Forested sky islands to urban desert remnants: N.S. Upham, D.C. Rivera, M. Pierce, J.M. Alston*, J.R. Baez*, M.E. Bucci*, G.J. De Leon*, B.M. Dean*, N.A. Hernández Hernández*, S.C. Hess*, M.F. Investigating the island biodiversity of Arizona Jones*, S. Kraberger*, R.D. Liao*, S. Mohammadian*, G.L. Post*, A.L. Robles Fernández*, S.M. Smith*, K.L. Vargas*, L.J. Zamora Chavez*, small mammals and their symbionts A. Varsani, S. J. Hall, D.M. Rowsey * = alphabetical Arizona Island CAP-LTER All Scientists' Meeting, 2024 Arizona State University, School of Life Sciences **Biodiversity** Project Premise People Sites **Species** other desert Urban ecosystems are rapidly growing in A) central Arizona. At the same time, the montane forests of nearby Madrean sky NORTH islands have been isolated for the past ~10,000 years. These habitat islands of varying ages and origins within a 4-hour

drive from metro Phoenix makes for a fascinating theater in which to study island biodiversity dynamics.

Questions

Diversity and abundance:

•Are biogeographic principles of speciesarea and -isolation effects sufficient to explain community assembly in urban islands relative to baselines from nearby natural habitat islands, or does urbanization lead to non-analog species assemblages?

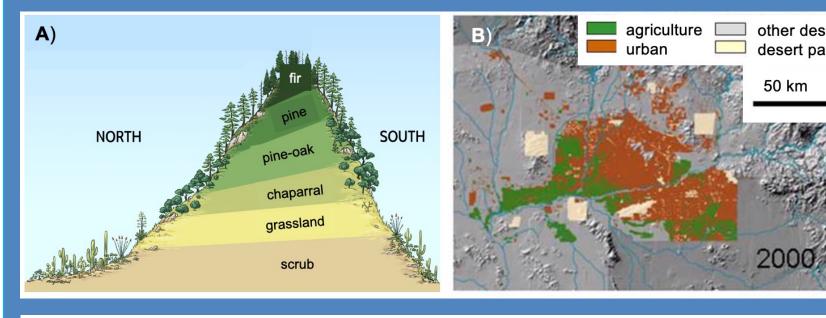
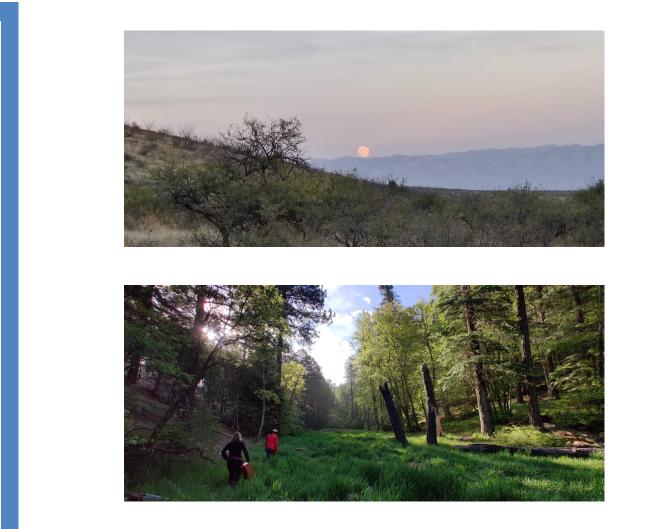


Fig. 1. Types of habitat islands in Central and SE Arizona, both (A) mountaintop sky islands of the Madrean system, and (B) urban islands in the Phoenix metro area. Sources: skyislandalliance.org, Chow (2011).









•Which species are present? At what abundances? Do some islands promote species with certain ecological traits (e.g., faster life history, greater dispersal ability, more general dietary niche)?

Ecological connectivity:

- To what extent are different species able to maintain gene flow across the metro Phoenix area?
- Does gene flow predict the sharing of symbionts (e.g., viruses) among sites?

