

The role of genetics in understanding landscape-level ecological processes

SPATIAL AND TEMPORAL LANDSCAPE PATTERNS across ecosystems have long been known to influence biological processes, but these processes often operate at scales that are difficult to study. The use of alternative methods like genetic markers can become a useful aid in the study of such patterns in ecology. Researchers can use a landscape-genetics approach to test hypotheses, as the authors did with the Lahontan cutthroat trout (*Oncorhynchus clarki henshawi*). They employed microsatellite DNA variation in a complex stream network in the Great Basin region of the western United States. Their analyses reflected patterns of dispersal, population stability, and local effective population sizes. In addition, the authors found that trout populations presumed to have greater proportions of migratory individuals or to originate from physically connected, large, or high-quality habitats had higher genetic variability and lower genetic differentiation than other populations. However, the opposite pattern was found in populations thought to contain largely nonmigratory individuals, suggesting behavioral isolation. Estimated effective sizes were small, and the authors identified significant and severe genetic bottlenecks in several populations that were isolated, recently founded, or that inhabited intermittent streams. Their results show the importance of grounding genetic inferences in ecological hypotheses and predictions, but also demonstrate that genetic patterns can reveal processes that may be quite unexpected.

Reference

Neville, H. M., J. B. Dunham, and M. M. Peacock. 2006. Landscape attributes and life history variability shape genetic populations in a stream network. *Landscape Ecology* 21:901–916.

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