

Supplementary Information for

Invasion genomics uncover contrasting scenarios of genetic diversity in a widespread marine invader

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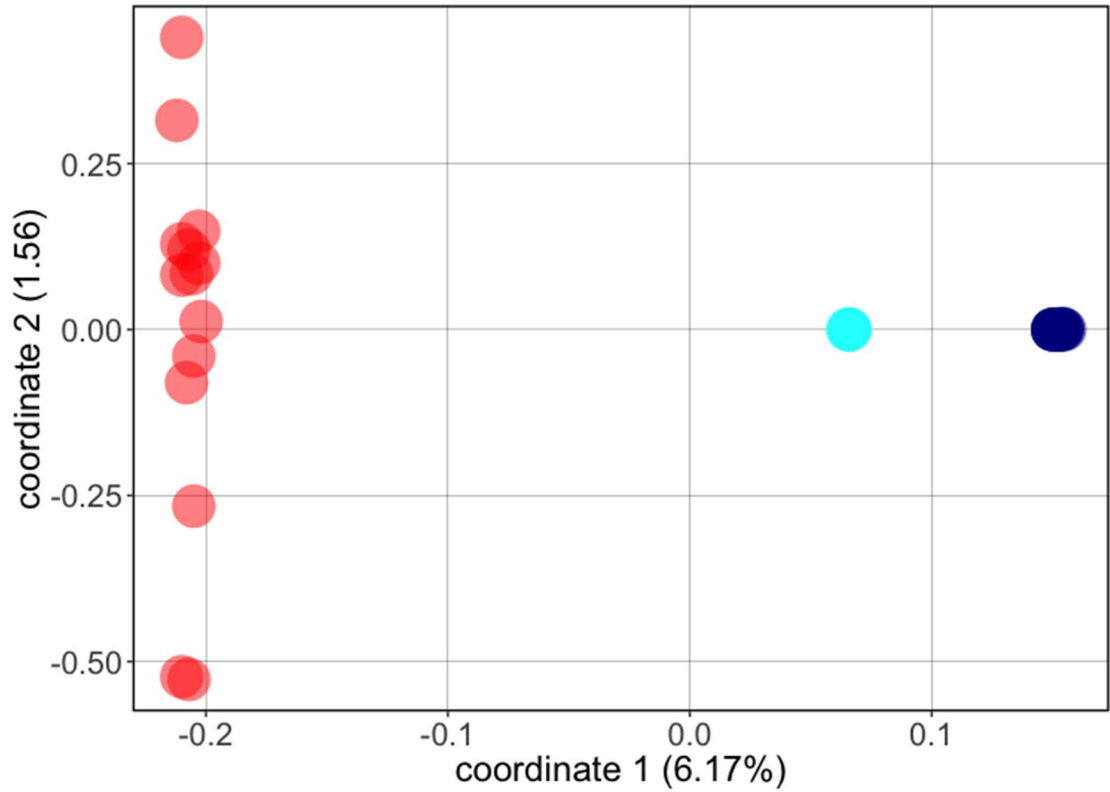


Fig. S1. PCA Plot for all native populations in our study including the northern (Woods Hole, blue) and the southern (Florida, red) populations together with the population from Chesapeake Bay (light blue) obtained from Verwimp et al. (2019). Note: kinship analyses confirm close relationship of all animals included in the Verwimp et al. (2019) analyses.

