Part II

SYMPOSIUM OF THE CALCOFI CONFERENCE

Lake Arrowhead, California

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GENETICS OF THE FAUNA OF THE CALIFORNIA CURRENT

The California Current is the dominant oceanographic feature on the west coast of North America. It profoundly affects the flora and fauna of the coast, from its influence on climate and upwelling to its effects on the transport and dispersal of organisms and their propagules.

A full understanding of the processes that promote or restrict the dispersal of organisms, and of the California Current's role in governing these processes, is necessary for the proper management of this ecosystem. We know that some genera contain dozens of species, and that others are represented by only a few species. Some species have distributions that separate obviously along known faunal breaks, whereas related species have continuous distributions along the coast. Some populations undergo great temporal cycles of expansion and contraction; others appear relatively stable over time.

Understanding spatial and temporal patterns of variation as they relate to physical and biological features of the California Current is a long-term goal of the CalCOFI program. Recently, a number of programs such as the joint NSF/NOAA GLOBEC (Global Ocean Ecosystem Dynamics) program have refocused interest on understanding the mechanisms that lead to patterns of variation in marine ecosystems, particularly larval transport processes and recruitment variation.

The purpose of this CalCOFI symposium was to examine the role that population genetics—specifically, emerging new techniques of molecular genetic analysis—can play in explaining the mechanisms that underlie observed patterns of spatial and temporal variation. In addition, we hoped to illustrate how population structure can be present but not readily detectable by other means. Finally, it was our intent to highlight the increasingly important role of genetic analyses in making management decisions about marine resources and protected species.

In the past, population geneticists (at least those with common sense!) investigated systems that had stable populations, well-defined barriers to gene flow (a mountain range or an isthmus would suffice), and well-determined times of separation (in the geologic past). Such conditions made it possible to identify population-level differences, and to make inferences about rates of movement among populations.

The study of genetic variability in oceanic populations has been problematic because these systems are inherently open and unstable. Barriers to migration (gene flow), if they exist, are often cryptic, incomplete, and intermittent. In addition, population size may vary by several orders of magnitude over periods of a few years, and the number of individuals that successfully contribute to a particular year class may be a small and nonrandom portion of the total population. These factors have made the application of traditional measures of genetic variation, and the statistical treatment of the data, difficult at best.

Initial studies of oceanic populations, primarily involving allozymes, often indicated no significant variation between putative populations. Quite likely this was because the time and degree of separation needed to produce divergence in allozyme frequencies by genetic drift were overwhelmed by the effects of continuous low levels of migration or by episodic mixing of populations.

Recently, investigators driven by curiosity—if not common sense—have begun to revisit the study of genetic variation in organisms that are influenced by complex and dynamic systems such as the California Current. The approach has been to use new genetic markers that evolve at faster rates, so that population-level differences can be observed in the face of higher levels of gene flow.

The organisms considered in the symposium ranged from marine mammals that forage in the current but are not subject to its physical transport effects, through benthic fish and invertebrates that rely on the current for dispersal of larvae, to calanoid copepods that are intimately associated with the hydrographic processes of the current throughout their lives.

The papers in the symposium proceedings illustrate a variety of approaches for determining genetic population structure. They include novel approaches to revealing larval dispersal patterns by studying introduced species and hybridization zones. They also address temporal as well as spatial patterns of diversity. Several papers provide insights into the analysis of molecular genetic data, and into using power analysis to apply confidence limits to conclusions.

The symposium marks the beginning of what promises to be a new era of investigations into the California Current. Genetic approaches have much to offer toward investigating processes of larval dispersal, recruitment variability, and historic population structure. Genetic considerations are being used increasingly as a management tool, and the conservation of genetic diversity is becoming an explicit goal of management.

Biomedical technology will continue to provide new and innovative tools for the study of marine population genetics. However, a true understanding of the processes that determine genetic structure in oceanic populations will continue to rely on multidisciplinary studies of the physical and biological environment. The development of modeling and statistical procedures that are appropriate for the analysis of marine populations is a research priority.

Russell D. Vetter

Participants in the Symposium of the CalCOFI Conference: Genetics of the Fauna of the California Current. *Left to right:* Russell Vetter, Robin Waples, Dennis Hedgecock, Jennifer Nielsen, Andrew Dizon, Joseph Neigel, Ronald Burton, Jonathan Geller, Ann Bucklin, and student representative Axayacatl Olivares.