



Wildlife surveillance

NASEM Valley Fever Workshop

Paris Salazar-Hamm, Ph.D.

Biorepositories can be leveraged for pathogen surveillance and discovery

- Biorepositories contain >225 million specimens
- Museum of Southwestern Biology ~250,000 tissues

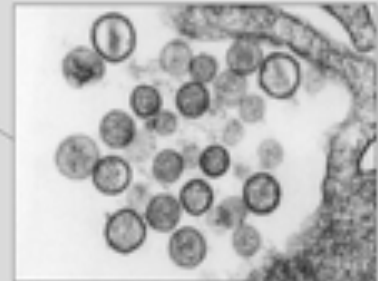




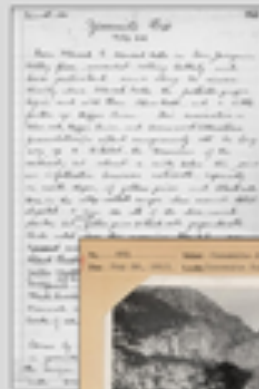
Geo-referenced locality



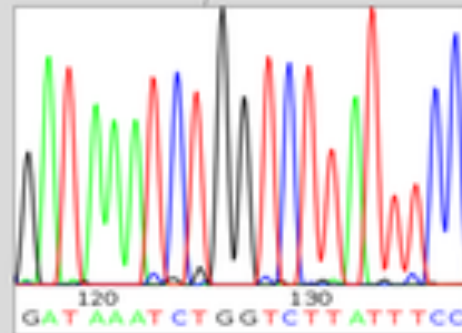
Ecto & endo parasites



Virus isolates



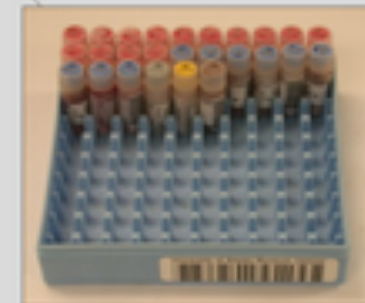
Field notes, ecological data



Genomic data



Publications



Ultrafrozen tissues

Biorepositories can be leveraged for pathogen surveillance and discovery



Batrachochytrium dendrobatidis
causing chytridiomycosis



Pseudogymnoascus destructans
causing white-nose syndrome



Ophidiomyces ophiodiicola
causing snake fungal disease



Hantavirus/Sin Nombre virus



SARS-CoV-2 causing COVID-19



Ebola and Marburg viruses
causing hemorrhagic fever

Breathing can be dangerous: Opportunistic fungal pathogens and the diverse community of the small mammal lung mycobiome

