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Introductory overview

Stability, equilibrium and molecular aspects of conservation in marine species

A major challenge in any genetic analysis of population structure is to gain a proper perspective on the relevant spatial and temporal scales that might be involved. For example, with respect to temporal considerations, a species might have restricted dispersal capabilities at most points in ecological time when we observe them, yet they might have broad ranges due to periodic, episodic, or accumulated movements over longer timescales, perhaps following major environmental changes or at other exceptional times.

In the marine environment, many species exhibit a phenomenon known as chaotic patchiness wherein there is great allele frequency variation on microspatial scales at any one time, yet also a temporal kaleidoscopic pattern in which allele frequencies can change quickly at a given locale. Thus, microspatial heterogeneity can be pronounced yet temporally variable such that if a species were assayed multiple times, different pictures of the particulars of population genetic structure might emerge. Many marine species have the potential for explosive reproduction by individuals such that cohorts of larvae, perhaps produced by relatively few breeding individuals, might be the lucky survivors that settle successfully and precipitate a large local change in allele frequency. In a few generations another cohort might come in, and so on. It is this kind of stochastic or chaotic patchiness, demographically driven, that might characterise many marine species. It is even possible that long-term decisions about where stocks exist could be misinformed when based on information gathered at any one slice in time. There is no obvious answer as to what should be done in this sort of situation, except to stress that ecologists and geneticists should at least be aware of the possibilities. It is important to try to come to grips with the spatial and the temporal scales over which population structure might exist. To accommodate temporal and spatial variation in allele frequencies, we need to devote effort to thinking of ways to couple ecological concepts with phenomena that take place episodically or over longer periods of time.

Another point often overlooked in genetic issues is that in most cases the biological world is unlikely to be at equilibrium between opposing evolutionary forces. Many of the traditional equilibrium models of population genetics involve unrealistic assumptions about the way real populations behave in the natural world. One consequence of this is that, despite talk about how the allozyme and DNA revolutions have revealed so much genetic variation in populations, the amount of variation in nearly all species is far less than predicted under neutrality theory if evolutionary effective population sizes approximate current-day population sizes. This statement applies with particular force to currently abundant species. Whether measured by allozymes or at the DNA level, actual levels of genetic variation usually are vastly lower than traditional neutrality expectations. From this perspective, genetic polymorphism is unexpectedly low (rather than high), and this finding is consistent with the possibility that evolutionary effective population sizes in most species are several orders of magnitude below those species' current standing crops. One good way to illustrate this is to consider, for example, some of the mega-abundant populations of particular zooplankton species that have been assayed genetically. These surely consist of many billions of individuals, and yet the coalescent depths in mitochondrial gene genealogies are consistent with evolutionary effective population sizes of the order of perhaps a hundred thousand or less. Similar arguments can be made for other currently abundant species. Historically, almost all species probably have fluctuated dramatically in population size, perhaps in association with speciation events or perhaps at other times in their recent evolutionary history. Species that are abundant today cannot have been abundant consistently through time or, they would have far more genetic variation and deeper coalescent depths than in fact they do.

This is just one line of argument that many natural populations are at non-equilibrium status. It is likely that populations of most species fluctuate dramatically in space and in time at least periodically, and by making field observations today we are merely capturing a snapshot view. Genetic analyses can help to add a temporal

dimension to our understanding because the current genetic architecture of a species in large part reflects that species' demographic past as well. Thus, genetic analyses can be informative and influence how we think about the biological world, and in general they indicate that this world is probably in a tremendous state of dynamism. For example, diseases or any of a wide range of environmental impacts can wipe out large fractions of a species and thereby cause dramatic fluctuations in population size.

Overall, marine organisms present some unusual challenges and opportunities for genetic analysis. Marine species generally are less accessible than those on land or in freshwater, so behavioral studies and observations of natural history are more difficult. This opens many opportunities for genetic analyses to reveal otherwise hidden aspects of a species' natural history. Marine organisms offer an exceptionally wide range of dispersal and migratory capabilities, and the geographic ranges of individual species can be vast. Life histories often include potentially enormous fecundity, and the capability for sudden explosive population increases. A high proportion of marine species are also of concern with respect to conservation, with many being harvested commercially on a large scale, in some cases illegally. Thus population management may involve economic, social, jurisdictional or forensic concerns. Molecular biology can play a role in many of these areas, uncovering previously unknown aspects of behavior, natural history, and population demography pertinent to decisions on population management and conservation.

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