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Evaluating Species Responses to Climate Change Using Ecological Niche Modeling and Genetic Data

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1 Introduction

The current and projected future warming trends together with degradation of habitats throughout much of the Great Basin and Columbian Plateau represent real threats to many species occupying these regions. If we can determine the impacts of past climatic changes on the distribution of species, we can obtain a better understanding of the future impacts of projected climatic trends on many species in these regions. My results with the Great Basin Pocket Mouse (Perognathus parvus) may be relevant to conservation ecologists and resource managers attempting to protect several Endangered Species Act candidates, such as the pygmy cottontail (Brachylagus idahoensis).

I used ecological niche modeling and molecular genetics to determine if P. parvus distribution shifted according to predictions of climate-driven habitat changes between the Last Glacial Maximum (LGM; when ice sheets were at their maximum between 26,500-20,000 years ago) and present time.

2 Predictions

I tested the null hypothesis that the species habitat requirements remain identical through time as climates change, and therefore P. parvus responded to the warming climate after the LGM by shifting its range (Fig. 1a, Hewitt 1996). If that’s the case, this range shift will be congruently supported by the ecological niche models and the genetic data. Alternatively, if the species habitat requirements do not remain identical through time, the genetic data will not support the niche models and show a different response to climate change, such as range stability despite the climatic changes (Fig. 1b).

3 Methods

To determine whether the species distribution shifted as predicted under the niche conservation model, I first used the methodology of ecological niche modeling to reconstruct the species current and LGM distributions. I employed the software Maxent (version 3.3) which evaluates environmental (e.g., climatic) data taken from the species occurrence records. This information on species environmental requirements was used to identify suitable habitat across the landscape and project species expected distribution on a map. Eighteen climatic variables were used to build the models, including precipitation, temperature, and diurnal range. The program was masked (limited to) the ecoregions where the species actually occurs.

Secondly, genetic patterns were used to evaluate the niche conservation model. I generated mitochondrial DNA sequences for 71 individuals of P. parvus. I calculated genetic variation among sampling localities which was then interpolated across the landscape in ArcGIS. The patterns of genetic variation can be used to infer which populations have recently expanded and which have remained stable over time according to available population genetic models (Fig. 2) (Hewitt 1996).

Results and Discussion

The LGM model generally projected a broader suitable habitat range than the current model, stretching southwest into the Mojave Desert and northward into Washington, Idaho, Wyoming, and Montana. The LGM model indicated unsuitable habitat within the eastern parts of the Great Basin, as opposed to more suitable habitat throughout the western Great Basin. Based on these models, I predicted a genetic signal of stable populations (Fig. 2a) in areas of overlap between the LGM and current models (Fig. 3, yellow shaded circles). I also predicted a genetic signal of populations in areas of recent expansion (Fig. 2b) as suitable habitat increased into the eastern Great Basin after the LGM (Fig. 3, red shaded circles).

Interpolated genetic variation across landscape (Fig. 4) did not match our predictions based on the models. The areas where we predicted a genetic signal of recent expansion did not exhibit lower genetic variation than areas where we predicted population stability. The highest genetic variation was detected within the northern parts of the species range, within the Columbian Plateau. The genetic variation within the Great Basin was overall lower, with the lowest values found within the western Great Basin.

In conclusion, my prediction of species response to the past climatic event under the assumption of niche conservation was not supported by contrasting the ecological niche model with the actual pattern of genetic variation. The disagreement between the models and genetic data implies that P. parvus did not shift its range predictably under this assumption, which could mean that the species habitat requirements did not remain identical between the two climatically very different time periods. Alternatively, environmental factors (e.g., soils) other than those associated with the climatic variables used to build the models might be important in shaping the species distributions through time.

4 References


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