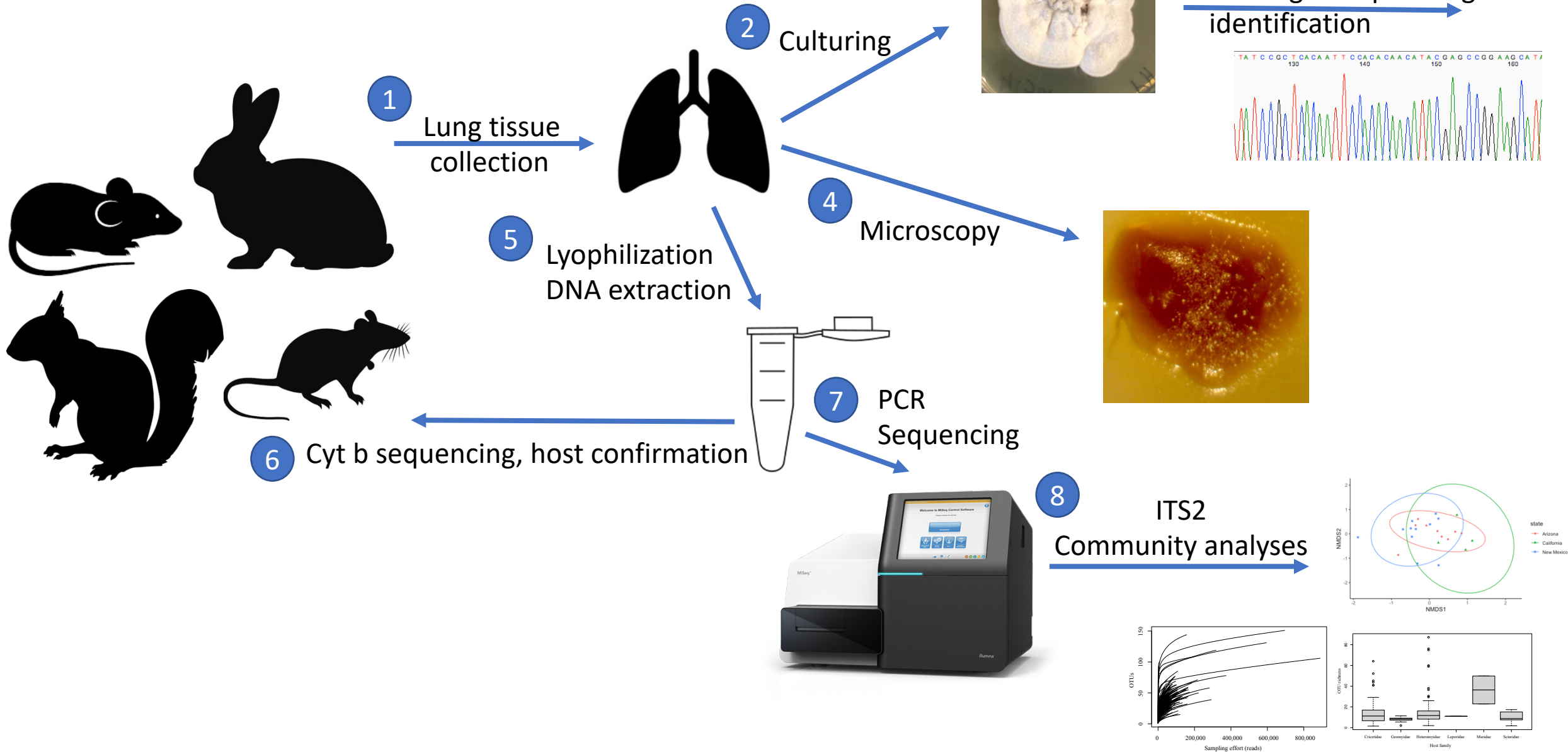
Paris S. Salazar-Hamm^{1*}, Kyana N. Montoya¹, Liliam Montoya²,
Kel Cook¹, Schuyler Liphardt¹, John W. Taylor²,
Joseph A. Cook^{1,3} and Donald O. Natvig¹

Front. Fungal Bio. 3:996574.
doi: 10.3389/ffunb.2022.996574

Questions

1. Can *Coccidioides* be detected in small mammals in the southwestern United States?
