# Suitability prevalence area index in late quaternary explains genetic diversity in Tassel eared Squirrels

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## Abstract

The current distributions of species do not always correspond to their historical distributions over evolutionarily significant periods. This is because environmental conditions are not static over time; species tend to distribute where conditions are most favorable.

It follows from this relationship between environment and species distribution that population size also varies with time. This variation in population size is related to the effective population size $N_e$, so that an index reflecting changes in environmental conditions in geography might be expected to be related to $N_e$ and thus to indicators of population structure such as the fixation index $F_{st}$. Thus, it is possible to relate patterns of changes in the distribution of species to the genetic structure of their populations using a statistical model that explains this relationship.

With this approach we can predict the geographic pattern of population structure from environmental information. This approach is strongly driven by advances in currently available climate simulations (Leonardi et al. 2023; Krapp et al. 2021), as well as next generation sequencing data, and supported by both ecological niche (Thorup et al. 2021; Nogués-Bravo 2009) and population genetics theories (Lira-Noriega and Manthey 2014).

In this work we propose a method to find the Suitability Prevalence Area (SPA) as an index with a double purpose: 1) to find endemic areas to delimit the historical distribution of the species and 2) to explain the patterns of genetic diversity.

To obtain the SPA, we performed a historical reconstruction of the geographical range back to 120 000 BC at 2 000 year intervals and recorded the environmental suitability at each site.

Subsequently, we delimited historical endemic areas to locations where the prevalence of suitability remained at 90% during this period. From the fixation index calculated with respect to populations in the historical endemic areas, a statistical model of the fixation index as a function of SPA was performed. With this statistical model, the fixation index values were projected to the current distribution to obtain a map with the geographic pattern of this index.

As a case study we consider squirrels (*Sciurus aberti*), a species currently distributed in disjunct patches from the southern Rocky Mountains in the United States to the northern Sierra Madre Occidental in Mexico for which it is possible to find reliable information on both the genetic structure of its populations and its current distribution (Bono et al. 2018; Burgin et al. 2018).

Our results reveal that suitability prevalence corresponds to the fixation index of *S. aberti* populations with respect to a source population. Populations closer to the historical endemic area present a higher genetic diversity and a lower $F_{st}$ value. Finally, this study allows us to add a biogeographic explanation to the results obtained with population genetic methods and to generate maps of this structure as tools to support conservation with a perspective that integrates both population genetics and historical patterns of species distribution.

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