1 **Electronic Supplementary Material 1 (ESM1):** Isolation by Resistance Across a Complex Coral
2 Reef Seascape
3
4 Table S1 Descriptive statistics of 15 sample sites across the Houtman Abrolhos Islands: sample
5 sizes (N), number of multi-locus genotypes (G), allelic richness (A_R), observed (H_O) and expected
6 (H_E) heterozygosity and inbreeding coefficients (F_{IS}). Bold values indicate significance
7 ($P \leq 0.05$).
8
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33 symmetric and so non-directional.
34
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36 subsampled dataset. Asterisks indicate p values using the full dataset.
37
38 Text Sl Details of the calculations for the forward projection matrix
39

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44

Group	Site	Latitude	Longitude	N	G	A_R	H_O	H_E	F_{IS}
Pelsaert	P1	-28.869	113.877	16	16	3.513	0.604	0.637	0.040
	P2	-28.898	113.923	14	14	3.327	0.610	0.594	0.012
	P3	-28.867	113.970	18	18	3.693	0.572	0.668	**0.175**
	P4	-28.862	113.988	14	14	3.217	0.500	0.591	**0.109**
	P5	-28.815	113.948	16	15	3.554	0.638	0.624	0.033
Easter	E1	-28.650	113.880	30	29	3.879	0.533	0.653	**0.181**
	E2	-28.699	113.780	25	25	3.903	0.597	0.644	0.102
	E3	-28.716	113.789	33	32	3.818	0.609	0.648	0.087
	E4	-28.740	113.809	26	26	3.810	0.600	0.654	0.091
	E5	-28.737	113.789	30	30	3.643	0.547	0.639	**0.143**
Wallabi	W1	-28.473	113.776	38	36	3.691	0.587	0.656	0.127
	W2	-28.480	113.784	24	20	3.812	0.629	0.663	0.049
	W3	-28.499	113.746	44	44	3.730	0.576	0.669	**0.152**
	W4	-28.435	113.743	37	30	3.395	0.597	0.617	0.009
	W5	-28.407	113.719	30	30	3.740	0.640	0.673	**0.067**

Table S2 Multiplex details and thermocycling conditions for the panel of microsatellite markers

Locus	Primer Sequence (5'-3')	Primer vol [10µM]	Flourescent tag	Multiplex
Amil2_018[1]	F-GCCCTCCTTAGGTGATTTAC	0.375	6-FAM	1
	R- ATCGTTTTGAGCAATCAGAC			
EST_063[2]	F-TATTGTAGTCGTTACGTAGGCT	0.065	VIC	1
	R-AACAATCGTGCATACTAGCTCA			
Amil2_022[1]	F-CTGTGGCCTTGTTAGATAGC	0.065	VIC	1
	R-AGATTTGTGTTGTCCTGCTT			
Amil2_002[1]	F-ACAAAATAACCCCTTCTACCT	0.100	6-FAM	2
	R-CTTCATCTCTACAGCCGATT			
EST_181[2]	F-TGATTGCTGAGAAAGCTAGAGAT	0.100	VIC	2
	R-GCCTCACCTTGCCTTGTACA			
EST_254[2]	F-GGTGACCAATCAGAGTCTTGA	0.125	PET	2
	R--TACACTTGCTATAGTAACTTGCT			
EST_016[2]	F-CTATCTGTGTATGATCAGGACTA	0.100	6-FAM	3
	R-TCCATCTGTTGTGGAAACTGGT			
WGS_153[2]	F- TTTCCAAGTTGCTGTGAGTACA	0.175	VIC	3
	R-CGGGTGCTAAGCTTGCTCAA			
EST_245[2]	F-CAGAATGATATTTCTGCAGCACT	0.200	VIC	4
	R-CGCAATCGAGATTATAGGAAGA			
EST_098[2]	F-ACAAATTGCGCTCAAGTTGATG	0.050	VIC	4
	R-ACGGCTGCGAAGGAGTCTAGT			

Thermocycling conditions for multiplexes are as follows: Initial activation step for 15 min at 95°C, followed by 35 cycles of denaturing for 30sec at 94°C, annealing for 90s at 50°C (Multiplex 1, 2, 3) or 60°C (Multiplex 4) and extension for 90s at 72°C, and a final extension step for 10min at 72°C. Primers from [1]vanOppen et al. (2007) and [2]Wang et al. (2009)

Table S3 Biophysical dispersal model parameters.

