

## Summary of research on population genetics of bobcats across the United States

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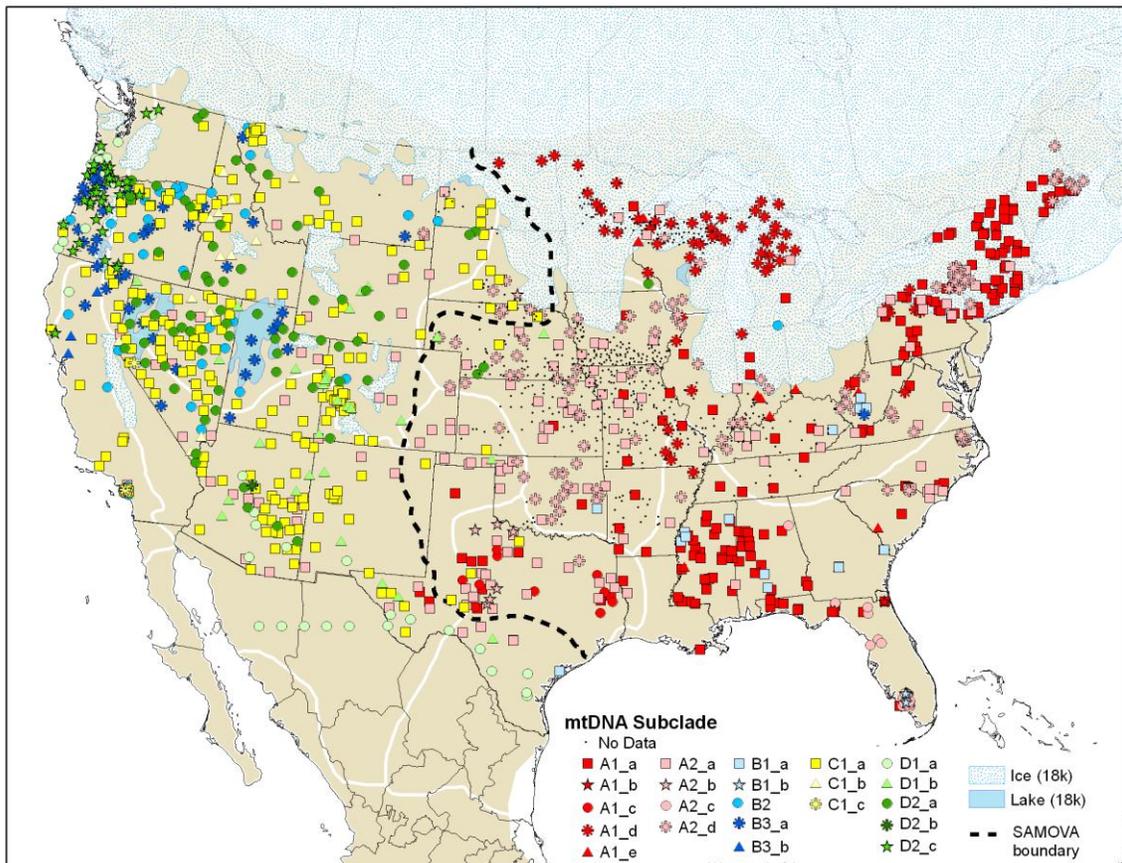
Genetic methods have increasingly become an integral component of conservation and management of wild animal populations. Genetic data can be useful for identifying population structure, which reveals how factors such as landscape barriers (such as roads, rivers, mountains, cities, or unsuitable habitat) or simply geographic distance influences animal movement and the potential for individuals to settle in new areas and interbreed. Understanding how and why bobcats are structured into populations can help to anticipate how they might respond to habitat loss, recover from local extinction, spread disease, or even evolve in response to long-term trends like global climate change.

In this study, we used genetic analysis to investigate the patterns and mechanisms of population structure for bobcats across the entire United States. We analyzed DNA (15 microsatellites and 1 KB mtDNA sequence) for over 1700 samples collected throughout the majority of the bobcat range, including samples from 9 of the 12 morphologically described subspecies. The sample set represents contributions from numerous furharvesters, state agencies, and biologists. The genetic data primarily distinguished bobcats in the eastern USA from those in the western half (Figure 1), even though there is no obvious physical barrier separating them. Instead, the data support a scenario of a *historical* midcontinent barrier. Bobcat populations in the east and west were likely separated by the relatively arid and treeless conditions in the center of the continent during the Pleistocene, but expanded around the time the glaciers receded (~11,000 years ago) and suitable habitat became more widely available.

