

# Effects of Ancient Climate Change on Population Size of *Thylamys* Mouse Opossums

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## Introduction

Species of the genus *Thylamys*, commonly known as fat-tailed mouse opossums, are small marsupials (Fig. 1). They reside in South America in Peru, Brazil, Chile, Bolivia, and Argentina, populating a variety of different habitats surrounding the Andes Mountains. These habitats include tropical and temperate habitats such as lowland savannas, mid-altitude cloud forests, and high deserts (e.g. Fig. 2; Giarla et al., 2010). The tropical and sub-tropical Andes Mountains in South America are a very biodiverse region (Myers, et al. 2000), making it an ideal area in which to study the impact of ancient environmental change. Three *Thylamys* species were studied, *T. sponsorius*, *T. pallidior*, and *T. venustus*, which were subdivided into haplogroups based on mitochondrial data from Giarla et al. (2010; Fig. 3).



Fig. 1 *Thylamys pallidior*

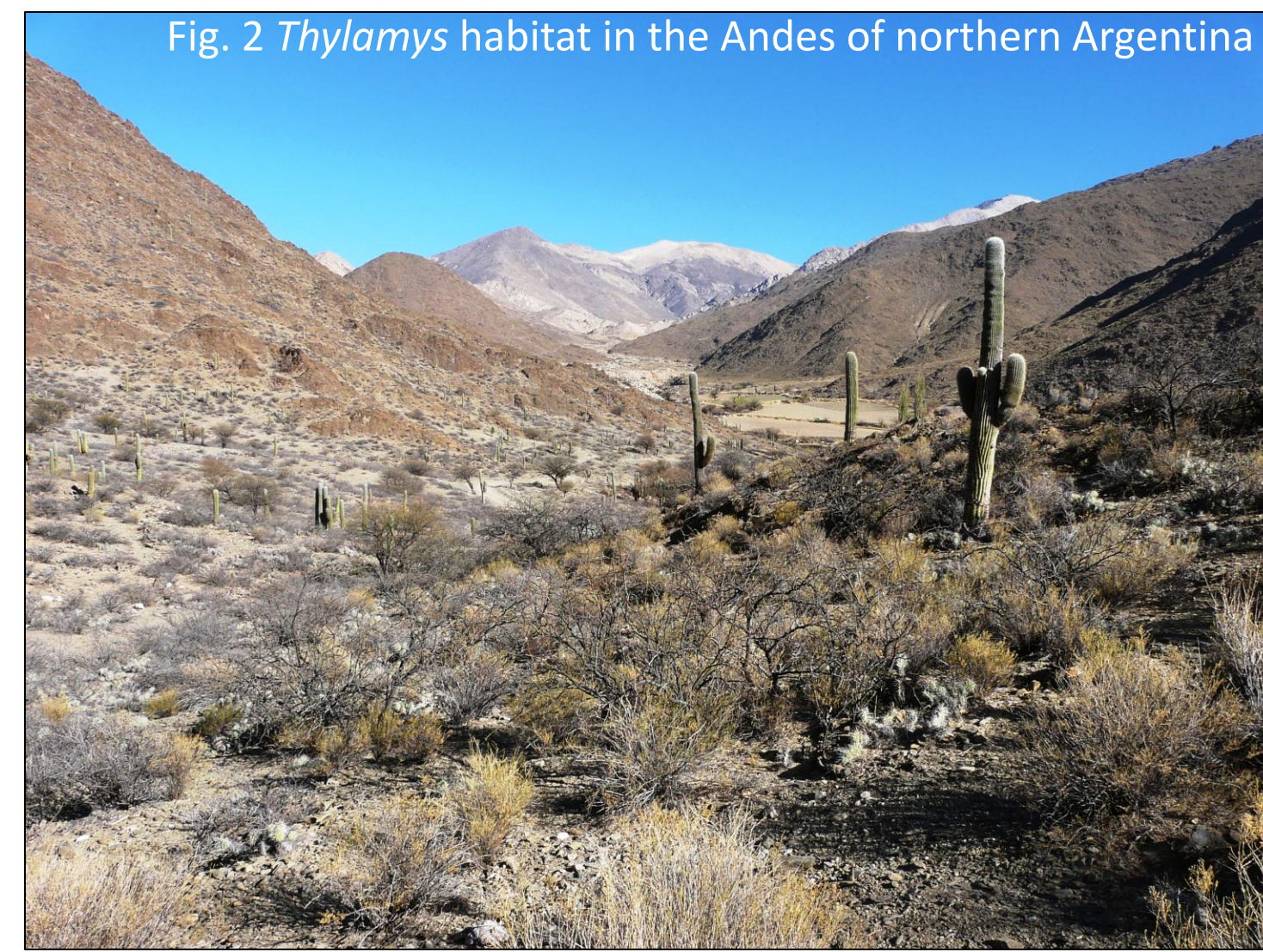
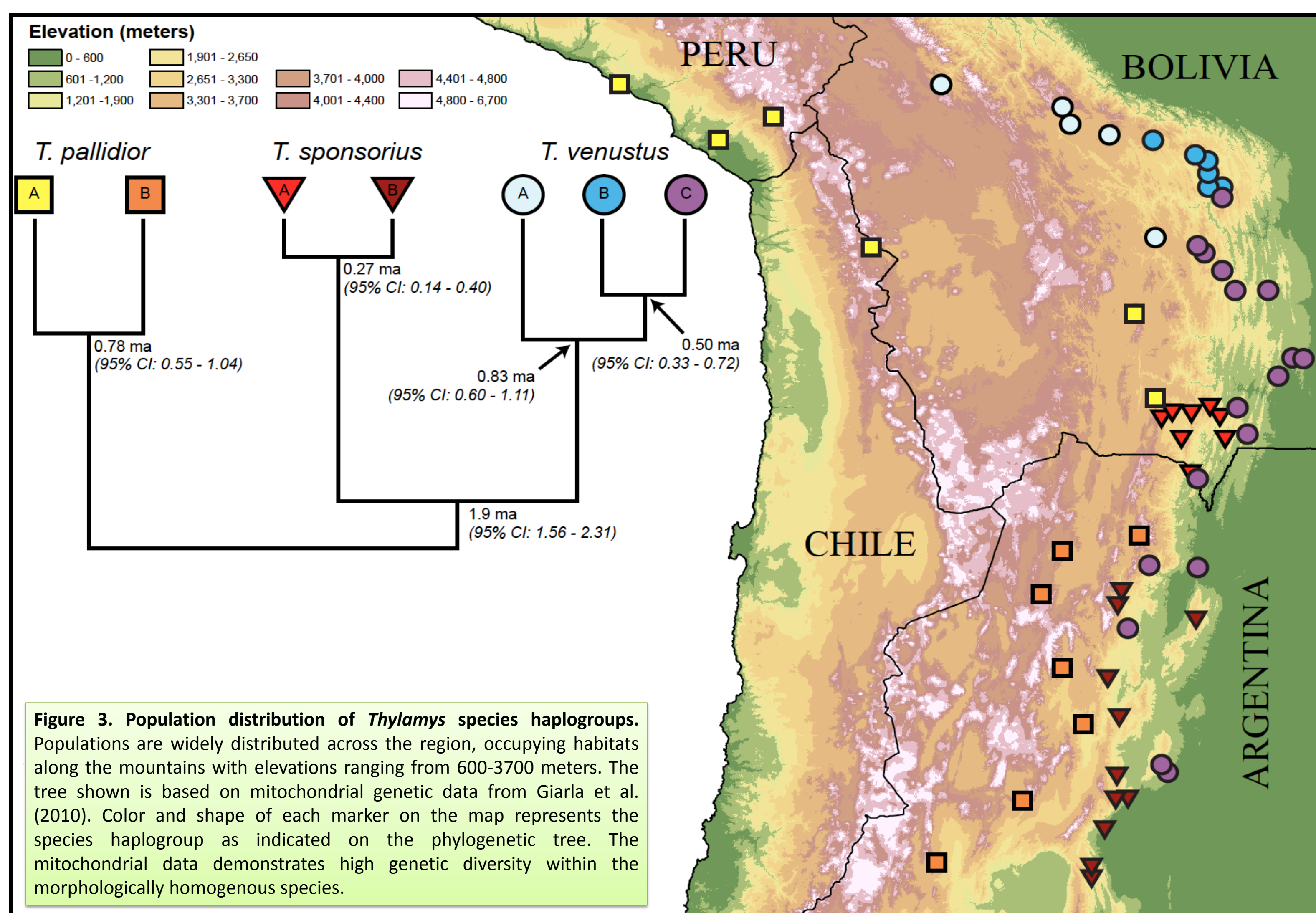