Parameter	Setting	Description
elSp	1	Release spacing
relSpUnits	Days	
relDuration	8	Maximum duration of a release
relDurationUnits	Days	
competencyStart	3	Date of settling eligibility
competencyStartUnits	Days	
settleChkFreq	1	Frequency of checking for settlement
settleChkFreqUnits	Days	
outputFreq	6	Frequency of output
outputFreqUnits	Hours	
vmgrt	FALSE	Include vertical migration behaviour?
mrate	0.06	Mortality rate
mUnits	Days	
mortalityType	Exponential	
diffusionType	Simple	
settlementType	FloatOver	
initialPositionType	Centroid	

Table S4 Diversity indices of the microsatellite markers at each sample site.

		Amil2_018	EST_063	Amil2_022	Amil2_002	EST_181	EST_245	EST_016	WGS_153	EST_254	EST_98
P1	N	16	16	16	16	16	16	16	16	15	16
	N_A	3	3	7	5	9	9	5	6	6	7
	N_E	1.135	1.636	3.507	3.683	3.391	6.024	3.436	5.172	4.737	3.631
	H_O	0.125	0.375	0.563	0.625	0.813	0.750	0.688	0.813	0.200	0.688
	H_E	0.119	0.389	0.715	0.729	0.705	0.834	0.709	0.807	0.789	0.725
	F_{IS}	-0.049	0.035	0.213	0.142	-0.152	0.101	0.030	-0.007	0.746	0.051
P2	N	14	14	14	14	14	14	14	12	14	14
	N_A	3	2	4	5	9	10	4	5	4	7
	N_E	1.156	1.415	3.039	2.178	4.723	7.686	2.631	4.056	2.465	3.063
	H_O	0.143	0.214	0.571	0.643	0.857	0.857	0.643	0.917	0.357	0.643
	H_E	0.135	0.293	0.671	0.541	0.788	0.870	0.620	0.753	0.594	0.673
	F_{IS}	-0.057	0.270	0.148	-0.189	-0.087	0.015	-0.037	-0.217	0.399	0.045
P3	N	18	18	18	18	18	17	18	15	17	18
	N_A	6	3	10	4	11	8	6	7	4	8
	N_E	1.427	1.906	4.235	2.339	5.445	5.070	3.465	5.000	1.710	4.349
	H_O	0.167	0.333	0.778	0.389	0.667	0.824	0.722	0.600	0.176	0.667
	H_E	0.299	0.475	0.764	0.573	0.816	0.803	0.711	0.800	0.415	0.770
	F_{IS}	0.443	0.299	-0.018	0.321	0.183	-0.026	-0.015	0.250	0.575	0.134
P4	N	14	14	13	14	14	14	14	11	10	14
	N_A	5	2	7	3	9	9	5	5	4	6
	N_E	1.352	1.324	2.541	1.840	5.091	6.323	2.722	3.408	2.667	4.356
	H_O	0.286	0.286	0.385	0.500	0.714	0.857	0.500	0.545	0.100	0.429
	H_E	0.260	0.245	0.607	0.457	0.804	0.842	0.633	0.707	0.625	0.770
	F_{IS}	-0.098	-0.167	0.366	-0.095	0.111	-0.018	0.210	0.228	0.840	0.444
P5	N	13	15	15	15	15	15	15	15	13	15
	N_A	2	4	6	6	9	8	5	6	6	9
	N_E	1.080	1.320	3.879	4.286	4.787	5.625	3.435	3.913	3.159	3.659
	H_O	0.077	0.267	0.867	0.533	0.867	0.733	0.800	0.733	0.308	0.867
	H_E	0.074	0.242	0.742	0.767	0.791	0.822	0.709	0.744	0.683	0.727
	F_{IS}	-0.040	-0.101	-0.168	0.304	-0.096	0.108	-0.129	0.015	0.550	-0.193
E1	N	28	29	28	29	29	29	29	29	28	29
	N_A	4	3	8	6	12	10	5	7	5	8
	N_E	1.456	1.503	2.266	2.905	6.728	6.007	3.831	5.965	2.761	4.237
	H_O	0.250	0.276	0.429	0.483	0.862	0.690	0.655	0.448	0.214	0.655
	H_E	0.313	0.335	0.559	0.656	0.851	0.834	0.739	0.832	0.638	0.764
	F_{IS}	0.202	0.176	0.233	0.264	-0.013	0.173	0.113	0.461	0.664	0.142
E2	N	25	25	25	25	25	24	25	20	22	25
	N_A	4	2	6	6	10	11	5	8	6	9
	N_E	1.130	1.523	4.072	2.694	5.388	6.698	3.086	6.154	3.006	4.386
	H_O	0.080	0.280	0.840	0.560	0.880	0.833	0.640	0.700	0.182	0.560
	H_E	0.115	0.343	0.754	0.629	0.814	0.851	0.676	0.838	0.667	0.772
	F_{IS}	0.306	0.184	-0.113	0.109	-0.081	0.020	0.053	0.164	0.728	0.275
E3	N	31	31	31	32	32	31	32	29	30	32
	N_A	6	4	6	6	12	12	6	7	4	8
	N_E	1.405	1.569	3.668	2.260	5.737	7.479	3.871	5.570	2.899	2.805
	H_O	0.194	0.323	0.677	0.438	0.844	0.903	0.688	0.724	0.033	0.688
	H_E	0.288	0.363	0.727	0.558	0.826	0.866	0.742	0.820	0.655	0.644
	F_{IS}	0.329	0.110	0.069	0.215	-0.022	-0.043	0.073	0.117	0.949	-0.068
E4	N	25	26	26	26	26	26	26	20	20	26
	N_A	4	2	6	6	10	9	5	7	4	7
	N_E	1.397	1.649	3.808	2.174	4.678	7.596	3.431	5.517	2.484	4.036
	H_O	0.240	0.385	0.769	0.346	0.769	0.769	0.769	0.700	0.250	0.654
	H_E	0.284	0.393	0.737	0.540	0.786	0.868	0.709	0.819	0.598	0.752
	F_{IS}	0.155	0.023	-0.043	0.359	0.022	0.114	-0.086	0.145	0.582	0.131
E5	N	30	30	30	30	30	30	30	26	29	30
	N_A	4	4	7	6	10	10	6	10	6	8
	N_E	1.506	1.410	2.885	2.479	5.114	6.228	4.138	6.288	3.025	2.736
	H_O	0.200	0.333	0.633	0.433	0.767	0.700	0.667	0.692	0.103	0.500
	H_E	0.336	0.291	0.653	0.597	0.804	0.839	0.758	0.841	0.669	0.634
	F_{IS}	0.405	-0.147	0.031	0.274	0.047	0.166	0.121	0.177	0.845	0.212
W1	N	36	36	34	36	35	34	36	32	30	35
	N_A	5	2	10	4	11	10	7	6	6	8
	N_E	1.461	1.564	3.375	2.296	5.684	6.964	3.465	4.785	2.299	4.083
	H_O	0.250	0.250	0.529	0.472	0.829	0.853	0.778	0.688	0.167	0.629
	H_E	0.316	0.361	0.704	0.564	0.824	0.856	0.711	0.791	0.565	0.755

