

Absence of cryptic species and population structure in *Lychnorhiza lucerna* (Cnidaria) from Southwestern Atlantic Ocean

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Abstract

Jellyfish may be a problem in some parts of the world, especially for sites with species with high biomass. One of the most relevant aspects is the understanding of the gene flow between the populations of these species and the detection of genetic isolation in certain regions and that can result in speciation processes. Aiming to evaluate the population genetic structure of the most representative species of large jellyfish in the Southwestern Atlantic, *Lychnorhiza lucerna*, the present study analyzed molecular markers (COI and ITS) of specimens from populations of Brazil, Venezuela and Argentina's coast. Our results indicated a strong gene flow among specimens of the most varied regions, so the species does not present an obvious structure in subpopulations. In our view, the species is structured in a "metapopulation".

Introduction

An important trait of planktonic species is the larval dispersal in spatiotemporal context. Population connectivity of certain species can be achieved by long-lived and oceanic larva that can reach great distances and disperse through large areas. A group of specimens with great larval dispersal may have a larger connectivity, and consequently the ability to reestablish after disturbances in certain regions. This scenario helps to understand patterns of gene flow, distribution and defining populations of jellyfish (Cnidaria) species around the world.

Materials and Methods

Data collection

The present study verify species and gene flow of specimens of a large scyphozoan jellyfish, *Lychnorhiza lucerna* (Fig.3), from 12 different sampling points (hypothetical populations) along Brazil, Venezuela and Argentina (indicated in Fig. 1.), defined previously to include most of the specie distribution. All samples were preserved in absolute alcohol and maintained in the freezer (-20°C).

DNA Extraction and analysis of samples

DNA were extracted using Agencourt® DNAdvance™ (Genomic DNA Isolation kit), and amplified using PCR technique, with molecular primers of COI (Dawson, 2005) and ITS (Dawson, 2004; Maronna, not published) genes. After there purified with AMPURE® kit (Agencourt®). The product purified were prepared to sequencing using the BigDye® (Applied Biosystems), with same primers conditions of the PCR's. The obtained sequences were edited using Geneious™ 9, and aligned with se same program in default parameters using MUSCLE (Edgar, 2004). Also was used the software MEGA7 for establish distance Kimura-2 patterns (Kimura, 1980; Tamura et al., 2011). The haplotype network were designed using a software PopArt 1.7 (Population Analysis with Reticulate Trees-<http://popart.otago.ac.nz/index.shtml>).



Fig 1 Distribution map with number of specimens in each sampling area.

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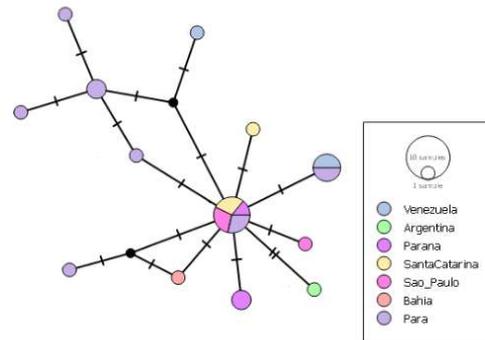


Fig. 2. Haplotype Network (Median-Joining Network) with 24 COI sequences from different populations

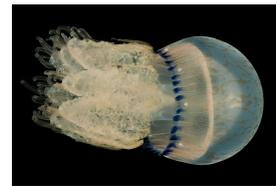


Fig.3. Specimen of *Lychnorhiza lucerna* from São Sebastião, SP. Image: Álvaro Migotto

Results and Discussion

Based on obtained sequences, we could confirm that specimens of *L. lucerna* from different localities present a low genetic variability (COI - K2P 0,002 and ITS - K2P 0,003), indicating a high connectivity and absence of cryptic species in this taxon. The specimens from more distant localities present at maximum 3 nucleotides of variation, a restricted genetic variability, therefore evidencing the high connectivity between specimens from different regions.

This result indicates the existence of a "metapopulation" with few biogeographic restrictions. This situation can be alarming in case of species with possibilities to population explosion (jellyfish blooms) because this condition can extend to all small groups depending on the factor triggering such blooms.

Global climate change is a key factor for understanding connectivity. Scenarios resulting from these changes can cause the global expansion of jellyfish populations, with the outcome of more connected populations and even a broader distribution of species as main consequences. A "metapopulation" pattern for a species with bloom potential would become dangerous for ecosystems and human affairs and they should be monitored.

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