

PRELIMINARY GLOBAL PHYLOGEOGRAPHY OF THE ENDANGERED DUSKY GROUPER, *EPINEPHELUS MARGINATUS*, AS REVEALED BY MITOCHONDRIAL DNA

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Abstract

The purpose of this study is to describe global phylogeography of *Epinephelus marginatus* using a mitochondrial DNA marker. *E. marginatus* is an economically important amphi-Atlantic marine fish found throughout the Mediterranean Sea that is facing extinction in the wild. The evaluation of genetic and biogeographic connectivity is a fundamental component of a species' conservation status. Genetic analyses revealed five discrete populations of *E. marginatus* throughout their global geographic range, where the northern Atlantic population represents a distinctly separate phylogenetic species. Estimated divergence time between the most ancestral population found in the northern Atlantic Ocean and the *nouveau*-Mediterranean Sea is on the order of two million years.

Keywords: *Biogeography, Mediterranean Sea*

Introduction

Known as the "King of the Mediterranean," the dusky grouper, *Epinephelus marginatus* is an iconic marine fish prized by recreational and commercial fishermen for its quality of flesh and steep market price. Present day they can be found within reefs and along rocky coastal shores up to 50 m depth throughout the Mediterranean Sea, along the east and south coasts of Africa as well as Brazil (Fig 1; [1]). Due to overexploitation and habitat degradation throughout their global range, this long-lived sedentary protogynous hermaphrodite, is considered at high risk of extinction in the wild [2]. Irrespective of their large and discontinuous distribution, *E. marginatus* is classified as a monotypic species. Despite amphi-Atlantic morphological cohesiveness, fundamental ecological and evolutionary processes generating biogeographical patterns leading to reproductive isolation calls into question systematic unification. A previous study by Gilles et al. [3] suggests that morphological and genetic evolution may be uncoupled in *E. marginatus* resulting in morphological similarities between regions regardless of extensive genetic divergence. The aim of this research is to determine systematic unification and describe global phylogeography of *E. marginatus*.

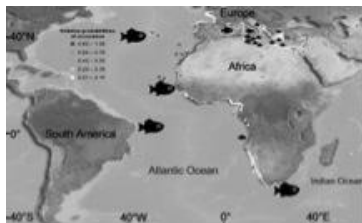


Fig. 1. Collection site map of 377 *Epinephelus marginatus* from 17 locations (fish symbol) in the Atlantic Ocean and Mediterranean Sea.

Materials and Methods

Samples from 377 *E. marginatus* individuals were collected from 17 localities and three continents from the Mediterranean Sea (Spain, Tunisia, N. Sicily and Linosa (IT), Malta and Hurd Bank [located E 12 NM from Malta], three locations along the Libyan north African shoreline to Egypt, Crete (GR) and N. Aegean Sea, east Atlantic (Angola, Senegal, South Africa), north-Atlantic (Azores, PT) and west Atlantic Ocean (Brazil). All *E. marginatus* were wild caught with the exception of samples from Crete, GR, which were F1 generation individuals donated from the Crete Aquarium. To assess global systematic unity of *E. marginatus* an integrative approach to molecular population genetics based on comparative phylogeography and coalescent based methodologies were conducted on a subset of 202 individuals using a 398 base pair catenated alignment of high density intraspecific variation from the mitochondrial control region (Fig 2). To avoid *a priori* assumptions of delimited populations, individual *E. marginatus* were assigned to spatially explicit genetic groups for comparative analysis downstream using GENELAND ver. 4.0.5 [4].

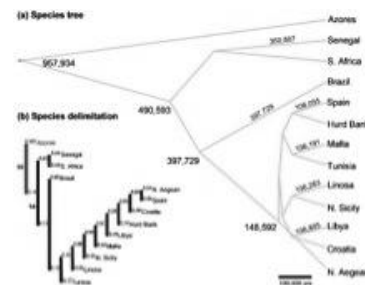


Fig. 2. (a) Consensus species tree with population divergence times and (b) species delimitation using the Poisson Tree Process.

Results

Eighty-eight distinct haplotypes containing 108 variable sites (plus three indels), of which 68 were parsimony informative, were represented between five spatially explicit global populations in the Azores, Brazil, Senegal, South Africa and the Mediterranean Sea with a collective modern effective population size estimate (N_{ef}) of around 4.4 million. The Azorean population was identified as the origin of species and currently represents a distinctly separate phylogenetic clade. The age of the *nouveau*-Mediterranean population is estimated to be around 150,000 Ma with a separation time from the origin of species on the order of two million years.

Acknowledgements: Many thanks to those that helped with sample collection: Dr Teresa Maggio (Palermo, Italy), Dr Sabina De Innocentiis (Rome, Italy), Dr Sandra Mollol-Martínez (Palma de Mallorca, Spain), Celia Schunter (Barcelona, Spain), Dr Daw Haddoud, R.A. Ban, A. Ariana, W.B. Gema (Tripoli, Libya), Dr Sanja Matic-Skoko and Dr Branko Glamuzina (Split, Croatia), Dr Grigorios Krey (Kavala, Greece), Dr Aspasia Sterioti (Crete, Greece), Dr Sergio Stefanni (Azores, Portugal), Dr Rodrigo Torres (Recife, Brazil), Dr Philip Heemstra and Dr Warren Potts (Grahamstown, South Africa) and all those at the South African Institute of Aquatic Biodiversity (SAIAB) who donated samples for this project.

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