	F_{IS}	0.208	0.307	0.248	0.163	-0.005	0.004	-0.093	0.131	0.705	0.168
W2	N	20	20	19	20	20	19	20	16	17	20
	N_A	3	3	7	5	11	10	6	8	4	8
	N_E	1.227	1.629	3.438	3.162	7.407	6.748	3.361	5.278	2.388	4.420
	H_O	0.200	0.350	0.579	0.450	0.950	0.895	0.750	0.688	0.118	0.800
	H_E	0.185	0.386	0.709	0.684	0.865	0.852	0.703	0.811	0.581	0.774
	F_{IS}	-0.081	0.094	0.184	0.342	-0.098	-0.050	-0.068	0.152	0.798	-0.034
W3	N	41	42	43	44	44	40	44	36	43	44
	N_A	6	3	9	5	11	10	8	8	4	8
	N_E	1.431	1.946	3.587	2.484	4.593	6.987	3.975	4.809	2.387	3.759
	H_O	0.220	0.357	0.605	0.614	0.795	0.875	0.727	0.556	0.163	0.432
	H_E	0.301	0.486	0.721	0.597	0.782	0.857	0.748	0.792	0.581	0.734
	F_{IS}	0.271	0.265	0.162	-0.027	-0.017	-0.021	0.028	0.299	0.720	0.412
W4	N	29	30	30	30	30	28	30	29	27	29
	N_A	4	2	6	4	11	8	7	7	5	7
	N_E	1.285	1.471	2.894	2.016	5.590	5.873	2.970	5.224	2.651	3.564
	H_O	0.241	0.333	0.600	0.600	0.867	0.786	0.667	0.552	0.074	0.621
	H_E	0.222	0.320	0.654	0.504	0.821	0.830	0.663	0.809	0.623	0.719
	F_{IS}	-0.088	-0.042	0.083	-0.191	-0.055	0.053	-0.005	0.318	0.881	0.137
W5	N	30	30	30	30	30	30	29	23	28	29
	N_A	6	3	8	6	7	11	6	6	5	8
	N_E	1.542	1.542	3.711	3.719	4.569	5.844	3.780	4.831	2.667	4.123
	H_O	0.200	0.367	0.733	0.633	0.767	0.800	0.828	0.739	0.214	0.690
	H_E	0.352	0.352	0.731	0.731	0.781	0.829	0.735	0.793	0.625	0.757
	F_{IS}	0.431	-0.043	-0.004	0.134	0.018	0.035	-0.125	0.068	0.657	0.089