Fig. 2 *Thylamys* habitat in the Andes of northern Argentina

**Climate change:** The specific time periods examined were the Pleistocene (2 million years ago – 10,000 years ago) and the Holocene (10,000 years ago – present). Since the peak of the last ice age, approximately 23,000 years ago, climates have grown increasingly warmer on earth. This warming affected the location, quality, and overall area of the habitats available to organisms. In turn, these shifts likely affected the population size, genetic diversity, and potential for speciation among organisms in these changing habitats (Hewitt, 2004). This warming is likely to have had profound effects on species that live in mountainous regions because their habitats are limited. The habitat of a species adapted to cool and dry montane regions will decrease in area when climates warm, becoming constricted to more isolated and higher-elevation parts of the mountain.

**Niche Conservatism:** The ecological concept of niche conservatism suggests that, over relatively short time-scales, organisms are expected to follow shifts in their habitat if it moves due to climate change rather than adapting to a new environment (Wiens and Graham, 2005). This is because range shifts might be less restricted than adapting to a new habitat. As climates warm, colder habitats decrease in size, limiting the areas where organisms that occupy these habitats can thrive.

**HYPOTHESIS:** The effective population sizes of *Thylamys sponsorius*, *T. pallidior*, and *T. venustus* have decreased since the last glacial maximum as a result of climate warming causing their habitats to move farther up the mountains and decrease in area.



## Methods

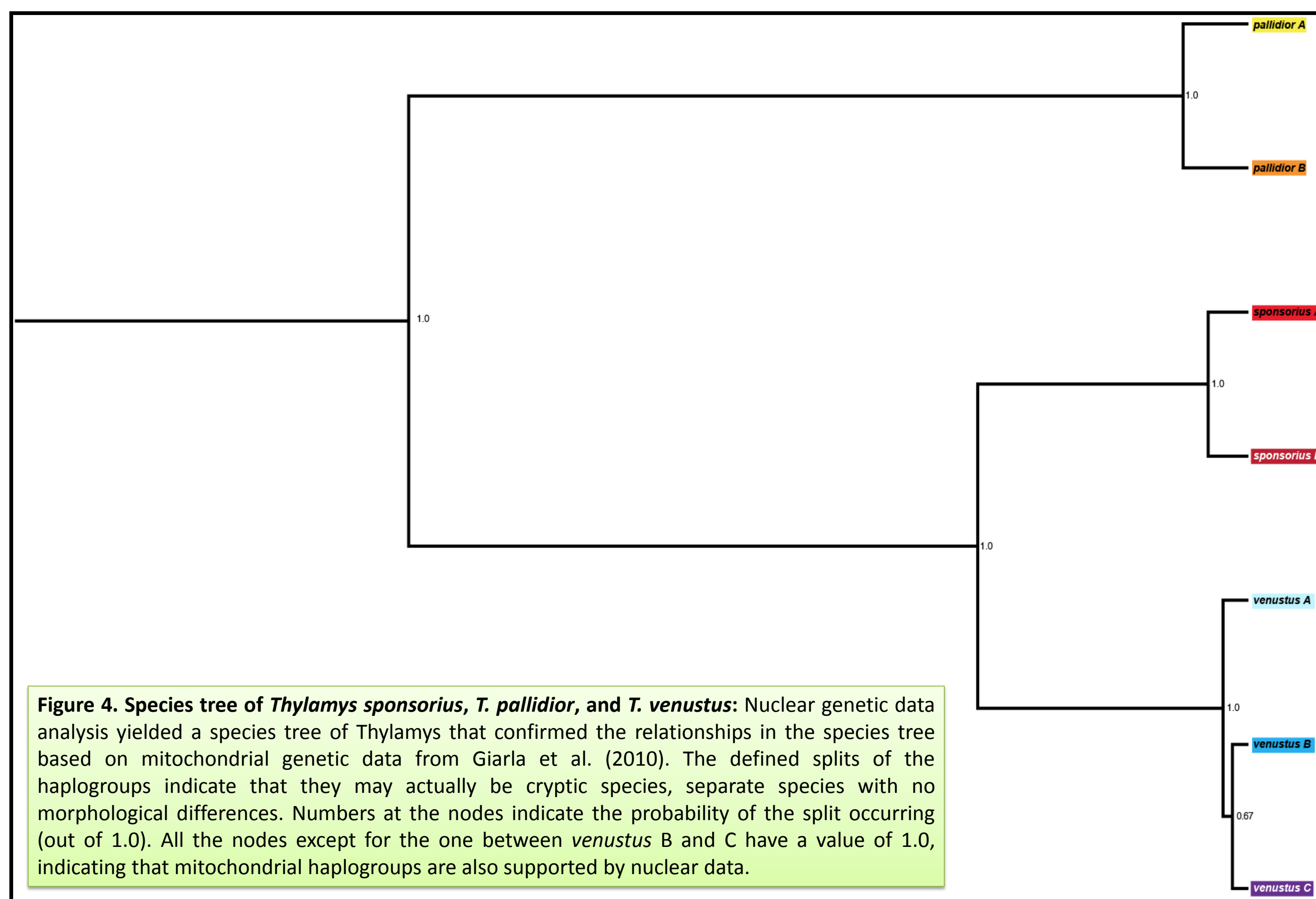
**PCR and Sequencing of Nuclear Loci:** Multilocus nuclear genetic data was used to examine the evolutionary history of *Thylamys* populations. Fifteen unlinked nuclear loci were amplified across multiple individuals for each species using Polymerase Chain Reaction (PCR). PCR products were sequenced by the BioMedical Genomics Center and the DNA sequences were edited using Sequencher software and aligned using Clustal X in preparation for data analysis.

