

DENSITY, DISPERSION AND GENETIC STRUCTURE OF *PARACENTROTUS LIVIDUS* (LAMARCK, 1816) NATURAL STOCKS IN THE SOUTH AEGEAN

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Abstract

Population structure of the edible sea urchin, *Paracentrotus lividus*, was studied over a three-year period in a South Aegean island. Spatial variations in population density and dispersion patterns were estimated. Sampling was carried out with a non-destructive method, the randomly placed frames technique, combined with *in-situ* registration of data. Mean population density was 13 ± 3.86 individuals/m², while the pattern of dispersion was random. The population genetic structure was also determined, using RAPD fingerprinting. *P. lividus* populations in Hellenic waters appeared to be panmictic and should be considered as a mixture stock over a large geographic scale.

Keywords : *Aegean Sea, Echinodermata, Density, Population Dynamics, Genetics.*

Introduction

Sea urchins are among the most important elements of the hard bottom benthos. In the Mediterranean Sea *Paracentrotus lividus* is one of the most abundant and widely distributed echinoderms. This edible and commercial sea urchin presents low mobility in adult stages. Therefore, its populations may exhibit high gene flow only when strong ecological or biogeographical barriers to dispersal are absent [1]. *P. lividus* is a well studied species, especially in the Western Mediterranean, where the depletion of its natural populations have lead to intense research effort for the management of its stocks [2], [3]. Contrarily, very few studies have been conducted in the Eastern Mediterranean, and even fewer in the South Aegean, where *P. lividus* has been traditionally harvested. The present work contribute to the study of *P. lividus* population structure in the Aegean Sea.

Materials and Methods

Sampling was carried out with SCUBA diving at three sites (A, B, C) along the coastline of Astypalea Island, at depths ranging from 2 to 10 m, in August 2003, November 2003, March 2004, October 2004, December 2004, June 2005, September 2005 and June 2006. The method of randomly placed frames, permitting *in-situ* counting, was applied to estimate population density and spatial dispersion (20 frames of 50 x 50 cm each) [4]. Morisita's index (I) was calculated to assess spatial dispersion and a chi-square test was used to determine the significance of deviation from random distribution [4]. Adult specimens from Astypalea (n=40), Amvrakikos Gulf (n=53, Ionian Sea), Pagasitikos Gulf (n=75, Central Aegean) and Chalkidiki (n=40, North Aegean) were used to determine the genetic structure of *P. lividus* populations in Hellenic waters. Genomic DNA was extracted from the gonads of each specimen using a modified Levitan's protocol [5]. Seven RAPD primer markers and eight loci were used for distance computation between and within populations. Analysis of Molecular Variance (AMOVA) was performed among and within populations. Total population differentiation value (Fst) was estimated, as well as its overall and pairwise gene flow (Nm) values. A UPGMA tree of genetic distance [6] was produced.

Results and Discussion

Mean population density of *P. lividus*, over all sites and sampling periods, was 13 ± 3.86 individuals/m². At each site a decrease in population density was evident at least twice during the study period. Two-way ANOVA showed significant spatial differences on mean population density ($F=9.37$ $p<0.05$), as well as temporal ones ($F=19.98$ $p<0.05$). The spatial differences were restricted to the reduced density of *P. lividus* at station A. Temporally, the abundance of sea urchins increased, gained maximum values in November 2003 and remained at high levels till March 2004; thereafter it declined, started to upturn in September 2005 and reached a second peak in June 2006. *P. lividus* individuals were randomly dispersed in most cases (I ranged from 1.05 to 1.32). These results indicate that *P. lividus* stocks undergo temporal fluctuations, probably linked to its reproductive output. The population seems to sustain the pressure of the local fisheries, since it retains overall high density, with no significant reduction on the mean test diameter (unpublished data). AMOVA permutation showed significant differences either among or within studied populations ($F_{st}=0.077$ $p<0.001$). Pairwise Fst values were statistically significant for all populations at all loci. These data, along with the high value of migrants per generation ($Nm=13.95$), imply near panmixis among populations. Cluster analysis showed low values of genetic distance even between the Aegean

and Ionian populations (Figure 1). Echinoderm species dispersal may occurs over long distances [8]. *P. lividus* populations in the Atlantic Ocean and the Mediterranean Sea appear to be panmictic within each, as gene flow occurs over large distances with no evidence of isolation by distance, indicating formidable plasticity to environmental or other pressures [1]. *P. lividus* populations, due to their panmictic nature in Hellenic waters should be considered as a mixture stock over a large geographic scale.

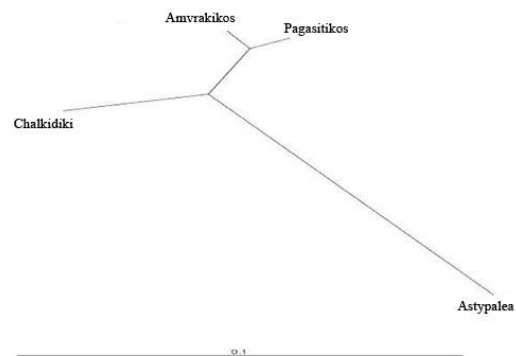


Fig. 1. UPGMA cluster analysis using Slatkin's genetic distance between the studied populations of *P. lividus*.

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