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## CAN DNA METHYLATION CONTRIBUTE TO EXPLAIN MORPHOLOGICAL VARIABILITY? THE CASE OF LOGGERHEAD TURTLE *CARETTA CARETTA*

The loggerhead turtle *Caretta caretta* is a common and threatened sea turtle in the Mediterranean Sea. It is listed in the Red List of Threatened Species of the International Union for Conservation of Nature (IUCN 2012) and, although it is widely studied, little is currently known about the relationships between its phenotype and genetic variability. In the last few years some authors observed the presence of individuals, collected in different parts of the Mediterranean Sea, with a variable number of carapacial and plastron scutes. In some cases, this variability makes the sound identification of the species difficult (e.g. MARGARITOU LIS and CHIRAS, 2011; TURKOZAN *et al.*, 2001; OLIVER, 2014). To date, no one tried to correlate these morphological anomalies with the genetic diversity of the species, even if several studies indicate that, beyond genetic variation, natural phenotypic variations can be generated through a suite of epigenetic mechanisms. Here we present some results about the possible correlation among the variability of the number of carapacial and plastron scutes and cytosine DNA methylation. Twelve specimens of *Caretta caretta*, collected from different parts of Sicily, were analysed. Morphological characters were used for the identification of the collected specimens according to the guidelines of MARQUEZ (1990). Four out of the twelve individuals showed an unexpected number of carapacial and plastron scutes making difficult the immediate and sound identification of the specimens as *C. caretta*. Afterwards, all the individuals were subjected to genetic analysis by the sequencing of a 243 bp fragment derived from the mitochondrial cytochrome b gene. Sequences analysis confirmed that all the individuals belong to the species *Caretta caretta*. Genomic DNA methylation level of cytosines was evaluated by dot blot analysis using antibodies against methylated cytosines. This analysis showed a reduced global level of methylated cytosines in the four "abnormal" individuals in respect to the other ones. We hypothesize that the variability of the number of scutes could be ascribed as an epigenetic effect probably due to the environmental parameters experienced by the embryos during incubation. This finding could have implications in our understanding of the pathways of morphological evolution and diversification in the chelonians.