



Figure S1. Bayesian clustering analysis showing the most likely number of clusters using: A) Evanno's method (K=2) and B) Puechmaille's method (K=1) in *Pinna nobilis* populations analysed with 19 microsatellite markers.

Table S1. Characterization of the 23 microsatellite loci used for this study. T_A primer annealing temperature, Null allele freq.: Null allele frequencies per locus. F_{IS}: inbreeding coefficient. N: number of individuals with reliable amplification, Na number of alleles. *p-value < 0.05, **p-value < 0.01, ***p-value < 0.001. Bold: high null allele freq. ^a González-Wangüemert *et al.*, 2014.

Multiplex	Locus	Primer sequences	Repeat type	T _A (°C)	Size range (bp)	Null allele freq.	F _{IS}	N	Na
1	15415	F: ACC ACT ACT CAT GCC TCA CC R: AAC GAA GGT CGG CTA TAA CG	(AC) ₁₆	53°C	237–261	0.02	0.042**	628	21
	11847	F: ACA CTC CAG TAC AAG TCA CAA ATG R: AGA ATG CCT GAG TGG GAC AG	(TGT) ₁₈	53°C	72–153	0.00	0.003***	767	34
	3.2^a	F: CCG AGG TCC CGT ATC ACA G R: TGC CCT TTG TGT CAT TAT TTCG	(ACC) ₁₂	53°C	194–248	0.02	0.036*	766	17
	10059	F: TTC TCC TCC GAA CCC TTC R: ATA AAT ACC CTT GCC GAC CT	(CA) ₁₃	53°C	101–131	0.15	0.298***	749	25
	6980	F: AGT CTG CAT AAC TTC CAC TGC R: GGC CAC CAG TAA GCT CTT TG	(ACC) ₁₀	53°C	190–245	0.03	0.063*	757	12
	1490	F: CTT CTG ATT GAC CGT AAG TG R: AAA CTC AGA CAA CGA GAC AA	(AAC) ₁₁	53°C	179–212	0.00	0.008	763	15
2	12107	F: TGC ATC TGC ATC GTG AGG R: TGG TGG TCA AGT GGG ATG AC	(CAT) ₈	55°C	110–119	-0.01	-0.008	771	7
	15584	F: TGA GGT GGA CGT CGC TTA AC R: GTC GAA GTC TCG TGC GAA AG	(TGT) ₁₃	55°C	221–272	-0.01	-0.012	761	20
	9902	F: TCT AAG GTG CTT GAT GTG GA R: TTA GAC GGA AAC CAT GTG TG	(GTCT) ₁₂	55°C	215–243	0.01	0.022	732	14
	4482	F: TAT CCA GCA AGA GCA CCA GC R: TGA CTT GGG TAC TGG GTT CG	(CAA) ₉	55°C	186–204	0.03	0.046	771	10

3	15096	F: AGT GCG TTG TTT CAA TTT CA R: TAG GCA AAT TTT CTC GCT CT	(GT) ₁₂	57°C	166–192	0.00	0.003*	763	17.52
	8995	F: AGT GGA AGA GAA GCC ATA CG R: TAC TTG ACG GAA ACC ATG TG	(GTCT) ₁₄	57°C	226–290	0.02	0.042*	717	18
4	5017	F: ACC GAA GTC GAG ATG GTT GG R: CTT CAC TGG CAC ACG ATG C	(GTT) ₁₀	60°C	207–231	0.05	0.107***	741	16
	4664	F: ACA TGC ATA CAT ACA AAC AAG TGC R: CCT TTC TGC CCG ACC TCT C	(ACAT) ₉	60°C	134–171	0.04	0.077***	632	17
	5.2^a	F: TTG CAT GTG CCA CCA TAA TC R: TTC ATA CCG ATG AGC CAA ATG	(ATAGT) ₁₁	60°C	182–217	0.00	0.023**	761	9
	13402	F: TCG TCA TCG TCA TCA TCG R: CTA ATG ATG CCC ATG GTT CT	(CAT)	60°C	163–214	0.11	0.227***	766	33
	6477	F: AAT CTC TTC CAG CAT CCA AG R: AGC GGT ACA CTC ACA CGT AA	(CAA) ₁₈	60°C	124–163	0.11	0.243***	763	18
	4.3^a	F: TGG ATC TAG ACT CTT TGT TTG TCT TC R: ACA GTG CCA TGC TAT GTT GC	(ATTT) ₁₇	60°C	238–322	0.05	0.107***	745	30
5	14763	F: AGC ATC TGG TAA CAC GAC GG R: TGG CGG CTC TAG AAA GAT TG	(TTG) ₁₄	63°C	146–185	0.01	0.031***	761	20
	3.5^a	F: CCT AGC CTA CAT TCC ATA TGTGC R: TCA TGT CTA TGT CAA ATG AAC TCG	(AAT) ₁₃	63°C	149–182	-0.01	0.008***	706	14
	9918R2	F: GTC TTT CTG TGC CGA TGT CTG R: GGA CGG GCC GAC CTA TCT	(ATCT) ₇	63°C	226–254	0.02	0.034***	761	12
	2287F1R1	F: AGG TCG AAT AGC AAT AAC AACAA R: GGC GTG GAG GTA AGA GTC AA	(ACA) ₁₂	63°C	89–122	0.00	-0.007	766	16
	9865	F: TCA GGG TTA GGG TTC CTC CT R: TTT GAC ACA GCG TGA CGT TT	(GTT) ₇	63°C	202–208	0.16	0.352***	757	8

Table S2. List of full siblings found in the study. N° Family: refers to the family cluster to which these individuals belong based on COLONY analyses; Individual: code of each full-sib individual; locality, depth: locality and depth where the individuals were sampled; width (cm): maximum shell width. The name of the locality is coded as in table 1.

N° family	Individual	Locality	Depth (m)	Width (cm)
5	STM_184	STM	7.8	18.6
	STM_448	STM	15	17.8
7	PORT_675	PORT	8	23.6
	STM_92	STM	6.3	23.4
17	RAT_419	RAT	21.6	19.9
	STM_850	STM	7.5	21.7
40	OLLA_497	OLLA	10.2	15.5
	STM_271	STM	18.1	20.1
72	PORT_553	PORT	7.8	22.5
	STM_609	STM	13.5	19.8
89	STM_530	STM	16.4	23
	STM_587	STM	13	21.4
10	OLLA_328	OLLA	10	21.5
	OLLA_500	OLLA	10	19.4