2. Can museum samples allow us to determine areas of Valley Fever endemicity?
3. How does the presence of *Coccidioides* affect the lung mycobiome?

Methods workflow



Questions

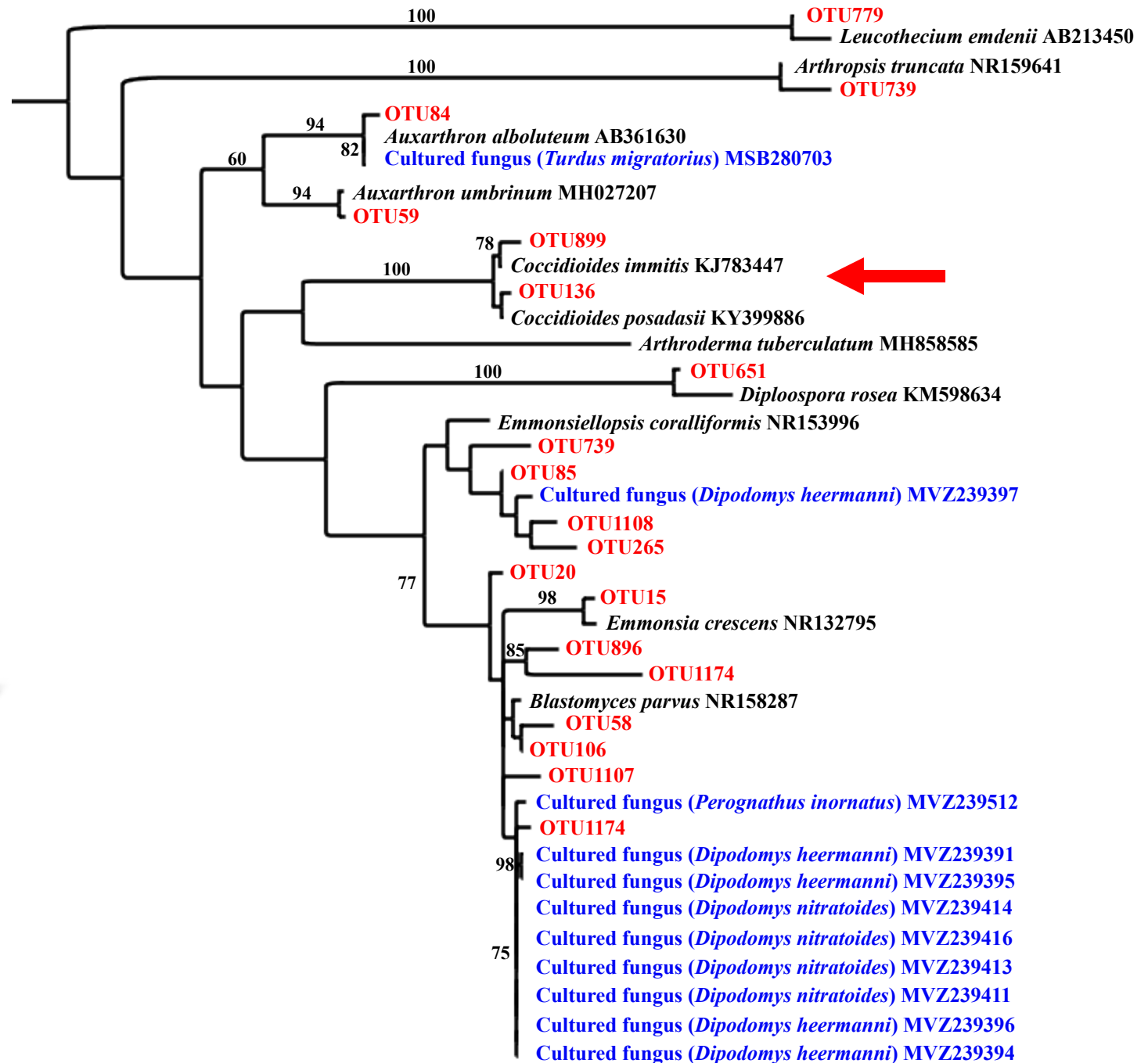
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Maximum likelihood tree of Onygenalean fungi