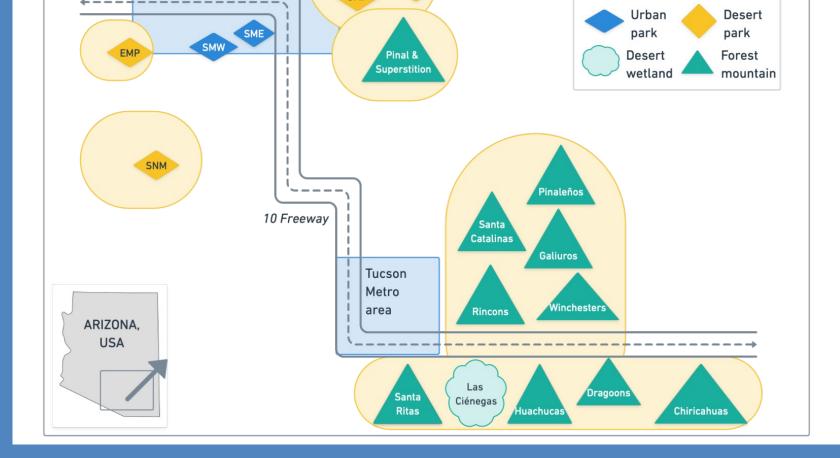
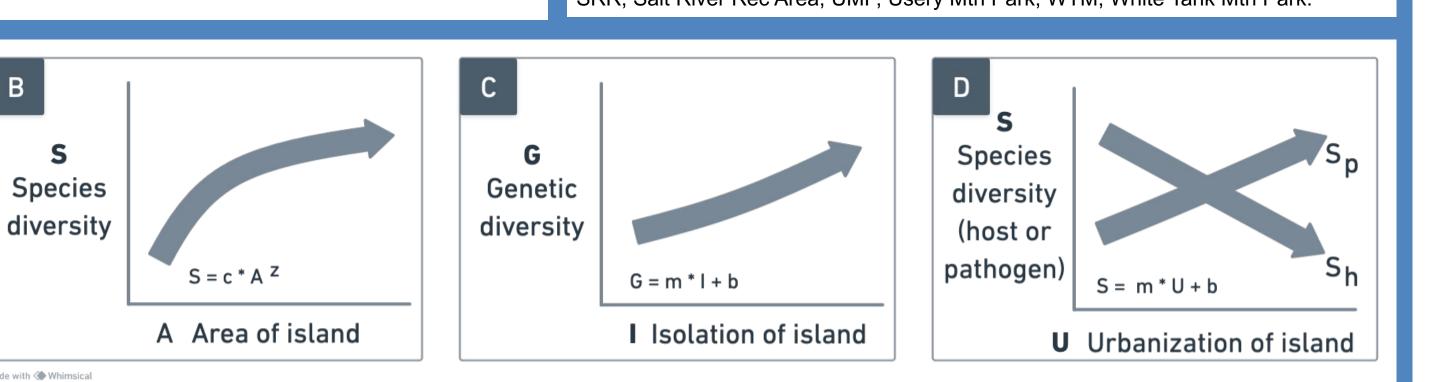


Fig. 2. Habitat islands of desert remnants in urban matrix vs. forested mountains in desert matrix targeted for sampling small mammals (rodents, bats, shrews) and their pathogens. (A) Simplified map of field sites (not to scale). Hypotheses to be tested, including the effects of (B) species-area, (C) isolation by distance (or time), and (D) urbanization. Abbreviations: DBG, Desert Botanical Garden; EMP, Estrella Mtn Park; LDP, Lost Dutchman St Park; MCM, McDowell Mtn Park; MVP, Mtn View Park; PWP, Piestewa Peak; SMW/SME, South Mtn Park west/east; SNM, Sonoran Des Nat Mon; SRR, Salt River Rec Area; UMP, Usery Mtn Park; WTM, White Tank Mtn Park.



