

## **MACROGEOGRAPHIC mtDNA DIFFERENTIATION IN THE MACARONESIAN PERIWINKLE, *LITTORINA STRIATA* (MOLLUSCA: CAENOASTROPODA)**

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The periwinkle *Littorina striata* (King and Broderip, 1832) is endemic in Macaronesia (*i.e.* Azores, Madeira, Canary Islands and Cape Verde Islands), where it is the dominant grazer on the intertidal rocky shores. The species is characterized by a conspicuous shell sculpture, form and size polymorphism, which shows a significant degree of ecological and geographical patterning. This shell morphology patterning seems to persist despite the species' planktonic larval development (*i.e.* dispersal capacity) and high level of macrogeographical gene flow. This latter was hitherto inferred from allozyme and RAPD data, revealing tendencies for macrogeographic patterns in allelic diversity, private alleles, heterozygosity and esterase banding profiles. Similar results were obtained via preliminary DNA-sequence analyses of two mitochondrial genes: cytochrome b and cytochrome oxidase subunit I. In the present contribution we increased the data for the mtDNA markers to test this tentative, but statistically non-significant, macrogeographic molecular differentiation. To this end, partial sequences of the mitochondrial cytochrome b and cytochrome oxidase subunit I genes were determined for individuals from all Macaronesian archipelagos. We combined the data of these two genes, determined the different haplotypes and their frequencies. Based on these results we computed a minimum spanning network and performed a nested clade analysis. This analysis confirms the previous data, indicating a limited macrogeographic patterning and supports the previously formulated colonisation hypothesis in which the Cape Verde Islands are believed to represent the center from which *L. striata* has colonised the remaining Macaronesian archipelagos. The tendency of differentiation between populations was further studied using AMOVA. This statistical test indicated that there is a significant macrogeographic differentiation between the three northern archipelagos (Azores, Madeira and Canary Islands) and the southern archipelago (Cape Verde Islands). Likewise, gene flow (*i.e.* Nm) estimates, indicated high gene flow between the three northern archipelagos, but limited flow between the northern and the southern archipelagos. These results are interpreted in function of the (historical) course of oceanic currents and the geological history of the Macaronesian archipelagos.