

Table S1: Haplotype frequencies of all *Bullia digitalis* samples in this study. Sequences have been submitted to GenBank with accession numbers OR238107 - OR238320

HAP#	EB	MB	MZ	STB	VB	MOS	MTB	KB	EK	TOTAL
HAP_1	17	16	1	0	1	0	0	0	1	36
HAP_2	1	1	0	0	0	0	0	0	0	2
HAP_3	1	1	0	0	0	0	0	0	0	2
HAP_4	1	1	0	0	0	0	0	0	0	2
HAP_5	1	0	0	0	0	0	0	0	0	1
HAP_6	1	1	0	0	0	0	0	0	0	2
HAP_7	1	0	0	0	0	0	0	0	0	1
HAP_8	1	0	0	0	0	0	0	0	0	1
HAP_9	0	0	1	0	0	0	0	0	1	2
HAP_10	0	0	0	0	0	0	1	1	2	4
HAP_11	0	0	0	0	0	0	0	0	1	1
HAP_12	0	0	0	0	0	0	0	0	1	1
HAP_13	0	0	1	0	0	2	0	0	3	6
HAP_14	0	0	0	0	0	0	0	0	1	1
HAP_15	0	0	0	0	0	0	0	0	1	1
HAP_16	0	0	1	1	1	0	2	2	4	11
HAP_17	0	0	0	0	0	0	0	1	1	2
HAP_18	0	0	0	0	0	0	0	0	1	1
HAP_19	0	0	0	0	0	0	0	0	1	1
HAP_20	0	0	3	1	2	2	2	0	1	11
HAP_21	0	0	0	0	0	0	0	0	1	1
HAP_22	0	0	0	0	0	0	0	0	1	1
HAP_23	0	0	0	0	0	0	0	0	1	1
HAP_24	0	0	3	1	1	2	0	2	2	11
HAP_25	0	0	0	0	0	0	0	0	1	1
HAP_26	0	0	0	0	0	0	0	0	1	1
HAP_27	0	0	1	0	0	1	0	0	1	3
HAP_28	0	0	0	0	0	0	0	2	0	2
HAP_29	0	0	0	0	0	0	1	1	0	2
HAP_30	0	0	2	0	2	0	0	2	0	6
HAP_31	0	0	0	0	0	0	0	1	0	1
HAP_32	0	0	0	0	0	0	0	1	0	1
HAP_33	0	0	0	0	0	0	0	1	0	1
HAP_34	0	0	0	0	0	0	0	1	0	1
HAP_35	0	0	0	1	0	0	1	1	0	3
HAP_36	0	0	0	0	0	0	1	1	0	2
HAP_37	0	0	0	0	0	0	0	1	0	1
HAP_38	0	0	0	0	0	0	0	1	0	1
HAP_39	0	0	0	0	0	0	0	1	0	1
HAP_40	0	0	1	1	0	0	1	1	0	4
HAP_41	0	0	0	0	0	0	0	1	0	1
HAP_42	0	0	0	0	0	0	0	1	0	1
HAP_43	0	0	0	0	0	0	0	1	0	1
HAP_44	0	0	0	0	0	0	0	1	0	1

