

Molecular insight into the population structure of common and spotted dolphins inhabiting the pelagic waters of the Northeast Atlantic

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Abstract Several cetacean species exhibit fine-scale population structure despite their high dispersal capacities and the apparent continuity of the marine environment. In dolphins, most studies have focused on coastal areas and continental margins, and they revealed differentiated populations within relatively small geographic areas, sometimes in conjunction with a specialisation for different habitats (ecotypes). We analysed the population genetic structure of short-beaked common dolphins (*Delphinus delphis*) and Atlantic spotted dolphins (*Stenella frontalis*) in the Azores and Madeira, the two most isolated archipelagos of the North Atlantic. The archipelago of the Azores is divided

into three groups of islands and stands 900 km away from Madeira. It is not known whether individuals migrate between groups of islands and archipelagos, nor whether distinct ecotypes are present. These questions were investigated by genetic analyses of 343 biopsy samples collected on free-ranging dolphins. The analyses consisted in sequencing part of the mitochondrial hyper-variable region, screening up to 14 microsatellite loci, and molecular sexing. Results did not unravel any population structure at the scale of the study area. Lack of differentiation matches expectations for spotted dolphins, which are transient in both archipelagos, but not for common dolphins, which are present year-round in the Azores and potentially resident. Absence of genetic structure over hundreds and even thousands of kilometres implies the existence of gene flow over much larger distances than usually documented in small delphinids, which could be achieved through individual movements. This finding indicates that population structure in oceanic habitat differs from that observed in coastal habitat.

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