Title
Patterns of Recruitment in Red Sea Urchins: A Population Genetics Approach

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Publication Date
2003-06-01

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Project Number: R/F-178
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Final Technical Narrative

Management of sea urchin fisheries is hampered by a lack of understanding of recruitment processes. Two issues are of particular importance. First, because their larvae develop in the plankton over a period of several weeks, sea urchins may experience long distance dispersal. This may lead to a disconnect between local management practices and recruitment since recruits may be derived from distant populations. Second, individual adult urchins have extremely high fecundity, so it is possible for relatively few females to produce ample supplies of recruits to maintain urchin abundance despite intensive fishing pressure.

The primary goal of the project was to employ a population genetic approach to assess the importance of high dispersal capability and high fecundity on recruitment processes in California sea urchins. Sea urchins are long-lived, so adult urchin populations result from many recruitment events spanning decades; since patterns of recruitment vary over time, any genetic signature of recruitment patterns will be blurred over time. In our previous Sea Grant supported work, Moberg and Burton (2000) found that smaller-size urchins were more genetically divergent than larger size urchins collected at the same locales. This would suggest that either: (1) the new recruits arriving at different places come from different source populations or (2) the recruits that arrive at different places derive from different animals within a common source; they are then transported differently because they were entrained in different water masses (due to spatial and/or temporal variability in local hydrodynamics. However, the smallest size class sampled by Moberg and Burton (2000) was up to 30 mm test diameter, so the animals may have been up to two years old. Here we obtained

a closer look at individual recruitment events by genotyping newly settled urchins from multiple spatial and temporal samples.

In order to obtain population genetic information from a series of recruitment events, we obtained samples of urchins within 2 weeks of their settlement for 16 recruitment events spanning six years and seven geographic locations. Mitochondrial DNA sequences (358 bases of the cytochrome oxidase subunit I gene) were obtained from a total 302 recruits. These data were analyzed in two ways in order to address the two different recruitment issues stated above. Levels of genetic differentiation were determined to assess the extent of dispersal between populations. Although this is not a strong test of dispersal since adult urchin populations show little genetic divergence, we found that recruits arriving at different geographic locales at the same time were generally genetically homogeneous. This result suggests, but does not prove, that the larval pool is well mixed. The second analysis compared levels of genetic diversity in each sample of recruits to that which would be expected based on sampling the adult population. The hypothesis that few adults participate in each recruitment event would be apparent from reduced levels of diversity in the recruits. Our data gave no evidence for such reduced genetic diversity in recruits. Hence, although small numbers of reproductive urchins have the potential for producing all the larvae that recruit at a given place and time, we found no evidence for such "sweepstakes" recruitment.

We encountered two major problems in carrying out this research. First, although we had hoped to focus our efforts on red urchins, collections of red urchin recruits were too few for population genetic analysis. Work shifted to analysis of purple urchins because sufficient material was available for the proposed investigations. Because purple urchins share the general life history features of red urchins, it is likely that our results on purple urchins apply to the more commercially valuable red urchins. Second, development of microsatellite loci proved difficult and time consuming. We have now developed primers for microsatellite loci in *Strongylocentrotus purpuratus* (purple urchin) and have developed one such marker in *S. franciscanus* (red urchin); additional loci have been deveoped by Don Levitan (Florida State

University) and we are now initiating population genetics work with these markers on both species. Hence the studies will be completed on other funds, hopefully by the end of 2004.

Current regulation of California sea urchin fisheries recognizes separate northern and southern California ecological regions with no subdivision within those regions. Genetic analysis did not reveal any significant population genetic structure (even between northern and southern California); hence, further subdivision of stocks for management purposes is not warranted at this time. The management implications of our work on genetic diversity of recruits is not yet clear. Genetic data suggest that large numbers of animals contribute to each recruitment event. This may, in turn, reflect current knowledge of fertilization biology that suggests that high population densities are required for successful fertilization. If this interpretation is correct, it supports efforts to establish no-take marine protected areas, where unfished urchin populations may reach high densities.

REFERENCES:

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