



A new approach to identifying drivers of local adaptation

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Local adaptation, the higher fitness a population achieves in its local “home” environment relative to other environments is a crucial phase in the divergence of populations, and as such both generates and maintains diversity. Local adaptation is enhanced by selection and genetic variation in the relevant traits, and decreased by gene flow and genetic drift.

Demonstrating local adaptation is laborious, and is typically done with a reciprocal transplant design [1], documenting repeated geographic clines [e.g. 2, 3] also provides strong evidence of local adaptation. Even when well documented, it is often unknown which aspects of the environment impose selection. Indeed, differences in environment between different sites that are measured during studies of local adaptation explain little of the variance in the degree of local adaptation [4]. This poses a problem to population management. Given climate change and habitat destruction, understanding the environmental drivers of local adaptation can be crucially important to conducting successful assisted migration or targeted gene flow.

In this manuscript, Macdonald *et al.* [5] propose a means of identifying which aspects of the environment select for local adaptation without conducting a reciprocal transplant experiment. The idea is that the strength of relationships between traits and environmental variables that are due to plastic responses to the environment will not be influenced by gene flow, but the strength of trait-environment relationships that are due to local adaptation should decrease with gene flow. This then can be used to reduce the somewhat arbitrary list of environmental variables on which data are available down to a targeted list more likely to drive local adaptation in specific traits.

To perform such an analysis requires three things: 1) measurements of traits of interest in a species across locations, 2) an estimate of gene flow between locations, which can be replaced with a biologically meaningful estimate of how well connected those locations are from the point of view of the study species, and 3) data on climate and other environmental variables from across a species' range, many of which are available on line.

Macdonald *et al.* [5] demonstrate their approach using a skink (*Lampropholis coggeri*). They collected morphological and physiological data on individuals from multiple populations. They estimated connectivity among those locations using information on habitat suitability and dispersal potential [6], and gleaned climatic data from available databases and the literature. They find that two physiological traits, the critical minimum and maximum temperatures, show the strongest signs of local adaptation, specifically local adaptation to annual mean precipitation, precipitation of the driest quarter, and minimum annual temperature. These are then aspects of skink phenotype and skink habitats that could be explored further, or could be used to provide background information if migration efforts, for example for genetic rescue [7] were initiated.

The approach laid out has the potential to spark a novel genre of research on local adaptation. In its simplest form, knowing that local adaptation is eroded by gene flow, it is intuitive to consider that if connectivity reduces the strength of the relationship between an environmental variable and a trait, that the trait might be involved in local adaptation. The approach is less intuitive than that, however – it relies not connectivity per-se, but the interaction between connectivity and different environmental variables and how that interaction alters trait-environment relationships. The authors lay out a number of useful caveats and potential areas that could use further development. It will be interesting to see how the community of evolutionary biologists responds.

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Appendix

Reviews by Ruth Hufbauer and Thomas Lenormand: <http://dx.doi.org/10.24072/pci.evolbiol.100034>