Table S5 Values of genetic differentiation (D_{est}) for 15 sample sites across the Houtman Abrolhos Islands. Significance values are above diagonal and bold values indicate significance based on a Bonferroni adjusted P-value of 0.005. D_{est} was strongly correlated with G'_{ST} (R = 0.998, P = 0.001).

	P1	P2	P3	P4	P5	E1	E2	E3	E4	E5	W1	W2	W3	W4	W5
P1		0.402	0.018	**0.001**	0.404	0.554	0.806	0.034	0.140	0.447	0.158	0.314	0.142	0.248	0.628
P2	0.003		0.033	0.010	0.005	0.420	0.759	0.631	0.752	0.628	0.852	0.236	0.404	0.374	0.289
P3	0.046	0.041		0.476	**0.001**	0.022	0.008	**0.000**	0.001	0.001	0.012	0.013	0.007	**0.000**	0.004
P4	0.091	0.053	0.000		**0.000**	0.008	**0.001**	**0.000**	**0.000**	0.001	0.009	0.001	**0.001**	**0.000**	0.003
P5	0.002	0.054	0.091	0.101		0.008	0.085	0.001	0.001	0.003	0.003	0.013	**0.000**	0.002	0.244
E1	-0.004	0.002	0.037	0.052	0.048		0.647	0.030	0.116	0.476	0.690	0.313	0.041	0.144	0.457
E2	-0.012	-0.010	0.044	0.070	0.020	-0.005		0.613	0.859	0.354	0.894	0.429	0.157	0.314	0.454
E3	0.026	-0.005	0.073	0.096	0.070	0.022	-0.003		0.717	0.120	0.588	0.070	0.156	0.022	0.017
E4	0.016	-0.010	0.064	0.086	0.064	0.014	-0.011	-0.006		0.064	0.701	0.181	0.700	0.043	0.067
E5	0.000	-0.006	0.060	0.071	0.054	-0.001	0.003	0.011	0.018		0.438	0.146	0.014	0.127	0.087
W1	0.013	-0.014	0.039	0.048	0.056	-0.006	-0.011	-0.003	-0.005	0.001		0.067	0.306	0.081	0.311
W2	0.007	0.011	0.047	0.079	0.043	0.006	0.002	0.018	0.013	0.013	0.020		0.037	0.075	0.189
W3	0.015	0.002	0.043	0.073	0.079	0.020	0.010	0.009	-0.006	0.024	0.004	0.025		0.004	0.005
W4	0.008	0.003	0.102	0.101	0.058	0.011	0.004	0.022	0.019	0.011	0.014	0.019	0.032		0.096
W5	-0.005	0.008	0.051	0.064	0.009	0.000	0.001	0.026	0.018	0.015	0.004	0.011	0.030	0.013	

Table S6 Migration Matrix of standardized probabilities of dispersal between sampling locations. Particles were considered to recruit to a sample site if they fell within a 1km buffer around each location within the recruitment eligibility window. Source of larvae are in columns and sinks are in rows. Data is from spawning across 4 years (2009-2012) and standardized across each sink sample site. Diagonal values represent self-recruitment.