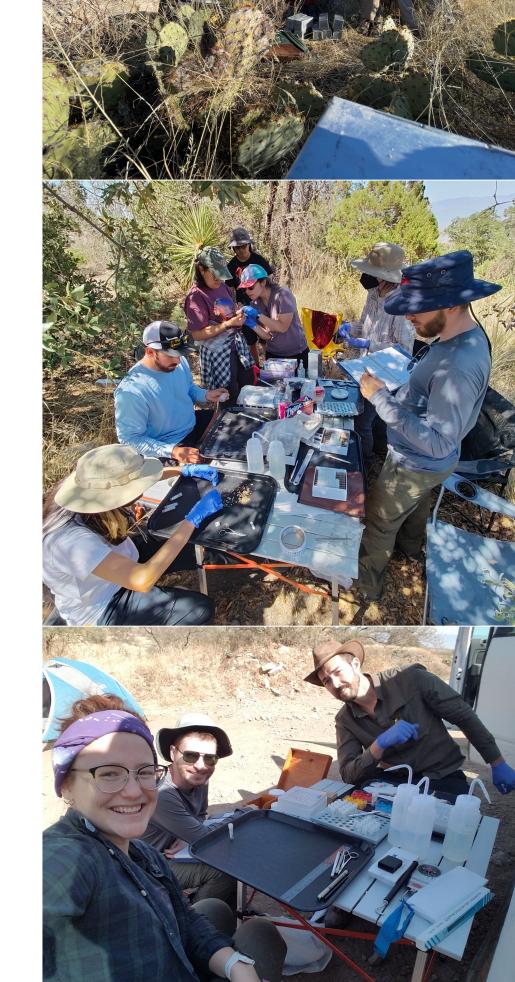












We are establishing a collaborative, multi-taxon effort to investigate the extent to which different wild species are able to remain ecologically connected – exchanging genes and symbionts – across varied habitat islands. This work builds on pilot studies of rodents and shrews in the Santa Catalina Mtns conducted from 2021-2023 with the ASU Natural History Collections. In 2024, we aim to start surveys of rodent, bats, and shrews in urban habitat islands of metro Phoenix (sampling mainly at CAP LTER sites) and in montane pine-oak/conifer forests of the Madrean sky islands (specifically the Galiuros, Winchesters, Dragoons, and Chiricahuas). Importantly, this work constitutes the first systematic surveys of small mammals at several of the sites, and the first efforts to preserve tissue samples (e.g., liver, kidney, lung, blood, feces) for metagenomic analyses of gene flow and symbiont sharing (i.e., sequencing of all DNA present in a given sample). Does the extent of current genetic connectivity predict the symbionts shared (i) among individuals?

Urban desert remnants

Average Percent Impervious Surface at CAPLTER Sites	Legend
The Central Arizona-Phoenix Long Term Ecological Research (CAP-LTER) project has been ongoing since 1997.	Average Percent Impervious Surfa • 0%-1%
Displayed here are 239 sites that previously or currently are monitored and their respective values for average percent impervious surface cover.	• 1% - 22%
Datasets were created by Jeff Haight through use of the CAPLTER Data Portal and the 2021 National Land Cover Database,	23%-42%43%-57%
Created by Morgan Pierce 01-11-24	• 57%-80%