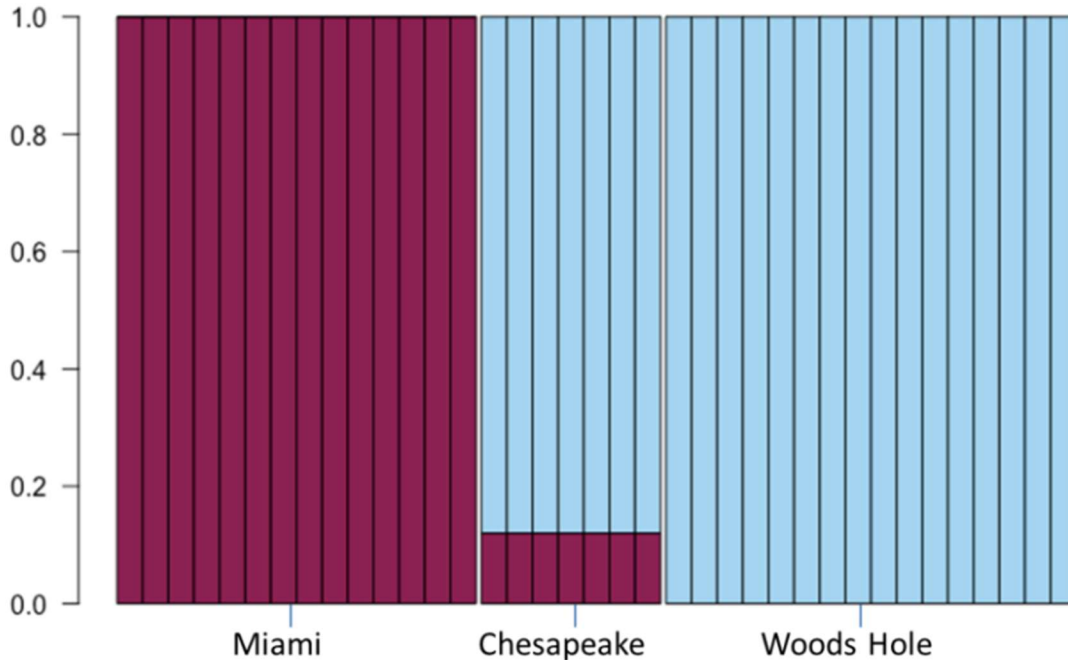


Fig. S2. Admixture analysis using Structure for all native populations in our study including the northern (Woods Hole) and the southern population (Florida) together with the population from Chesapeake Bay obtained from Verwimp et al. (2019). Individuals were assigned on the basis of the most likely K, in this case ($K = 2$). Admixture proportions are shown for all individuals, each individual represented by a vertical bar. Note: kinship analyses confirm close relationship of all animals included in the Verwimp et al. (2019) analyses. Recently, Verwimp et al. (2019) claimed a reduction of genetic diversity when comparing the native North American population (Chesapeake Bay) and the North Sea using a genotyping-by-sequencing approach. Re-analysis of Chesapeake Bay individuals from Verwimp et al. (2019) together with our individuals from Miami and Woods Hole using admixture analysis in Structure showed all Chesapeake Bay individuals to be introgressed, while no admixture was detected in Florida or Woods Hole. Hence, the Chesapeake Bay individuals included in Verwimp et al. (2019) are not the source population of the North Sea invasion and represent introgressed individuals with the southern native population, which would explain their higher genetic diversity.

Table S1. Sampling details including sampling location, number of individuals, geographical coordinates and first record of *M. leidy* in each location.

Location	Region	N	Year	Latitude	Longitude	First Record
Miami	Florida	15	2016	25°36'53"N	80°18'19"W	Native location
Woods Hole	New England	16	2016	41°31'21"N	70°40'28"W	Native location
Varna	Western Black Sea	16	2016	43°11'02"N	27°54'01"E	1986
Villefranche-sur-mer	Western Mediterranean	9	2016	43°41'18"N	7°18'53"E	2009
Sylt	North Sea	16	2016	55°01'01"N	8°26'25"E	2006

Table S2. Nucleotide diversity (π) calculated for each location, (a) using 1,632,777 SNPs after filtering for linkage disequilibrium and a 80% call rate and (b) using 77,103 SNPs after re-sizing to 9 individuals for each population. SE = Standard error.

Status	Location	a) full SNP set		b) re-sized SNP set	
		π	SE	π	SE
Native	Miami	0.13	0.006	0.12	0.006
	Woods Hole	0.06	0.004	0.06	0.005
Invasive	Varna	0.13	0.005	0.11	0.006
	Villefranche	0.10	0.006	0.09	0.006
	Sylt	0.08	0.006	0.06	0.005

Table S3. Coalescence approach using two different models to assess the invasion routes and stepping-stone range expansion of *Mnemiopsis leidyi* in western Eurasia. Fastsimcoal2 (I) separated into the southern and northern invasion events (a) and splitting the southern invasion into two scenarios with (b) a stepping stone range expansion from the Black Sea (Varna) to the western Mediterranean Sea (Villefranche) and (c) a direct secondary introduction from the native range (Miami, USA). Scenarios b and c are compared with the DIYABC model (II). Inferred parameter values included estimates of current effective population size (N_e) and their confidence intervals (CI). In Fastsimcoal2 mutation rate was allowed to vary (1×10^{-7} - 1×10^{-9}), the best model, was chosen using Akaike information criterion (AIC). Log likelihood ratio (logL), number of parameters estimated (N_p) and delta AIC, relative to the best model (dAIC). PSMC plot is based on the average mutation rate of northern and southern invasions (Ia) of 6.85×10^{-8} .

I) Fastsimcoal2							
a) Southern invasion	N_e	CI		Northern invasion	N_e	CI	
Miami	11,271	9,323	12,043	Sylt	4,283	3,713	4,498
Varna	11,606	10,093	13,405	Woods Hole	212,661	160,224	227,777
Villefranche	844	773	943				
Mutation rate	7.6×10^{-8}	7.3×10^{-8}	7.6×10^{-8}	Mutation rate	6.1×10^{-8}	5.7×10^{-8}	6.5×10^{-8}
b) Varna - Villefranche				c) Miami - Villefranche			
Miami	11,271	9,323	12,043	N Miami	20,450	15,560	28,276
Varna	11,606	10,093	13,405	N Varna	11,264	9,019	11,776
Villefranche	844	773	943	N Villefranche	758	713	852
Model comparison:	logL	N_p	AIC/dAIC		logL	N_p	AIC/dAIC
Varna - Villefranche	-584,310	4	1,168,128 / 0	Miami - Villefranche	-586,846	4	1,173,700 / 5,072
II) DIYABC		Best Model: Varna - Villefranche			N_e	CI	
				Miami	2850	816	8,300
				Varna	1880	561	5,920
				Villefranche	397	161	905

SI References

C. Verwimp, L. Vansteenbrugge, S. Derycke, T. Kerkhove, H. Muylle, O. Honnay, T. Ruttink, I. Roldán-Ruiz, K. Hostens, Population genomic structure of the gelatinous zooplankton species *Mnemiopsis leidyi* in its nonindigenous range in the North Sea. *Ecol. Evol.* **10**, 11-25 (2019).