## ANALYSIS OF MITOCHONDRIAL DNA VARIATION VIA PCR-SSCP REVEALS MICRO- AND MACROGEOGRAPHIC GENETIC HETEROGENEITY IN THE PLANKTONIC DEVELOPING PERIWINKLE, MELARAPHE NERITOIDES (CAENOGASTROPODA, LITTORINIDAE)

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The distribution of the marine gastropod, Melarhaphe neritoides, covers a relatively wide geographic area, ranging from the Mediterranean, the eastern Atlantic coast (until the Azores) to Norway. An important factor enabling migration over long distances, is the lona-lived planktotrophic larval stage that characterizes the life-cycle of this marine snail. A good dispersal ability is often related with high levels of gene flow which is expected to have a homogenizing effect on population genetic variation. This was confirmed in previous studies based on allozyme and DNA sequence data which revealed very low levels of variation and a lack of significant differentiation between populations of M. neritoides on a wide geographic scale. For the current study, we used PCR-SSCP analyses to obtain haplotype frequency data for a short mtDNA fragment (cytochrome oxidase 1) from 40-50 individuals in seven populations across the species range. In contrast to the previous studies, haplotype diversity was found to be extremely high with significant frequency differences between several of the studied populations. By counteracting the gene flow that potentially could be displayed between populations, other factors must thus have contributed to the currently observed population genetic structure of M. neritoides. These may be abiotic factors such as e.g. (historical) barriers, ocean currents and climatic changes, but also biotic factors such as e.g. the ability of the species to adapt to local environmental conditions for the settlement of viable populations.