Trends in Ecology & Evolution

Rigorously linking the pattern and mechanism of coevolutionary diversification

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We were pleasantly amused by the title of Arnqvist's article, which caused one of us (J.F.A.T.) to wax nostalgic about graduate school at Harvard in the late 1970s and recall a Yiddishism applicable here to our discussion of editorial evaluation. At that time, announcements for seminars in Richard Lewontin's laboratory were printed with a graphic of an obviously stressed and profusely sweating caricature of a scientist, who looked like he was stepping out of the pages of a Robert Crumb comic, carrying a briefcase on which 'Schmarvard' was boldly written. It poked good fun at laboring to present one's work in what was cartooned as a hypercritical and anxiety-provoking environment. We hope authors will not be unduly stressed in identifying the right journal to present their research, but will nevertheless be diligent in reviewing journal standards and contents to determine appropriateness for submission. Authors should not feel discouraged about submitting their work to a highly ranked primary journal, but should rather acknowledge their responsibility to be mindful of the manuscript content required for different venues in making such decisions. If in doubt, email enables rapid communication with editors to offer an opinion. And authors should of course be aware they have options in these transitional times of science publishing.

References

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Ten years lost at sea: response to Manel and Holderegger

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Manel and Holderegger [1] (hereafter MH) present a review of the methodological and conceptual advances that have occurred in the field of landscape genetics during the 10 years since the publication of Manel *et al.*'s [2] seminal review. MH proceed to discuss the future of the discipline, focusing on potential applications in terms of adaptation to global change and the conservation of natural resources. MH dedicate a section of their review to the progress made in the subfield of 'seascape genetics' [3]. However, MH refer solely to an approach in which genetic data can be combined with biophysical oceanographic models to investigate environmental influences on larval dispersal. The larval dispersal study by Selkoe *et al.* [4] is presented as a representative example of the research being conducted to understand the influence of ocean currents on patterns of gene flow. Although we agree that important progress has been made in the study of environmental influences on the genetic patterns of the larval stages of marine species (e.g., [5–7]), we wish to note that significant advances in understanding the seascape genetics of highly migratory species, such as cetaceans, were entirely omitted from the review [8–12].

MH also recommend that the field of seascape genetics would benefit from larger-scale sampling to capture wide-ranging patterns of connectivity and from also being more aware of progress being made in terrestrial landscape genetics, because the methodological and statistical concepts are broadly the same [1]. In elucidating how oceanographic features have influenced the genetic structure of cetacean species and their populations, the studies we wish to highlight have been conducted at broad spatial scales, and have used and adapted many of the techniques employed by terrestrial landscape geneticists; thus, researchers working in the field of seascape genetics are already addressing the issues considered pertinent by MH.

Prior to the birth of 'landscape genetics', Fullard *et al.* [8] presented correlations for the long-finned pilot whale (*Globicephala melas*), which suggested population isolation occurs between areas of the ocean that differ in sea surface temperature. Building on this concept, Mendez *et al.* [9] found significant correlations between genetic discontinuities of franciscana dolphin (*Pontoporia blainvillei*), off the coast of Argentina, and more complex oceanographic climatologies; Mendez *et al.* [9] described this isolating mechanism as one of 'isolation by environmental distance (IBED)'. A comparative study on the humpback dolphin (*Sousa* spp.) in the Western Indian Ocean proved that the principles of IBED could be generalized to other cetacean species and geographic areas [10]. Seascape genetic studies have also been undertaken to investigate the environmental factors shaping the distribution of intraspecific genetic diversity. In an impressive global study, Amaral *et al.* [11] demonstrate how marine productivity and sea surface temperature are correlated with the genetic structure of the

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short-beaked common dolphin (*Delphinus delphis*). Given the tight linkage between oceanic conditions and prey behavior, such studies demonstrate ways in which to potentially track the biological effects of ongoing climate change and also inform marine reserve design. Moreover, examination of Pleistocene climatic conditions has provided insights into the phylogeography and demographic history of the common dolphin (*Delphinus* spp.) at the global scale [12]; information that could be of great importance in predicting the ecological and evolutionary consequences of future changes in oceanographic conditions [12].

We present this summary in an effort to provide a more complete picture of where progress in the field of seascape genetics currently stands, and to provide a more concrete baseline from which the seascape genetics research community can continue to innovate and improve our understanding of the genetic patterns and processes of marine species. Notwithstanding, we whole-heartedly agree with MH on their concluding remark, that the fields of land and seascape genetics have much to contribute in defining units for conservation and for understanding how the trajectories of uniquely evolving entities will be affected by global climate change.

References

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Reply to Kershaw and Rosenbaum

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We agree with Kershaw and Rosenbaum [1] that our discussion on seascape genetics was limited and we thank them for developing on the importance of the work that has already been conducted in the seascape genetics of highly migratory species such as cetaceans, which we did not incorporate in our review [2]. It is obvious that the past 10 years have not been lost at sea. However, the main objective of our review was not to cover any particular field of landscape or seascape genetics in a broad way, because reviewing 10 years of landscape genetics (which is not a completely new scientific field, but based on older concepts of spatial genetics [3]) is already a wide topic in itself and asks for brevity. For an overview of seascape genetics only, we recommend the reader to consult the recent review of Liggins *et al.* [4].

Kershaw and Rosenbaum [1] suggest that seascape genetics studies have already been conducted on a broad spatial scale. This is certainly true for cetaceans and larger fishes. However, even the broad-scale studies mentioned by Kershaw and Rosenbaum [1] are based on the analysis of a small number of sampling sites (ranging from four [5] to seven [6]), limiting the power of statistical tests to elucidate spatial genetic patterns, functional connectivity, or adaptive genetic response to the environment. In the work of Fullard *et al.* [5], Mantel tests were applied to test for isolation by distance from only four sites for the long-finned pilot whale, which is hardly sufficient to obtain statistical support. This is what one would not like to see in future landscape or seascape genetic analysis, although we are aware of the difficulty of sampling organisms in marine ecosystems. The example that we chose as representative of seascape genetics [7] tested the relationship between genetic differentiation and seascape variables (environmental associations) from at least 17 sampling sites and for three reef species using a refined statistical regression method (mixed linear model).