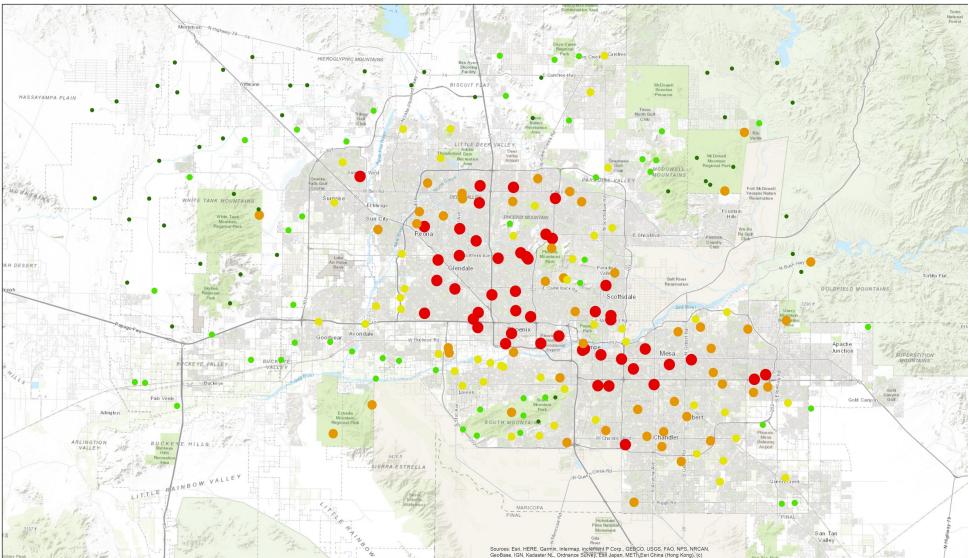


Fig. 3. Possible sampling sites across an urbanization gradient in Metro Phoenix

Forested sky islands

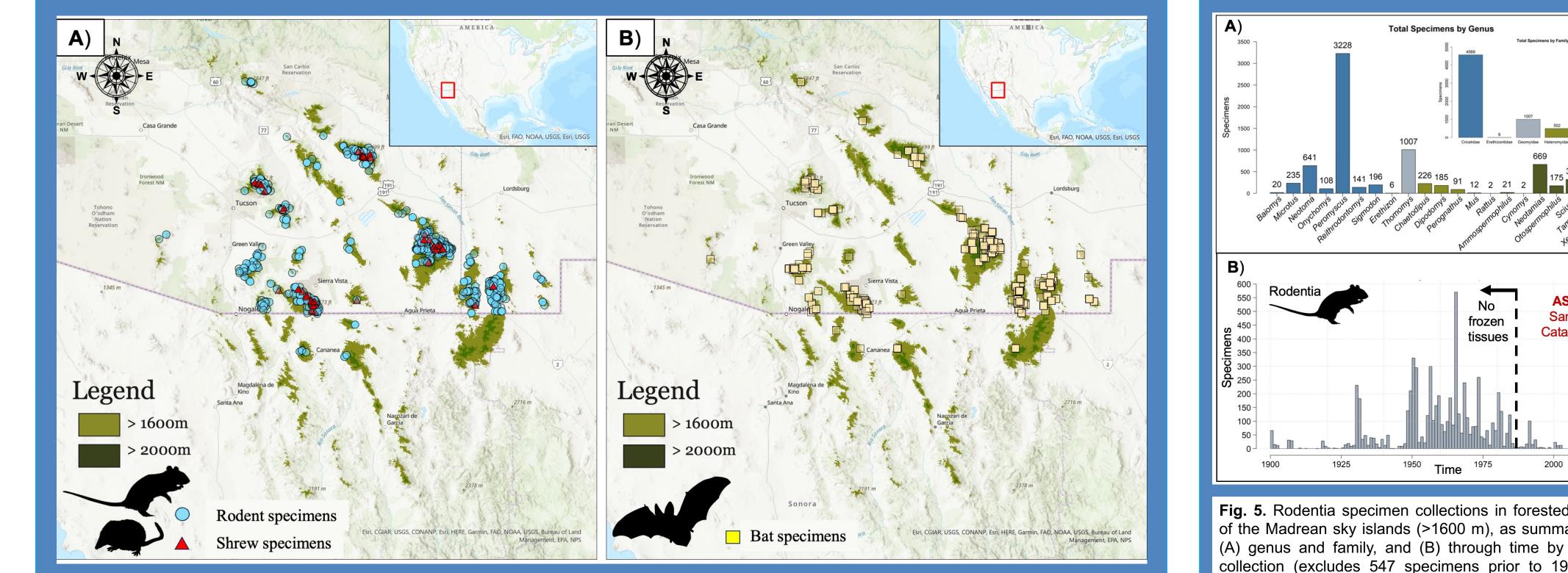
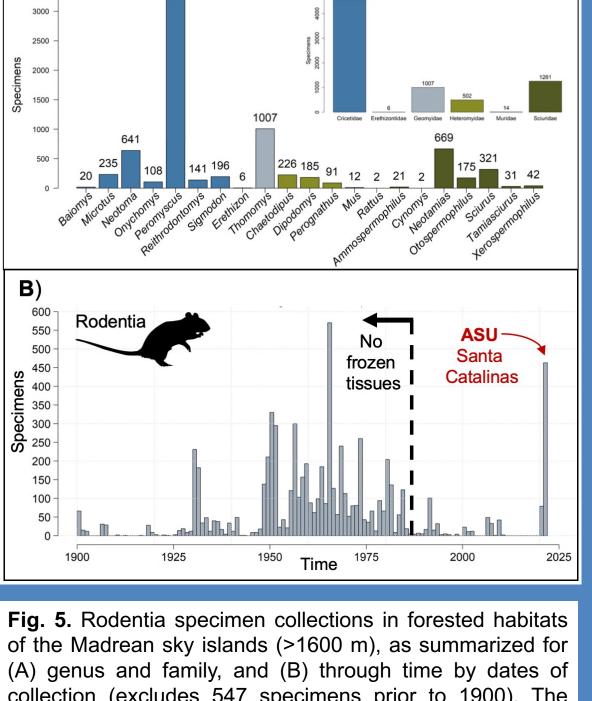
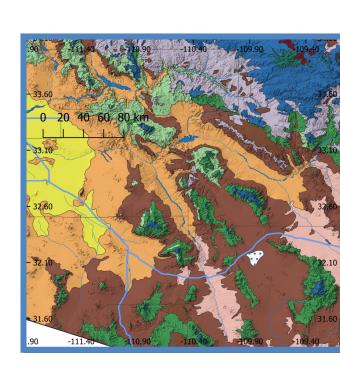


Fig. 4. All known records of preserved specimens for small mammals in the Madrean sky islands, summarized for (A) Rodentia (blue circles) and Eulipotyphla (red triangles); and (B) Chiroptera (yellow squares). Note the large gaps in sampling on several mountains. Pine-oak habitats >1600 m are shown in light green, while conifer habitats >2000 m are in dark green. Records download: Global Biodiversity Information Facility (GBIF) on 10 July 2023.