HAP_45	0	1	0	0	0	0	0	0	0	1
HAP_46	0	1	0	0	0	0	0	0	0	1
HAP_47	0	1	0	0	0	0	0	0	0	1
HAP_48	0	1	0	0	0	0	0	0	0	1
HAP_49	0	0	0	0	0	2	0	0	0	2
HAP_50	0	0	0	0	0	1	0	0	0	1
HAP_51	0	0	0	1	0	1	0	0	0	2
HAP_52	0	0	0	0	0	1	0	0	0	1
HAP_53	0	0	0	0	0	1	0	0	0	1
HAP_54	0	0	0	0	0	1	0	0	0	1
HAP_55	0	0	0	0	0	1	0	0	0	1
HAP_56	0	0	0	0	1	1	1	0	0	3
HAP_57	0	0	0	0	0	1	0	0	0	1
HAP_58	0	0	0	0	0	1	0	0	0	1
HAP_59	0	0	0	0	0	1	0	0	0	1
HAP_60	0	0	0	0	0	1	0	0	0	1
HAP_61	0	0	0	0	0	1	0	0	0	1
HAP_62	0	0	0	0	0	1	0	0	0	1
HAP_63	0	0	0	0	0	1	0	0	0	1
HAP_64	0	0	0	0	0	1	1	0	0	2
HAP_65	0	0	0	0	0	1	0	0	0	1
HAP_66	0	0	0	0	0	0	1	0	0	1
HAP_67	0	0	0	0	0	0	1	0	0	1
HAP_68	0	0	0	0	0	0	1	0	0	1
HAP_69	0	0	0	0	0	0	1	0	0	1
HAP_70	0	0	0	0	0	0	1	0	0	1
HAP_71	0	0	0	0	0	0	1	0	0	1
HAP_72	0	0	0	0	1	0	1	0	0	2
HAP_73	0	0	0	0	0	0	1	0	0	1
HAP_74	0	0	0	0	0	0	1	0	0	1
HAP_75	0	0	0	0	0	0	1	0	0	1
HAP_76	0	0	0	0	0	0	1	0	0	1
HAP_77	0	0	0	0	0	0	1	0	0	1
HAP_78	0	0	1	1	0	0	1	0	0	3
HAP_79	0	0	0	0	0	0	1	0	0	1
HAP_80	0	0	0	0	0	0	1	0	0	1
HAP_81	0	0	0	0	0	0	1	0	0	1
HAP_82	0	0	0	0	0	0	1	0	0	1
HAP_83	0	0	2	0	0	0	0	0	0	2
HAP_84	0	0	1	0	0	0	0	0	0	1
HAP_85	0	0	1	0	0	0	0	0	0	1
HAP_86	0	0	1	0	0	0	0	0	0	1
HAP_87	0	0	1	0	0	0	0	0	0	1
HAP_88	0	0	2	0	0	0	0	0	0	2
HAP_89	0	0	1	0	0	0	0	0	0	1
HAP_90	0	0	1	0	0	0	0	0	0	1
HAP_91	0	0	1	0	0	0	0	0	0	1
HAP_92	0	0	0	1	0	0	0	0	0	1

HAP_93	0	0	0	1	0	0	0	0	0	1
HAP_94	0	0	0	1	0	0	0	0	0	1
HAP_95	0	0	0	1	0	0	0	0	0	1
HAP_96	0	0	0	1	0	0	0	0	0	1
HAP_97	0	0	0	1	0	0	0	0	0	1
HAP_98	0	0	0	1	0	0	0	0	0	1
HAP_99	0	0	0	0	1	0	0	0	0	1
HAP_100	0	0	0	0	1	0	0	0	0	1
HAP_101	0	0	0	0	1	0	0	0	0	1
HAP_102	0	0	0	0	1	0	0	0	0	1
HAP_103	0	0	0	0	1	0	0	0	0	1
HAP_104	0	0	0	0	1	0	0	0	0	1
HAP_105	0	0	0	0	1	0	0	0	0	1
HAP_106	0	0	0	0	1	0	0	0	0	1
HAP_107	0	0	0	0	1	0	0	0	0	1
HAP_108	0	0	0	0	1	0	0	0	0	1
HAP_109	0	0	0	0	1	0	0	0	0	1
HAP_110	0	0	0	0	1	0	0	0	0	1
N	24	24	26	14	21	25	28	25	27	214
H	8	9	19	14	19	21	26	21	20	110

Table S2. Mismatch analyses under the population and range expansion models, for individual and combined samples of *B. digitalis*, and for *B. rhodostoma* (Br) for six south coast samples (SC) combined. τ : relative time since expansion (with 5 – 95 % quartiles); Estimated number of effective immigrants ($2N_e m$) and estimated initial (θ_0) and present-day (θ_1) population size (with 5 – 95 % quartiles); *SSD*: Sum of Squared Deviation; *Hri*: H Harpending’s raggedness index; $\infty = 99\ 999$. Significance indicated as: * $p \leq 0.05$; ** $p \leq 0.01$; *** $p \leq 0.001$; **** $p \leq 0.0001$. Site labels as in Fig.4