**Species Tree Analysis:** Data from fifteen nuclear loci and one mitochondrial locus were used to estimate a species tree among haplogroups. Instead of simply joining all of the different loci together into one large dataset (a technique that has been known to lead to spurious results [Heled and Drummond 2010]), each locus was modeled independently. The resulting pool of independent gene trees was used to estimate the overall "species tree", a representation of population splitting over time. The species tree analysis was run using the StarBeast algorithm in the BEAST software package (v. 1.7.1; Drummond et al. 2012).

**Population Size Changes Over Time:** In order to trace population size changes over the past 50,000 years, Bayesian skyline plots (BSPs) were constructed using BEAST v 1.7.1. Genetic data were calibrated to an absolute timescale by constraining the mitochondrial loci to a strict "molecular clock" of 0.05 substitutions per site per year and allowing the program to estimate the evolutionary rates for each of the nuclear genes relative to this fixed rate (Heled and Drummond 2008).

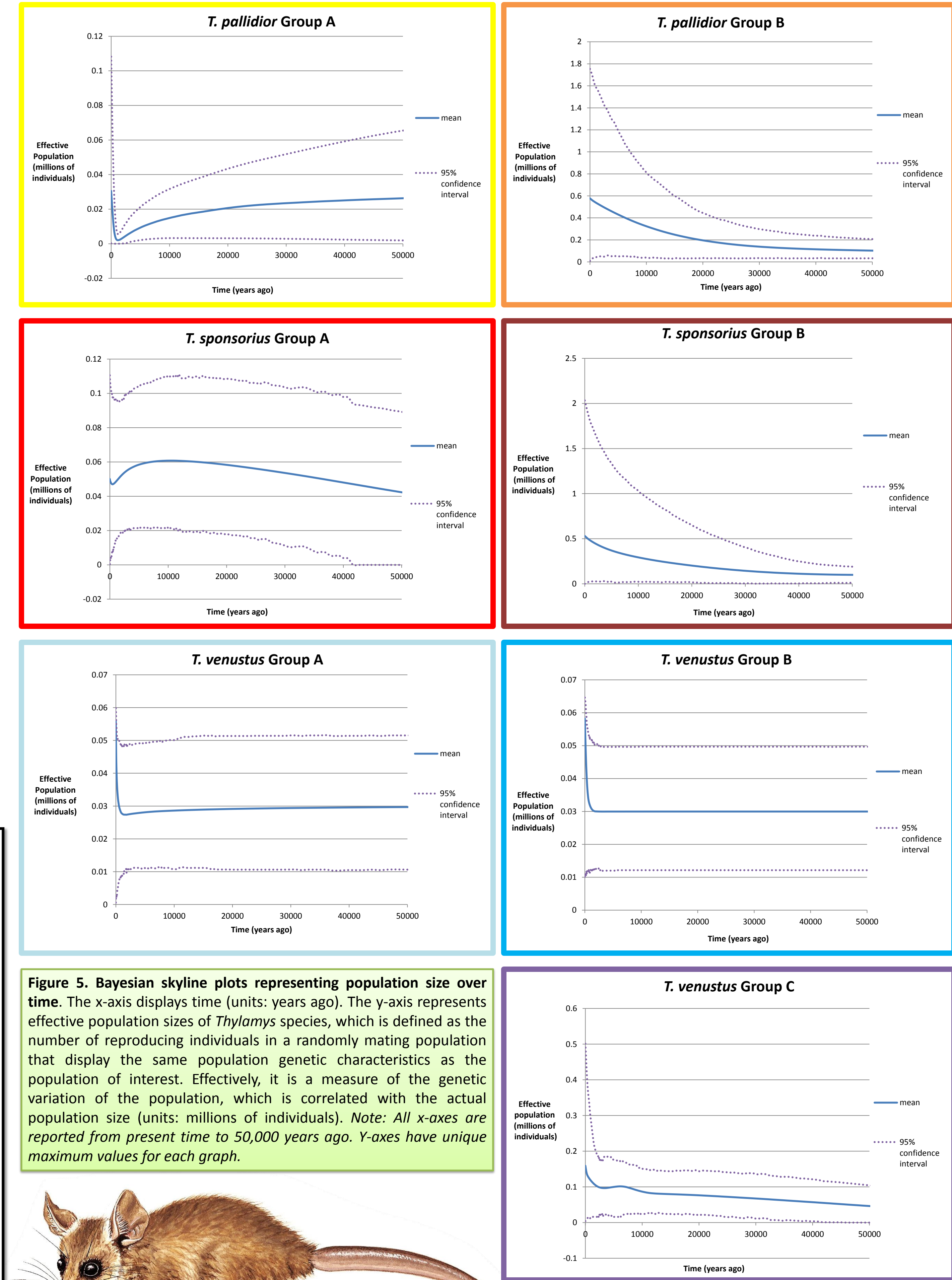
## Results and Discussion

Most of the results did not support the hypothesis, as an increase or no change in population size was observed for many of the species haplogroups. However data from *T. sponsorius* Group A and *T. pallidior* Group A supports the hypothesis by exhibiting decreases in population sizes. *T. venustus* Groups A and B had steady population sizes. *T. pallidior* and *T. sponsorius* B Groups along with *T. venustus* Group C had population increases. These results do not support the hypothesis. A possible explanation for an increase in population size could be that their populations are migrating further south to cooler climates. Populations of these species haplogroups occur further south than the other haplogroups (see Fig. 3 map). Migration southward would provide colder climate habitats without decreasing the habitat sizes. This possible explanation is also supported by the concept of niche conservatism. This explanation could be observed as support to climate warming affecting population sizes.



