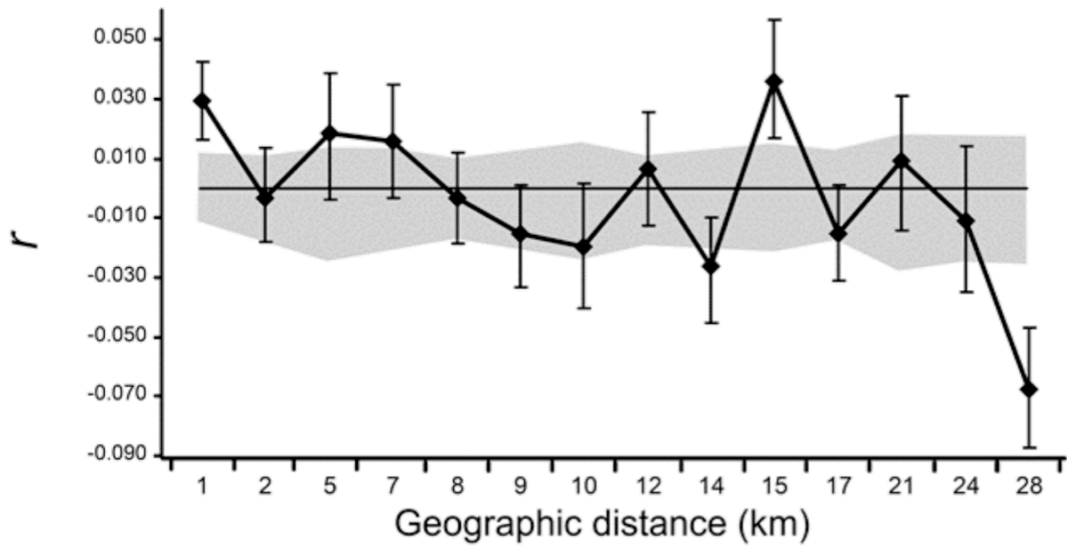


Fig. S2. Spatial autocorrelation correlogram for *Pyura doppelgangera* in the Adelaide metropolitan area. The correlogram depicts the autocorrelation parameter r at a scale of kilometres comparing all six sites. Geographic distances represent the end point of a particular 1 km distance class. The shaded areas represent the 95% confidence interval under the assumption of panmixia, beyond which the hypothesis of no spatial autocorrelation is rejected, and the error bars represent confidence intervals around r .

LITERATURE CITED

Cornuet JM, Ravigné V, Estoup A (2010) Inference on population history and model checking using DNA sequence and microsatellite data with the software DIYABC (v1.0). BMC Bioinformatics 11:401