	EB	MB	MZ	StB	VB	MOS	MtB	KB	EK	Total	Br (SC)
Population Expansion Model											
τ	0.0 (0 - 0.07)	0.0 (0 - 0.3)	1.8 (0.7 - 6.2)	4.1 (2.7 - 8.3)	5.8 (3.5 - 7.3)	3.8 (3.05 - 6.3)	3.9 (3.0 - 6.8)	4.1 (3.0 - 5.2)	2.5 (1.4 - 6.0)	2.6 (0.6 - 5.4)	0.7 (0.4 - 1.6)
θ_0	0.0 (0.0 - 0.0)	0.0 (0.0-0.003)	2.06 (0.0 - 5.7)	1.9 (0.0 - 4.9)	0.02 (0.0-1.8)	1.05 (0.0 - 1.5)	1.3 (0.0 - 2.2)	0 (0.0 - 0.6)	1.6 (0.0 - 3.9)	5.7 (0.0 - 14.2)	0.0 (0.0-0.08)
θ_1	∞ (99869 – ∞)	∞ (99869- ∞)	∞ (11.5 – ∞)	∞ (26.3 – ∞)	71.39 (27.6 – ∞)	∞ (26.2 – ∞)	∞ (28.1 – ∞)	∞ (23.1 – ∞)	718.75 (16.1 – ∞)	52.031 (15.3 – ∞)	∞ (10.6 - ∞)
<i>SSD</i>	0.30***	0.36***	0.006	0.005	0.004	0.031*	0.004	0.007	0.0007	0.011	0.14 ***
<i>Hri</i>	0.16	0.073	0.031	0.020	0.016	0.12**	0.018	0.03	0.014	0.012	0.038
Spatial (Range) Expansion Model											
τ	12.2 (0.07 - 22.6)	12.2 (0.2 - 16.7)	1.8 (0.9 - 5.0)	4.2 (2.6 - 7.5)	5.0 (3.3 - 7.1)	3.8 (2.6 - 5.9)	3.9 (2.7 - 6.2)	4.1 (2.4 - 5.0)	2.5 (1.4 - 5.0)	2.4 (0.8 - 13.1)	0.7 (0.3 - 6.3)
θ	0.6 (0.0007-1.9)	1.1 (0.0007-2.2)	2.06 (0.0007-6.0)	1.9 (0.0007-5.6)	0.7 (0.0007-2.4)	1.0 (0.0007-2.7)	1.3 (0.0007-3.5)	0.007 (0.0007-1.7)	1.7 (0.0007-5.3)	5.8 (0.003-15.3)	1.5 (0.001-4.1)
$N_e m$	0.5 (0.08 – ∞)	0.2 (0.1 – ∞)	∞ (8.4 – ∞)	∞ (63.3 – ∞)	117.8 (42.8 – ∞)	1467.9 (58.08- ∞)	∞ (69.7 – ∞)	∞ (44.2 – ∞)	2369.5 (23.5 – ∞)	43.46 (1.7 – ∞)	∞ (0.9 - ∞)
<i>SSD</i>	0.01	0.007	0.006	0.005	0.005	0.031**	0.004	0.007	0.0007	0.011	0.0054
<i>Hri</i>	0.156	0.073	0.031	0.02	0.016	0.119**	0.0180	0.03	0.0140	0.012	0.038

Table S3: Allozyme diversity statistics for *B. digitalis*, including sample size (N), average expected heterozygosity over all polymorphic loci (H_E), allelic richness based on a sample of 40 individuals (AR) and F_{IS} . Raw data are available in Grant & da Silva Tatley (1997)

Site	Abb.	coast	N	H_E	AR	F_{IS}
Luderitz	Lud	W	85	0.129	2.52	0.045
Lambert's Bay	Lam	W	87	0.130	2.52	-0.018
Yzerfontein	Yze	W	100	0.150	2.66	-0.016
Ou Skip	OuS	W	99	0.164	2.39	-0.025
Muizenberg	Mui	S	100	0.148	2.74	0.018
Mnandi	Mna	S	49	0.151	2.88	-0.064
Strand	Str	S	81	0.161	3.09	0.009
Sedgefield	Sed	S	44	0.096	2.15	0.069
Maitland	Mai	S	94	0.127	2.31	0.051

Table S4. Allozyme F_{ST} (14 polymorphic loci) between samples of *Bullia digitalis* from the west and south coasts of southern Africa. Below diagonal: F_{ST} . (bold: $P < 0.01$, italics: $P < 0.05$). Above diagonal: number of loci with a $P < 0.05$ in genic tests for each pairwise comparison.

