Public Abstract

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Title:Factors affecting abundance, physiology, and fine-scale genetic differentiation of the western slimy salamander (Plethodon albagula)

At its core, landscape genetics seeks to identify the spatial processes shaping the observed patterns of genetic diversity across the landscape, but most landscape genetic studies are predominantly exploratory and lack well-established hypotheses. To increase understanding of process-driven patterns in landscape genetics, I studied the western slimy salamander (Plethodon albagula) in east-central Missouri with three specific questions: (1) Where are salamanders on the landscape, and what environmental factors influence local abundance? (2) Is there a physiological constraint underlying the observed patterns of distribution and abundance? (3) How is spatial genetic structure shaped by abundance and physiology across the landscape? I utilized a combination of abundance modeling, spatial quantification of water loss using plaster of Paris models, and landscape genetics analyses to assess the factors contributing to genetic differentiation across a 1300 ha landscape.

I found that abundance of salamanders was best predicted by canopy cover, topographic position (ridge, slope, ravine), and the interaction between wetness and solar exposure. The spatial relationships of these factors are such that abundance is predicted to be highest in forested ravines with lower solar exposure. Plaster models deployed across the landscape served as surrogates for live salamanders to quantify rates of water loss. I found that rates of water loss across the landscape were inversely related to predicted abundance, suggesting that water loss is likely a physiologically-limiting process underlying the distribution of salamanders. Finally, I determined that genetic distances were significantly correlated with ecological surfaces, and that the independent landscape features underlying these processes were poor predictors of genetic differentiation. My results highlight the importance of understanding basic ecological and physiological factors as mechanisms for interpreting spatial genetic patterns.