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ORIGINAL ARTICLE

Connectivity and stock composition of loggerhead turtles foraging on the North African continental shelf (Central Mediterranean): implications for conservation and management

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Abstract

The loggerhead turtle, *Caretta caretta*, is a highly migratory species with a complex life cycle that involves a series of ontogenetic habitat shifts and migrations. Understanding the links amongst nesting populations and foraging habitats is essential for the effective management of the species. Here we used mixed stock analysis to examine the natal origin of loggerhead turtles foraging on the North African continental shelf off Tunisia, one of the most important Mediterranean neritic habitats. An 815-bp fragment of the mitochondrial DNA control region was sequenced from 107 individuals sampled from 2007 to 2009. No temporal variation in haplotype frequencies was detected. Juveniles (n = 87) and adults (n = 23) exhibited weak but significant genetic differentiation that resulted in different stock compositions. Libya was the main source population but the proportion of turtles from this rookery was higher in adults (median = 80%) than in juveniles (median = 35%). Western Greece was the second most important contributing population. Juvenile stock composition derived from mixed stock analysis and the estimates produced by numerical simulation of hatchling dispersion in the Mediterranean Sea were significantly correlated, supporting the recent theory that loggerheads imprint on possible future neritic habitats during the initial phase of their life. This association was not significant for adults, suggesting that other factors contribute to shaping their distribution. Overall, our results show that human activities on the South Tunisian continental shelf pose an immediate threat to the survival of the Libyan rookery.

Introduction

Protecting highly migratory species presents a unique conservation challenge because populations are typically comprised of a complex system of inter-connected subpopulations that use widely separated and ecologically disparate habitats (Webster *et al.* 2002; Martin *et al.* 2007; Taylor & Norris 2010). Stress occurring at one location may detrimentally affect population levels in many distant areas (Watson *et al.* 2011). Recognizing the natal origin of individuals present in non-breeding habitats and understanding the factors that shape population connectivity, *i.e.* the geographical linking of individuals or populations between stages of an animal's life cycle, is crucial for our ability to manage these species effectively (Martin *et al.* 2007; Maffucci *et al.* 2006; Bjorndal & Bolten 2008; Taylor & Norris 2010). Despite its importance, connectivity in marine systems is still not completely