Lud	Lam	Yze	OuS	Mui	Mna	Str	Sed	Mai	
–	4	5	7	3	4	4	2	2	Lud
0.0061	–	3	3	4	4	5	3	2	Lam
0.0278	0.0162	–	4	5	3	6	3	5	Yze
0.0206	0.0170	0.0179	–	6	4	8	5	3	OuS
0.0100	0.0030	0.0134	0.0162	–	2	3	4	3	Mui
0.0280	0.0187	0.0031	0.0245	<i>0.0070</i>	–	0	3	4	Mna
0.0231	0.0166	<i>0.0086</i>	0.0221	<i>0.0059</i>	0.0000	–	4	5	Str
0.0407	0.0329	0.0414	0.0474	0.0263	0.0263	0.0196	–	2	Sed
0.0033	0.0023	0.0165	0.0175	0.0043	0.0144	<i>0.0096</i>	0.0204	–	Mai

Table S5: Genetic differentiation at allozyme loci. Within population expected heterozygosity (H_S) and F_{ST} over all populations (F_{ST}), number of significant pairwise tests (# sign), number of possible pairwise tests given lack of polymorphism in some samples at some loci (# tests) and percentage of significant tests of all possible tests (% sign) is shown.

Locus	H_S	F_{ST}	# sign	# tests	% sign
Ark	0.05	0.044	17	33	52%
Est-1	0.53	0.012	26	36	72%
Est-3	0.01	0.027	6	8	75%
Gl-1	0.53	0.031	29	36	81%
GPI-1	0.02	0.006	4	36	11%
Idh-1	0.11	0.013	10	36	28%
Idh-2	0.02	0.009	1	33	3%
Mdh-1	0.01	0.006	0	26	0%
Mdh-2	0.01	0.013	0	15	0%
Mpi	0.07	0.016	13	36	36%
Odh	0.03	0.014	4	33	12%
Pgd	0.30	0.013	13	36	36%
Php	0.23	0.026	13	36	36%
Sdh-1	0.02	0.010	1	33	3%
Grand Total	0.14	0.022	137	433	32%

Table S6. Geographic distances between samples of *Bullia digitalis* from southern Africa used for allozyme analysis.

Lud	Lam	Yze	OuS	Mui	Mna	Str	Sed	Mai	
0									Lud
671	0								Lam
853	182	0							Yze
898	227	45	0						OuS
1004	333	151	106	0					Mui
1018	347	165	120	14	0				Mna
1041	370	188	143	37	23	0			Str
1465	794	612	567	461	447	424	0		Sed
1761	1090	908	863	757	743	720	296	0	Mai

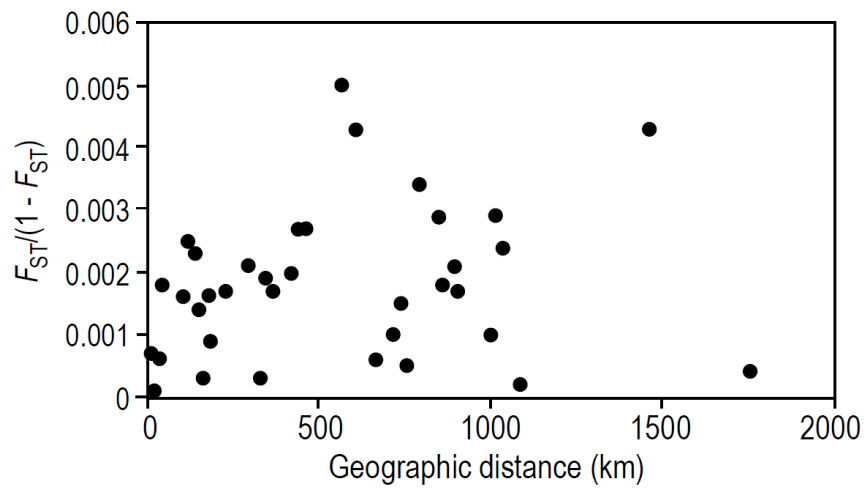


Figure S1. Isolation by distance (IBD) between populations of *Bullia digitalis* along southern African shores from Lüderitz, Namibia to Port Elizabeth, South Africa based on allozyme data. Allozyme genetic distances between populations were not significantly correlated with shoreline distance between samples ($r^2 = 0.037$, $p = 0.257$).