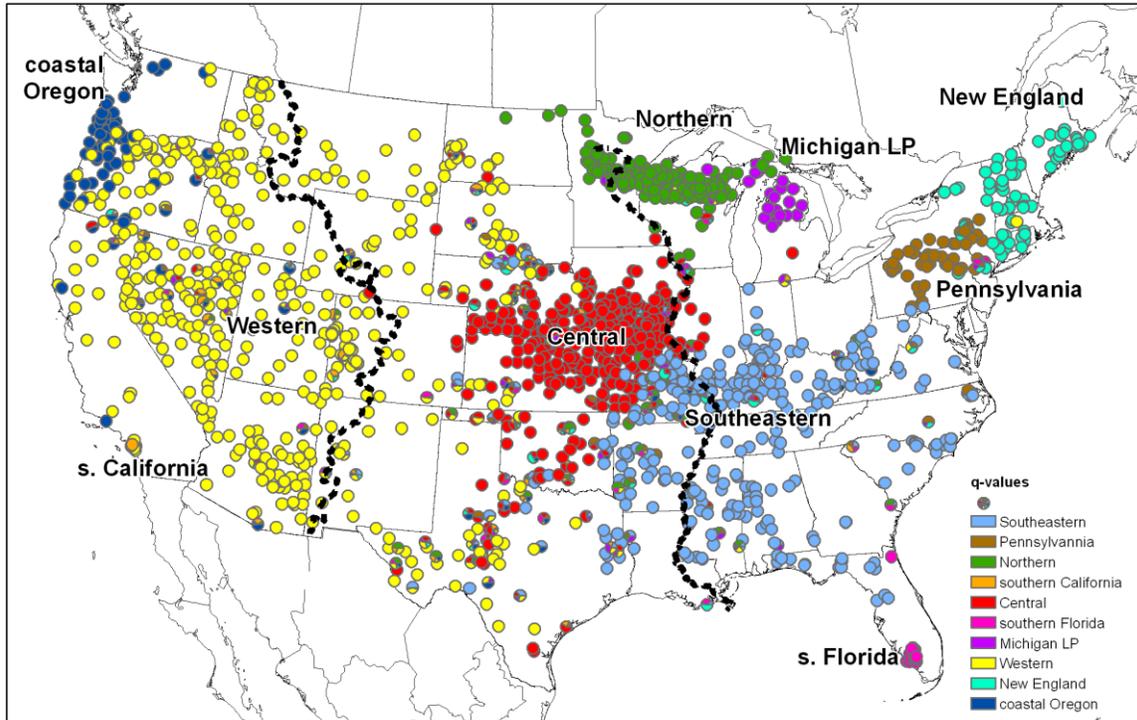
Within the two main bobcat lineages, additional substructure is evident, particularly in the eastern bobcats (Figure 2). Recent habitat loss and extirpation in places such as the Midwest and mid-Atlantic region seem to be contributing to population genetic structure. However, two prominent topographic features – the Mississippi River and Rocky Mountains – were not supported as significant genetic barriers. Ecological regions and environmental variables explained a small but significant proportion of genetic variation across the bobcat range. Although we only had a few samples from Mexico, they had unique genetic sequences. The finding suggests additional genetic variation may reside in Mexico's bobcats and warrants additional sampling to investigate the potential distinctiveness of Mexico's bobcat population. Overall, this study emphasizes that large scale landscape changes, whether caused by glaciers or human activities, have ecological and evolutionary effects even for a highly mobile generalist like the bobcat.

As a carnivore and furbearer, the bobcat is a species of ecological and economic importance, and the understanding of population structure that we have gained through this study is beneficial for properly managing and conserving this species. Bobcat populations do not correspond to political boundaries, as we found that most genetic units occur across several states. These findings suggest management strategies for this

species should involve regional cooperation, as management decisions in one state may influence bobcat populations in surrounding states. This may be especially relevant for states in which bobcats are still absent from portions of the landscape, as expansion may depend largely on the population dynamics in neighboring states. Another relevant finding from our study is that bobcats in eastern and western U.S. have had distinct evolutionary histories, and may be adapted to the particular environments they inhabit. Thus, from an evolutionary standpoint, it is important in the future to maintain healthy populations from both regions. Furthermore, our limited data on Mexico indicate the need for further research into the potential uniqueness of the federally endangered Mexican bobcat, which may be of particular conservation and evolutionary importance.



**Figure 1.** Distribution of mtDNA subclades. The dashed black line represents the approximate location of a genetic boundary between eastern and western bobcats. The map also illustrates the location of ice sheets and lakes during the last glacial maximum, and the white lines reflect bobcat morphological subspecies.



**Figure 2.** Assignment of individuals to each of the 10 bobcat subpopulations inferred from genetic (microsatellite) analysis. The black dashed lines depict two prominent topographic features – the Continental Divide in the west and the Mississippi River in the east – which did not appear to function as significant genetic barriers at this spatial scale.