

RESEARCH ARTICLE

Biocomplexity in Populations of European Anchovy in the Adriatic Sea

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Abstract

The sustained exploitation of marine populations requires an understanding of a species' adaptive seascape so that populations can track environmental changes from short- and long-term climate cycles and from human development. The analysis of the distributions of genetic markers among populations, together with correlates of life-history and environmental variability, can provide insights into the extent of adaptive variation. Here, we examined genetic variability among populations of mature European anchovies ($n = 531$) in the Adriatic (13 samples) and Tyrrhenian seas (2 samples) with neutral and putative non-neutral microsatellite loci. These genetic markers failed to confirm the occurrence of two anchovy species in the Adriatic Sea, as previously postulated. However, we found fine-scale population structure in the Adriatic, especially in northern areas, that was associated with four of the 13 environmental variables tested. Geographic gradients in sea temperature, salinity and dissolved oxygen appear to drive adaptive differences in spawning time and early larval development among populations. Resolving adaptive seascapes in Adriatic anchovies provides a means to understand mechanisms underpinning local adaptation and a basis for optimizing exploitation strategies for sustainable harvests.

Introduction

A growing body of evidence indicates that marine organisms with potentially dispersive planktonic larvae can show genetically patchy distributions that may be uncorrelated with spatial complexity [1, 2]. This unexpected genetic population structure has been attributed to natural