

Population genetics of the invasive ctenophore *Mnemiopsis leidyi* in Europe reveal source-sink dynamics and secondary dispersal to the Mediterranean Sea

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Marine Ecology Progress Series 485: 25–36 (2013)

Supplement. This document contains additional information concerning the significance of population differentiation in terms of diversity and divergence: Table S1 gives pairwise F_{ST} and associated significance values for comparison between all sites of the population genetic overview; Tables S2 & S3 show the significance of observed differences in genetic diversity, in the northern time series and the southern invasion, respectively. As such they refer to the diversity levels depicted in Figs. 2b & 5b of the main manuscript; Table S4 documents our attempts to formalize the results within the framework of coalescence theory using the program MIGRATE-N (Beerli 2006) and shows the non-convergence of model probabilities irrespective of parameters and settings

Table S1. *Mnemiopsis leidyi*. Pairwise genetic differences between populations (above diagonal) and associated p-values (lower diagonal). Significant F_{ST} values are indicated with an *. Calculated according to Weir & Cockerham (1984), implemented in the software Genetix (Belkhir 1996), analysis based on 6 microsatellite loci

	GM-PA	GM-GB	GM-PC	NWA-WH	NO-HE09	KA-KRS	BA-KB08	BA-KB09	BA-FEM	BA-BB09	BS-B	BS-U	BS-T	CAS-I	MS-ISD	MS-BS	MS-MS
GM-PA		0.000	0.000	0.242*	0.321*	0.282*	0.253*	0.253*	0.226*	0.230*	0.051*	0.067*	0.044*	0.068*	0.180*	0.088*	0.105*
GM-GB	0.617		0.009	0.268*	0.349*	0.309*	0.281*	0.284*	0.253*	0.257*	0.053*	0.068*	0.032*	0.075*	0.178*	0.076*	0.096*
GM-PC	0.627	0.091		0.230*	0.305*	0.270*	0.242*	0.241*	0.216*	0.218*	0.046*	0.062*	0.042*	0.080*	0.140*	0.075*	0.089*
NWA-WH	0.000	0.000	0.000		0.030*	0.015*	0.006	0.000	0.002	0.003	0.257*	0.269*	0.295*	0.305*	0.304*	0.294*	0.270*
NO-HE09	0.000	0.000	0.000	0.000		0.003	0.027*	0.021*	0.031*	0.029*	0.348*	0.346*	0.378*	0.383*	0.395*	0.373*	0.359*
KA-KRS	0.000	0.000	0.000	0.002	0.198		0.016*	0.006	0.015*	0.016*	0.303*	0.310*	0.339*	0.345*	0.351*	0.341*	0.313*
BA-KB08	0.000	0.000	0.000	0.036	0.000	0.004		0.000	0.001	0.006	0.271*	0.281*	0.309*	0.315*	0.320*	0.308*	0.283*
BA-KB09	0.000	0.000	0.000	0.428	0.002	0.163	0.915		0.000	0.000	0.275*	0.288*	0.317*	0.330*	0.331*	0.317*	0.290*
BA-FEM	0.000	0.000	0.000	0.224	0.000	0.002	0.283	0.784		0.000	0.246*	0.256*	0.282*	0.291*	0.292*	0.280*	0.257*
BA-BB09	0.000	0.000	0.000	0.150	0.000	0.001	0.034	0.516	0.916		0.247*	0.257*	0.283*	0.294*	0.294*	0.281*	0.259*
BS-B	0.002	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		0.043*	0.008	0.070*	0.130*	0.070*	0.042*
BS-U	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001		0.056*	0.094*	0.164*	0.118*	0.106*
BS-T	0.001	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.192	0.000		0.086*	0.165*	0.051*	0.059*
CAS-I	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.001	0.000	0.000		0.258*	0.167*	0.168*
MS-ISD	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		0.164*	0.111*
MS-BS	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000		0.044*
MS-MS	0.001	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.007	0.000	0.000	0.000	0.000	0.000	

Table S2. *Mnemiopsis leidyi*. Pairwise comparison of the mean number of alleles for all 7 loci (calculated after rarefaction) using paired *t*-tests after repeated-measures ANOVA. Sites in North Sea (NO-HE), Western Baltic (BA-KB) and South Central Baltic (BA-BB) were compared for all samples from 2008, 2009 and 2010

	BA-BB08-10	BA-KB08-10
BA-KB08-10	0.084	–
NO-HE08-10	4.6e ⁻⁰⁵	4.6e ⁻⁰⁵

Table S3. *Mnemiopsis leidyi*. Pairwise comparison for mean number of alleles (calculated after rarefaction), *t*-test (with pooled SD) between populations after 1-way ANOVA. Populations from the native Gulf of Mexico (GM-GB, GM-PA, GM-PC), the primary invaded Black Sea (BS-U, BS-T, BS-B) and putative secondary invasions in Caspian and Mediterranean Sea (CAS-I, MS-BS, MS-MS, MS-ISD) were compared

	Gulf of Mexico	Black Sea
Black Sea	0.0137	–
Caspian & Mediterranean	0.0012	0.0564

Table S4. MIGRATE-N outputs for several runs of *Mnemiopsis leidyi* analysis. MIGRATE-N parameters and settings: if not stated differently parameters were left as default, and for all calculations the Brownian motion model was used. Static heating schema with 4 chains with temperatures: 1, 1.5, 3.0 and 1 000 000. For the parameters Theta and M, uniform prior distributions were set 1–100 with a delta of 1. Markov Chain settings: we used one long chain recorded over 10 000–50 000 steps after a burn-in of 10 000–50 000 discarded trees and 2 replicates. In later runs we increased burn-ins to 1 000 000 and replicates to 20. Please note that convergence was not only judged upon the model probability, but also on posterior distributions of parameters Theta and M not depicted here. Convergence could not be achieved irrespective of model parameters or run settings

Model	Run settings			Model parameters and probability	
	Burning	Sampling	Replicates	Run	Log-probability (Bezier)
(i)	10 000	10 000	2	1	-1 110 969
				2	-1 242 942
(ii)	10 000	10 000	2	1	-1 606 640
				2	-1 437 567
	50 000	50 000	2	1	-2 402 068
				2	-1 574 676
(iii)	10 000	10 000	2	1	-1 374 987
				2	-1 741 783
	1 000 000	10 000	20	1	-2 070 142
				2	-2 329 555

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