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

Repeated invasions of European waters by the ctenophore Mnemiopsis leidyi offer a unique opportunity to study population dynamics and dispersal in gelatinous zooplankton. Here we followed population establishment in two recently invaded areas, the North and Baltic Sea, and analysed changes in population structure during a 3-yr interval using 7 highly polymorphic microsatellites (representing 191 alleles). A second goal was to reconstruct routes of recent invasive range expansion into the Mediterranean Sea. During the study period (2008-2010) populations in North Sea and Western Baltic Sea maintained their allelic composition with virtually unchanged levels of genetic diversity and between-population differentiation. This demonstrates that gene flow between the two regions was limited and indicates successful reproduction in both areas. In contrast, at the eastern distribution limit in the central Baltic (Bornholm Basin) the same measures fluctuated between years and genetic diversity decreased from 2008-2010. In concordance with prior ecological observations, this supports the view that here M. leidyi formed a sink population. In the area of recent range expansion (Mediterranean Sea) we observed high population differentiation for a holoplanktonic species. Among Mediterranean samples collected at sites in Spain, France and Israel pairwise differentiation was between $F_{st} = 0.04-0.16$. Despite such differentiation, Bayesian clustering and phylogeographic analysis support the hypothesis that all Mediterranean M. leidyi result from a secondary introduction originating in the Black Sea. Our study contributes to growing evidence that multiple invasions of the same species can vary in their degree of genetic diversity and demonstrates how genetic markers can help to resolve whether gelatinous plankton species form self-sustaining populations.

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