SINK	SOURCE														
	P1	P2	P3	P4	P5	E1	E2	E3	E4	E5	W1	W2	W3	W4	W5
P1	**0.000**	0.021	0.634	0.180	0.009	0.031	0.037	0.004	0.008	0.000	0.010	0.010	0.027	0.014	0.015
P2	0.000	**0.066**	0.731	0.159	0.004	0.000	0.007	0.000	0.000	0.000	0.020	0.004	0.004	0.000	0.004
P3	0.000	0.697	**0.082**	0.000	0.042	0.042	0.000	0.000	0.000	0.000	0.138	0.000	0.000	0.000	0.000
P4	0.000	0.555	0.000	**0.305**	0.140	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000
P5	0.000	0.911	0.015	0.056	**0.000**	0.015	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000
E1	0.140	0.210	0.185	0.071	0.136	**0.005**	0.009	0.116	0.100	0.028	0.000	0.000	0.000	0.001	0.000
E2	0.126	0.025	0.001	0.123	0.113	0.161	**0.000**	0.000	0.024	0.007	0.130	0.111	0.084	0.063	0.031
E3	0.437	0.029	0.118	0.246	0.008	0.027	0.002	**0.012**	0.001	0.006	0.025	0.024	0.031	0.019	0.016
E4	0.002	0.016	0.102	0.116	0.001	0.084	0.001	0.141	**0.213**	0.260	0.008	0.013	0.016	0.017	0.009
E5	0.035	0.093	0.199	0.268	0.000	0.017	0.000	0.109	0.026	**0.186**	0.011	0.008	0.024	0.017	0.006
W1	0.113	0.000	0.000	0.000	0.000	0.044	0.070	0.118	0.150	0.125	**0.133**	0.086	0.138	0.017	0.006
W2	0.171	0.000	0.000	0.000	0.000	0.035	0.022	0.059	0.204	0.079	0.140	**0.067**	0.138	0.083	0.002
W3	0.002	0.000	0.000	0.000	0.000	0.179	0.065	0.015	0.012	0.047	0.337	0.207	**0.057**	0.046	0.035
W4	0.073	0.000	0.000	0.000	0.000	0.023	0.131	0.119	0.080	0.091	0.099	0.058	0.170	**0.151**	0.005
W5	0.036	0.000	0.000	0.000	0.000	0.016	0.036	0.084	0.040	0.146	0.153	0.048	0.165	0.170	**0.107**

Table S7 Results from Mantel tests between DOR and F_{ST} when jacknifing across all loci.

Loci Removed	Mantel r	P
Amil_018	0.37263	0.004
EST_63	0.36209	0.002
Amil_022	0.39531	0.003
Amil_002	0.23407	0.020
EST_181	0.38652	0.003
EST_245	0.38265	0.005
EST_016	0.38154	0.004
wgs_153	0.36847	0.003
EST_98	0.38915	0.003

