

Isolation by distance and low connectivity in the peppery furrow shell *Scrobicularia plana* (Bivalvia)

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Marine Ecology Progress Series 462: 111–124 (2012)

Supplement 1. Additional haplotype diversity and occurrence data

Table S2. *Scrobicularia plana*. Haplotype occurrence, nucleotide diversity (π) and haplotype diversity (h) at each sampled site with corresponding standard deviation

Code	Site	h 01	h 02	h 03	h 04	h 05	h 06	h 07	h 08	h 09	h 10	h 11	h 12	h 13	h 14	h 15	h 16	h 17	h 18	h 19	h 20	h 21	h 22	h 23	h 24	h 25	h 26	h 27	h 28	h 29	h 30	h 31	h 32	h 33	h 34	h 35	h 36	h 37	h 38		
TRO	Trondheim, Norway	16	0	0	0	0	1	0	0	0	2	0	3	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	1	0	3	0	
TJ	Tjärnö, Sweden	21	0	0	2	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
WS	German Wadden Sea	24	0	0	0	1	1	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	
BA	Balgzand, Netherlands	21	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
TER	Terneuzen, Netherlands	23	0	0	1	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	3	0	0	0	0	0	0	0	0	0		
KB	Killala Bay, Ireland	17	0	0	1	0	1	0	1	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	
CLO	Clonakilty Estuary, Ireland	24	0	0	1	0	1	0	0	1	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	
PLY	Plymouth, England	16	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
KL	King's Lynn, England	21	0	0	0	0	2	0	0	0	1	0	2	0	0	0	1	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1
RO	Roscoff, France	13	0	0	0	2	2	0	0	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
MP	Moeze Plaisance, France	13	2	0	0	1	1	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
AS	Astúrias, Spain	13	1	1	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PV	Ponte Vedra, Galicia, Spain	6	0	0	0	0	0	0	0	0	0	0	0	0	0	2	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
CA	Caminha, Portugal	17	0	0	0	0	1	2	0	1	1	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
AL	Tavira, Algarve, Portugal	9	1	0	0	0	0	0	2	0	1	0	0	0	1	0	0	1	2	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
CZ	Cádiz, Spain	7	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	1	0	0	0	0	0	0	2	0	0	0	0	0	0	0	0	0	0	0	
AG	Agadir, Morocco	13	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	
PI	Pisa, Italy	10	0	0	0	8	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	0	5	1	1	1	1	1	1	0	0	0	0	
sum		284	4	1	5	14	12	3	1	5	5	1	5	1	1	4	11	1	1	5	1	1	1	1	1	1	1	1	2	5	5	1	1	1	1	1	1	1	3	1	

Code	Site	h39	h40	h41	h42	h43	h44	h45	h46	h47	h48	h49	h50	h51	h52	h53	h54	h55	h56	h57	h58	h59	h60	h61	h62	h63	h64	h65	sum	(SD)	h (SD)
TRO	Trondheim, Norway	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	29	0.0027 (0.0019)	0.6872 (0.0905)
TJ	Tjärnö, Sweden	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	26	0.0007 (0.0008)	0.3508 (0.1172)	
WS	German Wadden Sea	0	0	0	0	0	0	0	0	0	1	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	32	0.0015 (0.0012)	0.4375 (0.1072)	
BA	Balgzand, Netherlands	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	0	0	0	27	0.0008 (0.0009)	0.3932 (0.1136)	
TER	Terneuzen, Netherlands	0	0	0	0	0	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	29	0.0009 (0.0009)	0.3695 (0.1097)	
KB	Killala Bay, Ireland	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	23	0.0010 (0.0010)	0.4625 (0.1283)	
CLO	Clonakilty Estuary, Ireland	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	29	0.0007 (0.0008)	0.3202 (0.1116)	
PLY	Plymouth, England	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	20	0.0012 (0.0011)	0.3684 (0.1351)	
KL	King's Lynn, England	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	30	0.0014 (0.0012)	0.5103 (0.1087)	
RO	Roscoff, France	0	0	0	0	1	1	1	0	1	0	0	0	0	0	0	0	0	0	0	0	0	0	0	1	1	1	25	0.0020 (0.0015)	0.7333 (0.0952)	
MP	Moeze Plaisance, France	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	19	0.0016 (0.0014)	0.5380 (0.1330)	