**SIGNIFICANCE:** This project is significant in a broader context than just studying the changes in *Thylamys venustus*, *T. pallidior*, and *T. sponsorius* population sizes. It leads to a better understanding of speciation of the *Thylamys* genus and of the evolutionary history of *Thylamys* in general, a genus that has received little attention from researchers. In addition, it provides an illustration of population shifts that have occurred with climate change. While not all of the data supports the hypothesis, another possible explanation related to climate change could be a reason for the increase of some population sizes. The population decreases that have occurred raise concerns for the existing genetic diversity of these subgroups.

This study is also important to conservation. Conservation of mammal diversity is especially critical in an extremely biodiverse region such as the Tropical Andes, an area facing extensive habitat degradation due to human activity (Myers et al., 2000). This study could help biologists tailor their conservation efforts to the specific needs of *Thylamys* species. Ultimately, this project arouses the question: what will happen in the future if the climate continues to grow warmer? Could more climate changes lead to significant shifts in population sizes or even possible extinction of *Thylamys* species that live in the Andes?



## Acknowledgements

I would like to acknowledge my faculty mentor, Dr. Sharon Jansa. I would also like to thank EEB Ph.D. candidate Tom Giarla for his help, support, and guidance throughout this research project. Funding for this project was provided by the University of Minnesota Undergraduate Research Opportunity Program and a National Science Foundation Grant to TCG and SAJ.

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