Figure S1 Principle component analyses of three measures of genetic differentiation (F_{ST}, G_{ST}, D_{est})
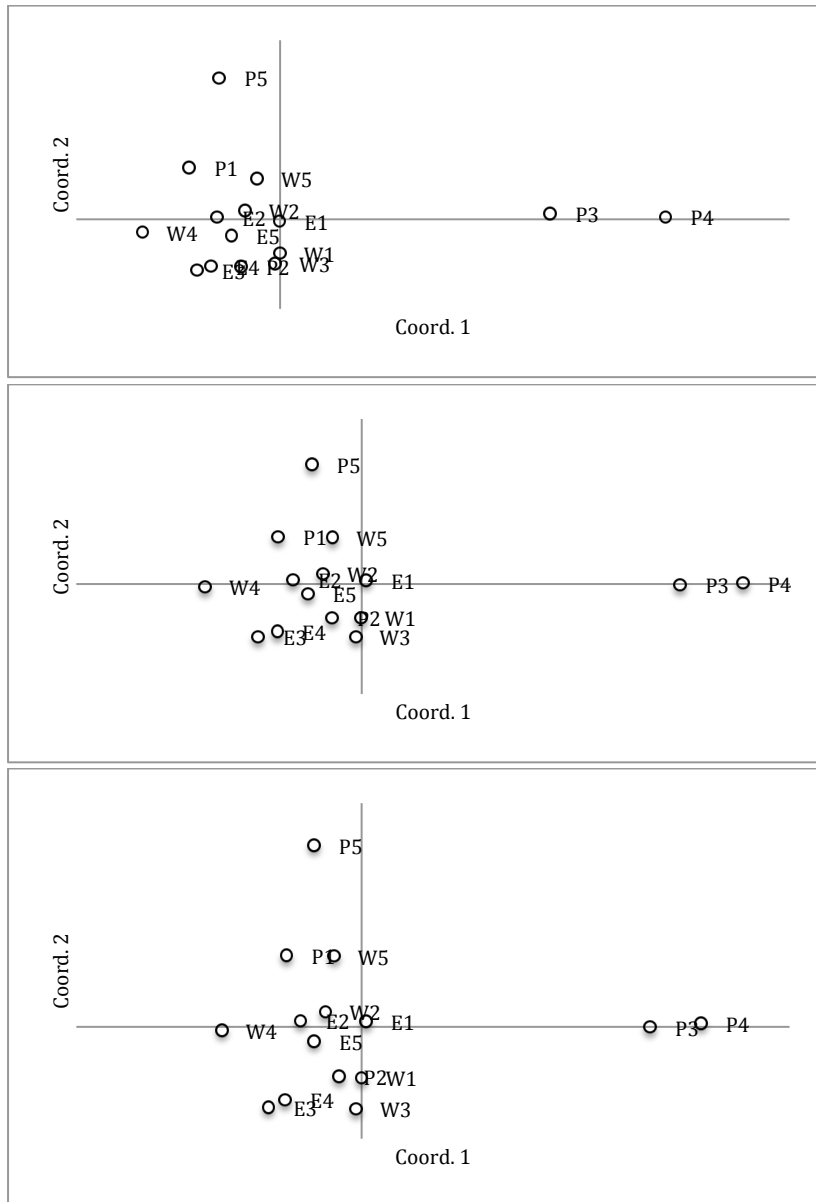
Figure S2 Results from GENELAND identifying $K = 3$ as the most likely number of clusters in the dataset. Results from 10 independent runs sorted by posterior probabilities are also provided.
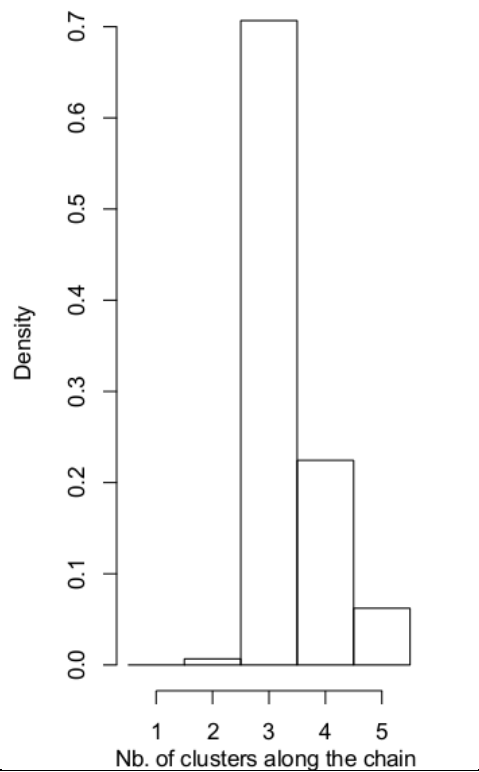
Replicate	K	Post. prob.
10	3 (73.6 %)	-8254.622905
1	4 (50.2 %)	-8554.019901
8	3 (49.5 %)	-8561.681974
6	2 (44.8 %)	-8650.811328
5	4 (56.7 %)	-8853.093507
3	3 (72.6 %)	-8964.203876
7	3 (69.7 %)	-8989.092028
4	3 (48.3 %)	-9206.017057
9	1 (41.9 %)	-9238.745992
2	3 (91.8 %)	-9996.340419