Table S4. *Scrobicularia plana*. Mean (range) haplotype diversity (h) in the mtDNA cytochrome-*c*-oxidase I gene for several marine bivalve species

Species	Geographic region	h	Source
<i>Anomalocardia brasiliiana</i>	NW Atlantic Ocean	0.67 (0.45–0.85)	Arruda et al. (2009)
<i>Austrovenus stutchbur</i>	SW Pacific Ocean	0.85 (0.58–0.97)	Ross et al. (2012)
<i>Brachidontes</i> spp.	Indian Ocean, Pacific Ocean and Mediterranean/Red Sea	0.98 (0.97–1.00)	Terranova et al. (2007)
<i>Brachidontes exustus</i>	Gulf of Mexico and NW Atlantic Ocean	0.88 (0.55–0.98)	Lee & Ó Foighil (2004)
<i>Cerastoderma edule</i>	NE Atlantic Ocean	0.63 (0.14–0.93)	Krakau et al. (2012)
<i>Cerastoderma glaucum</i>	NE Atlantic Ocean and Southern Europe	0.63 (0.21–0.91)	Tarnowska et al. (2010)
<i>Mercenaria mercenaria</i>	NW Atlantic Ocean	0.84 (0.86–0.95)	Baker et al. (2008)
<i>Mytilopsis sallei</i>	Indian Ocean and Pacific Ocean	0.69 (0.52–0.79)	Wong et al. (2011)
<i>Mytilus coruscus</i>	NW Pacific Ocean	0.87 (0.72–0.92)	Shen et al. (2009)
<i>Mya arenaria</i>	NW Atlantic Ocean, NE Pacific Ocean and North Sea	0.39 (0.00–0.65)	Strasser & Barber (2009)
<i>Pinna nobilis</i>	Mediterranean Sea	0.67 (0.40–0.81)	Rabaoui et al. (2011)
<i>Ruditapes decussatus</i>	Mediterranean Sea	0.49 (0.17–0.76)	Gharbi et al. (2010)
<i>Ruditapes philippinarum</i>	NW Pacific Ocean	0.96 (0.80–1.00)	Mao et al. (2011)
<i>Scrobicularia plana</i>	NE Atlantic Ocean and Southern Europe	0.52 (0.32–0.86)	This study
<i>Spisula</i> spp.	NW Atlantic Ocean	0.73 (0.42–0.86)	Hare & Weinberg (2005)
<i>Tridacna crocea</i>	Indo-West Pacific Oceans	0.91 (0.80–1.00)	DeBoer et al. (2008)
<i>Tridacna maxima</i>	Indo-Malay Archipelago and Red Sea	0.94 (0.59–1.00)	Nuryanto & Kochzius (2009)