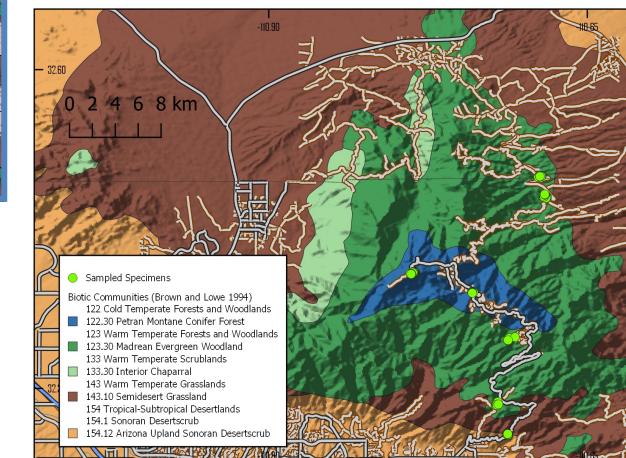


collection (excludes 547 specimens prior to 1900). The date of 1985 is used as a rough point after which collectors began freezing animal tissues for DNA analysis. The recent increase in rodent specimens is due to the 2021-2023

Pilot study: Santa Catalina Mountains



In 2021-2023, we sampled rodents and shrews at 10 sites for 400 trap-nights each using Sherman folding live-traps. Sites were matched to the plant and insect sampling of Moore et al. (2013).



Viruses

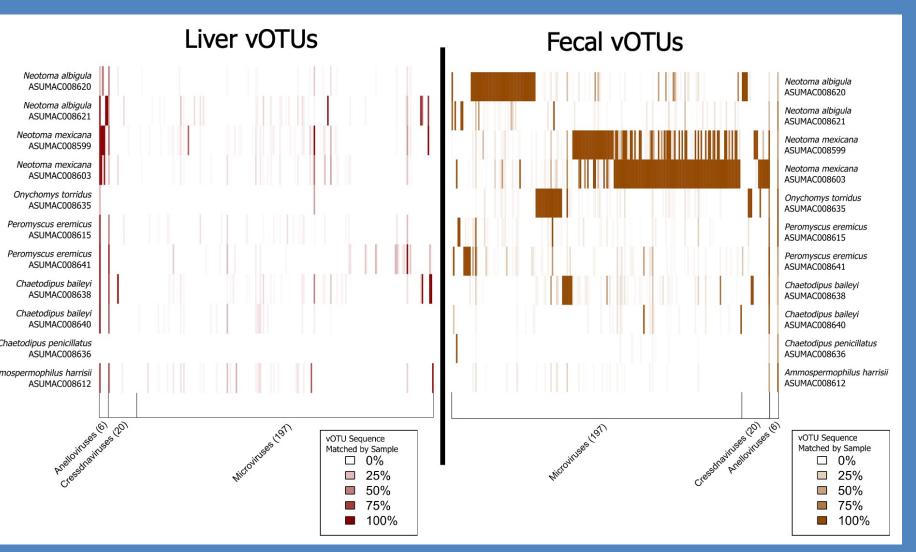


Fig. 6. Double-stranded DNA viruses collected from 11 rodent specimens, comparing viral taxa (vOTUs) from liver tissue versus feces. Results include: Anelloviruses – 6 OTUs from 3 specimens (all from liver); Cressdnaviruses – 20 OTUs from 6 specimens (most from feces); Microviruses – 197 OTUs from 9 specimens (most from feces).

Rodents and shrews

Summary statistics:

- 1651 tissue samples
- 369 individuals
- 150 voucher specimens

o 12 different tissue samples, 4 different voucher specimen prep types

315 specimen images

Taxonomy:

16 species, 9 genera, 4 families. 2 orders

- Cricetidae
 - Neotoma albigula, N. mexicana, Onychomys torridus, Peromyscus boylii, P. eremicus, P. leucopus, P. maniculatus/melanotis?, *Reithrodontomys fulvescens, R. megalotis, Sigmodon ochrognathus*
- Heteromyidae
 - Chaetodipus baileyi, C. intermedius, C. penicillatus
- Sciuridae
 - Ammospermophilus harrisii, Neotamias dorsalis
- Soricidae
- Sorex monticolus