Figure S3 Scatterplot showing the relationship between genetic distance matrices based on subsampled v. entire dataset.
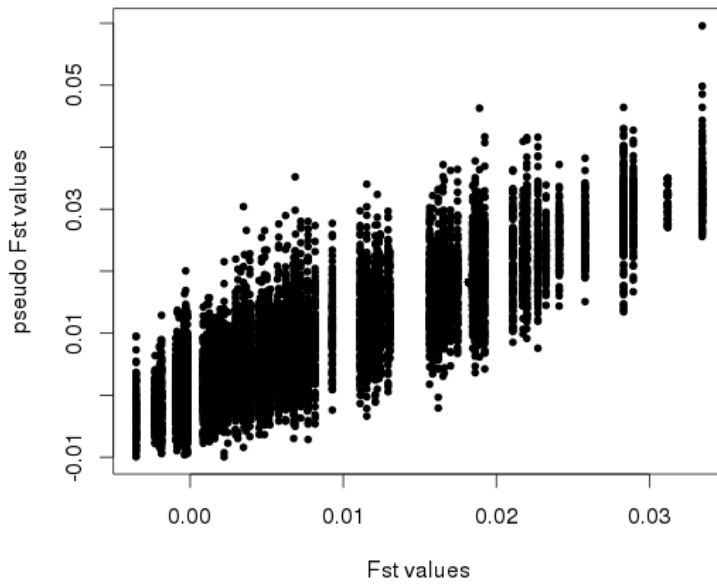
Figure S4 Matrix of similarity (Nei 1987) based on the forward projected migration matrix standardised migration matrix at t = 0 (above) and when forward projected 10 generations (below). Red indicates high levels of similarity and blue low levels of similarity. The matrix is symmetric and so non-directional.

Figure S5 Histograms showing distribution of *P* values from the Mantel tests based on the subsampled dataset. Asterisks indicate *P* values using the full dataset.

Geographic distance

Mantel p-value

Derived oceanc resistance

Mantel p-value
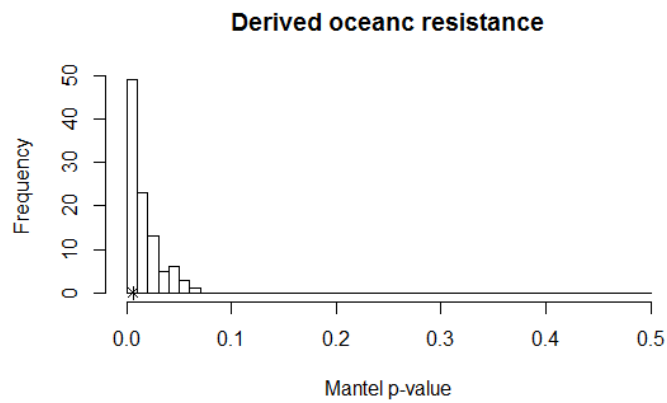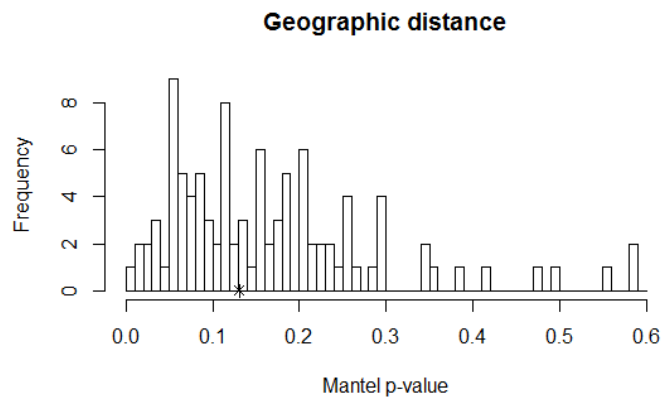
Text Sl Details of the calculations for the forward projection matrix

The migration matrix was projected forward in time to examine the probability of populations being connected over multiple generations using the formula $Q_t = \overline{AK}^t$, where $A = \overline{MB + I}$ (the top bar indicates row-normalisation) and Q_t is a state matrix representing the constitution of each adult population at each adult population at time t (rows) in terms of the relative contribution from each source population at $t = 0$ (columns), B is a diagonal matrix of per capita birth rates, K is a diagonal matrix of relative carrying capacity and I is an identity matrix with the same dimension as M, and t is the number of generations projected [62]. The forward-projected matrix was calculated using $t = 10$, and identity matrices were applied for B and K since turnover rates were assumed constant at one juvenile per individual per generation, and all populations were assumed to be equal in size. When using higher birth rates the matrix rapidly converged to the eigenvalues and so higher values were avoided. The projection model does not take into account post-settlement mortality, which would act to slow the rate of convergence; however, without any spatial biases the relative patterns would not be affected.