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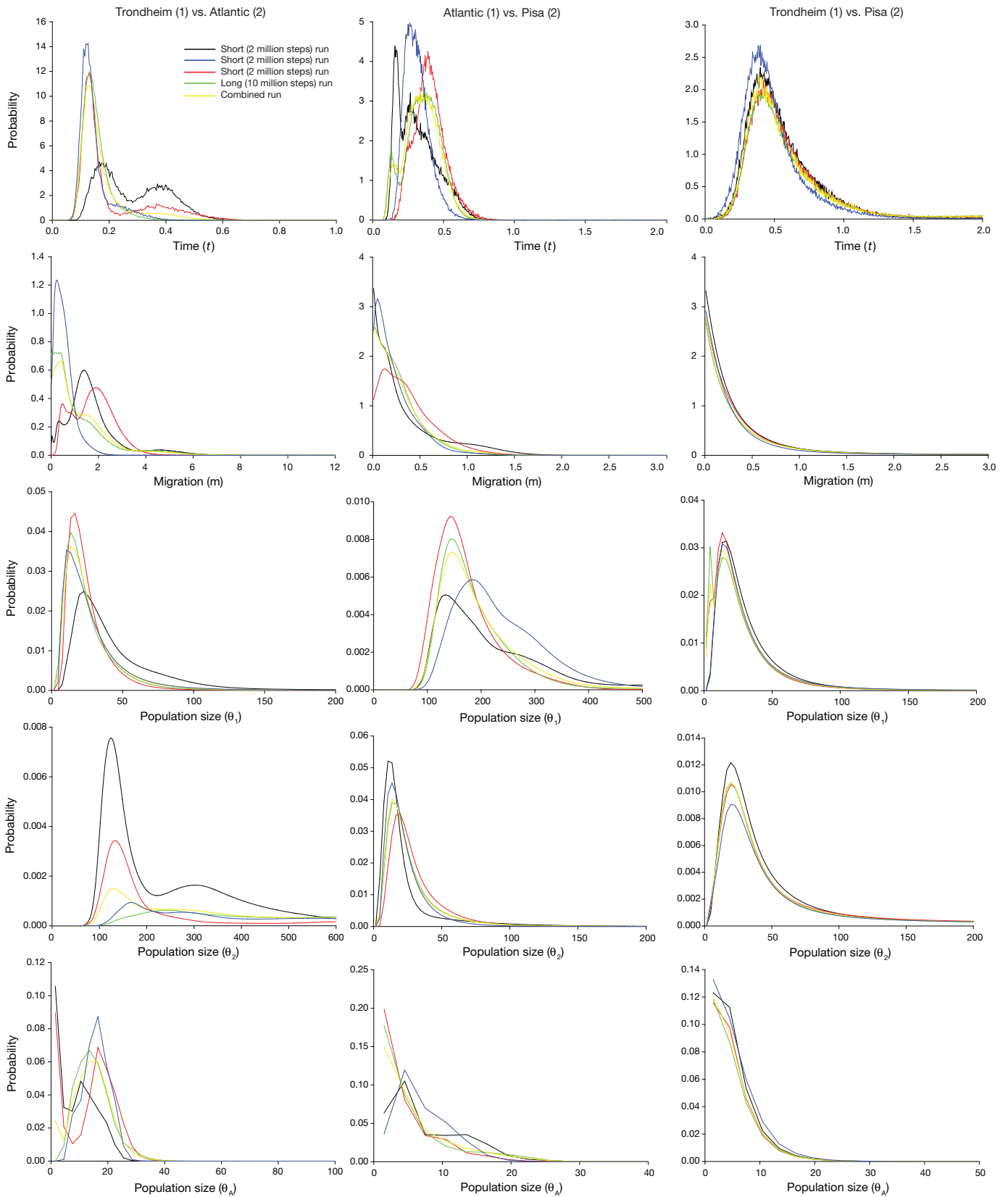


Fig. S1. *Scrobicularia plana*. Marginal posterior probability distributions for isolation with migration analytic (IMa) parameters of 3 distinct models: Trondheim vs. Atlantic, Atlantic vs. Pisa and Trondheim vs. Pisa. For each model, 4 IMa independent runs were completed: black, blue and red lines represent the three 2 million step runs, while green corresponds to one 10 million step run and yellow to the combined run. Population size parameters (θ) are shown for current populations (1 and 2) and their ancestral population (A), along with migration rate (μ , substitutions sequence⁻¹ yr⁻¹) and time since last split (t). Note that values correspond to model parameter estimates. For corresponding demographic parameter estimates see Table 4 in the main article