

POPULATION, ECOLOGY AND GENETIC CHARACTERISTICS OF THE MEDITERRANEAN BOX JELLYFISH *CARYBDEA MARSUPIALIS* IN THE ISLAND OF MALTA

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Abstract

The main aims of this study were to investigate the environmental parameters associated with blooming events of *Carybdea marsupialis* and to genetically compare the box jellyfish in Malta to other Mediterranean and Atlantic samples. The numbers of adult individuals, as well as abiotic and biotic factors were monitored *in situ* and analysed statistically. Phenological patterns were determined and the abundance of *C. marsupialis* at the Maltese sites was shown to be strongly and positively correlated with sea water temperature. Genetic analysis indicated a high degree of homology between the sequences derived from the analysed Mediterranean specimens, which was not apparent in the genetic material derived from specimens from the Eastern Atlantic (Cadiz).

Keywords: Genetics, Population Dynamics, Mediterranean Sea

Introduction

The jellyfish *Carybdea marsupialis* (class Cubozoa) is an endemic species of the Mediterranean (Bordehore, 2014, Geroun et al, 2015). Previously not considered to be a blooming species in the Central and Western Mediterranean, in recent years unusually high densities of the species have been recorded in South-East Spain [1] Tunisia [3], Malta [2] where they negatively impact the marine ecology and tourism of these affected regions. This study aims to provide data on the factors affecting the abundance of these organisms in Malta.

Methods

C. marsupialis populations were monitored bi-monthly within two Maltese embayments (Birzebbugia and Msida), between July 2014-2015. The sites were selected as these studies had shown that they support year-round populations and are sufficiently distant from each other. Abiotic and biotic factors at each selected site, as well as morphological parameters, diagonal bell width, gastric cirri width, bell height, pedalia width and inter-rhopalia width were recorded. Correlations between abiotic and biotic parameter seasonal values were investigated, using the IBM SPSS Statistics package 19. Concurrently, a comparative study of 18S and 28S rDNA from Maltese specimens (n=24), and from reference specimens from the Mediterranean (off Denia) and Atlantic (off Cádiz) coastal waters of Spain was carried out. Five reference samples were studied for each site, with the exception of the sample from Cadiz where one sample was used.

Results and Discussion

The Mann-Whitney U-test was used to reveal strong statistically-significant spatial differences between morphometric measurements with inter-population differences in these values seemingly related to the levels of zooplankton at each site. Overall, population numbers showed a strong seasonality for the duration of the study, with similar phenological patterns exhibited at both sites. The appearance of juvenile stages was recorded at the end of May 2015, with the abundance of adult stages peaking at their highest densities between June-July. The population numbers then declined between February and absence persisted till early-May 2015. PCA and Spearman's Rank Coefficient were used to determine which factors primarily drove the observed seasonal changes in abundance recorded. Abundance was strongly and positively correlated with surface sea water temperature. Negative correlations were recorded between population numbers, nitrate and chlorophyll concentration. Genetic studies of the 18S-28S rDNA regions demonstrated uniformity between the Spanish (Mediterranean population only) and Maltese samples (>98.0% homology). Greater differences were recorded between the genetic sequences of the Mediterranean populations and that of the Atlantic (Cádiz) specimen (~80.0% homology). Less pronounced differences were recorded between the Denia and Birzebbugia samples, whilst all the remaining Maltese samples clustered together, suggesting an element of genetic drift between the Maltese populations. Analysis of the morphometric data confirmed that the Maltese *C. marsupialis* specimens were morphologically similar to the

specimens found in Olivia, Baha and Denia (Spain). The negative correlation between jellyfish abundance and phytoplankton and chlorophyll concentration appear at face value to be contradictory. We postulate that Cubomedusae population peaks do track the peaks in phytoplankton (and hence chlorophyll) abundance. However this occurs after a certain lag, with the Cubomedusae abundance responding to the subsequent peak in the abundance of mesoplankton, upon which they prey. The high homology at the 18S-28S rDNA region in the Mediterranean *Carybdea* specimens is compatible with their pelagic nature. Absence of high homology between the sample from Cádiz and the Mediterranean samples may possibly reflect mis-identification or the presence of a different *Carybdea* species. Further genetic studies with larger numbers of *Carybdea marsupialis* are thus recommended. This study highlights the importance of amalgamating both morphometric and genetic tools as a taxonomic tool within the Cubomedusae.

References

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