Illumina OTUs = red

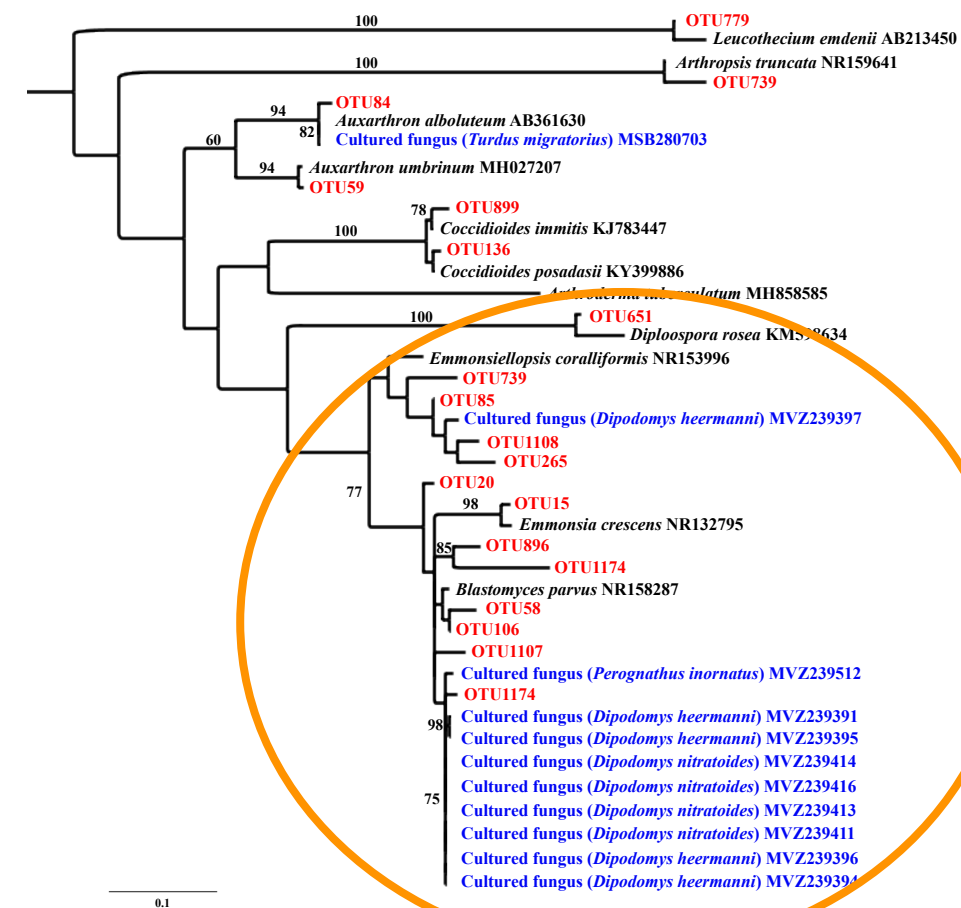
Cultures = blue

GenBank = black

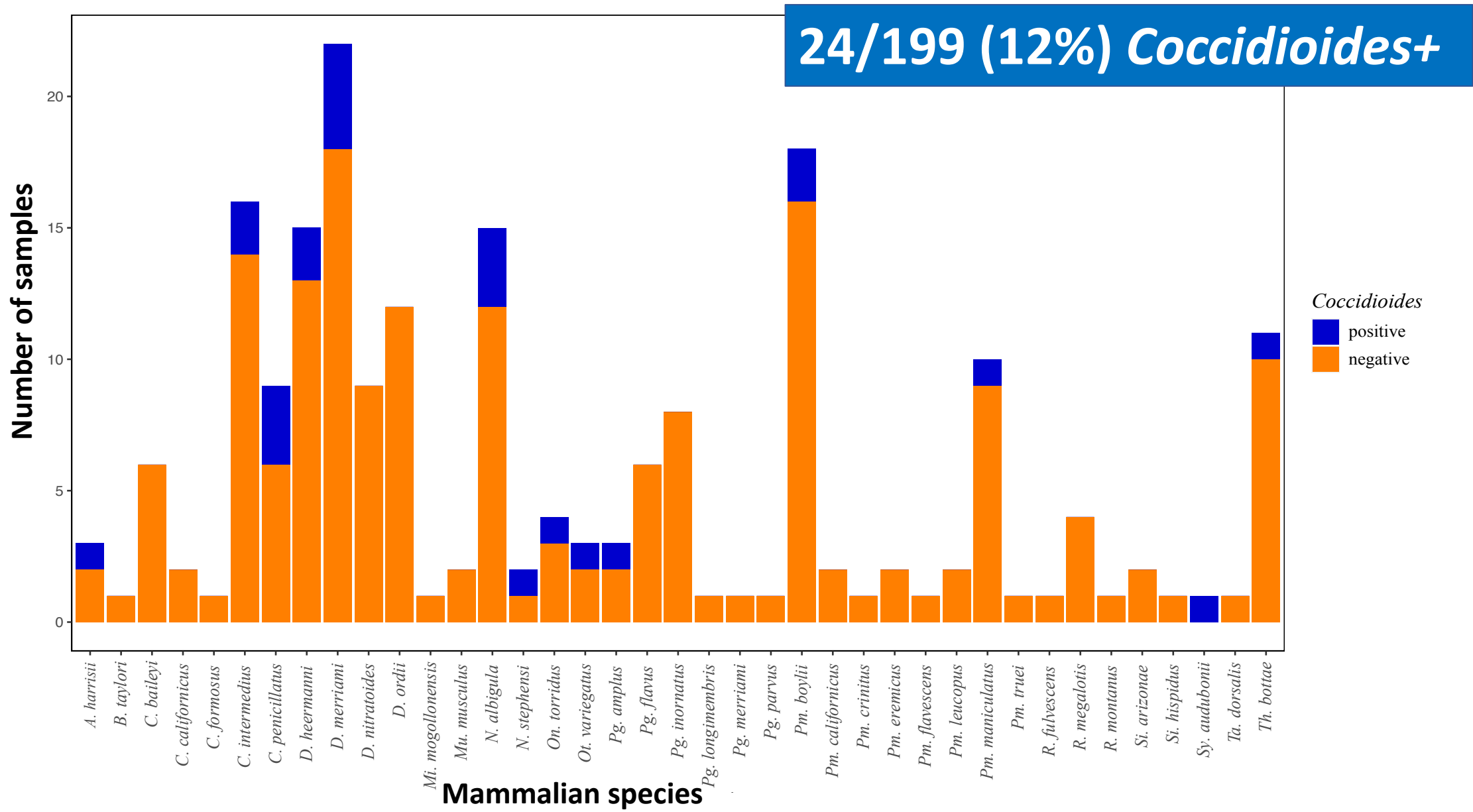


Ilan S. Schwartz, Chris Kenyon, Peiying Feng, Nelesh P. Govender, Karolina Dukik, Lynne Sigler, Yanping Jiang, J. Benjamin Stielow, José F. Muñoz, Christina A. Cuomo, Alfred Botha, Alberto M. Stchigel, G. Sybren de Hoog

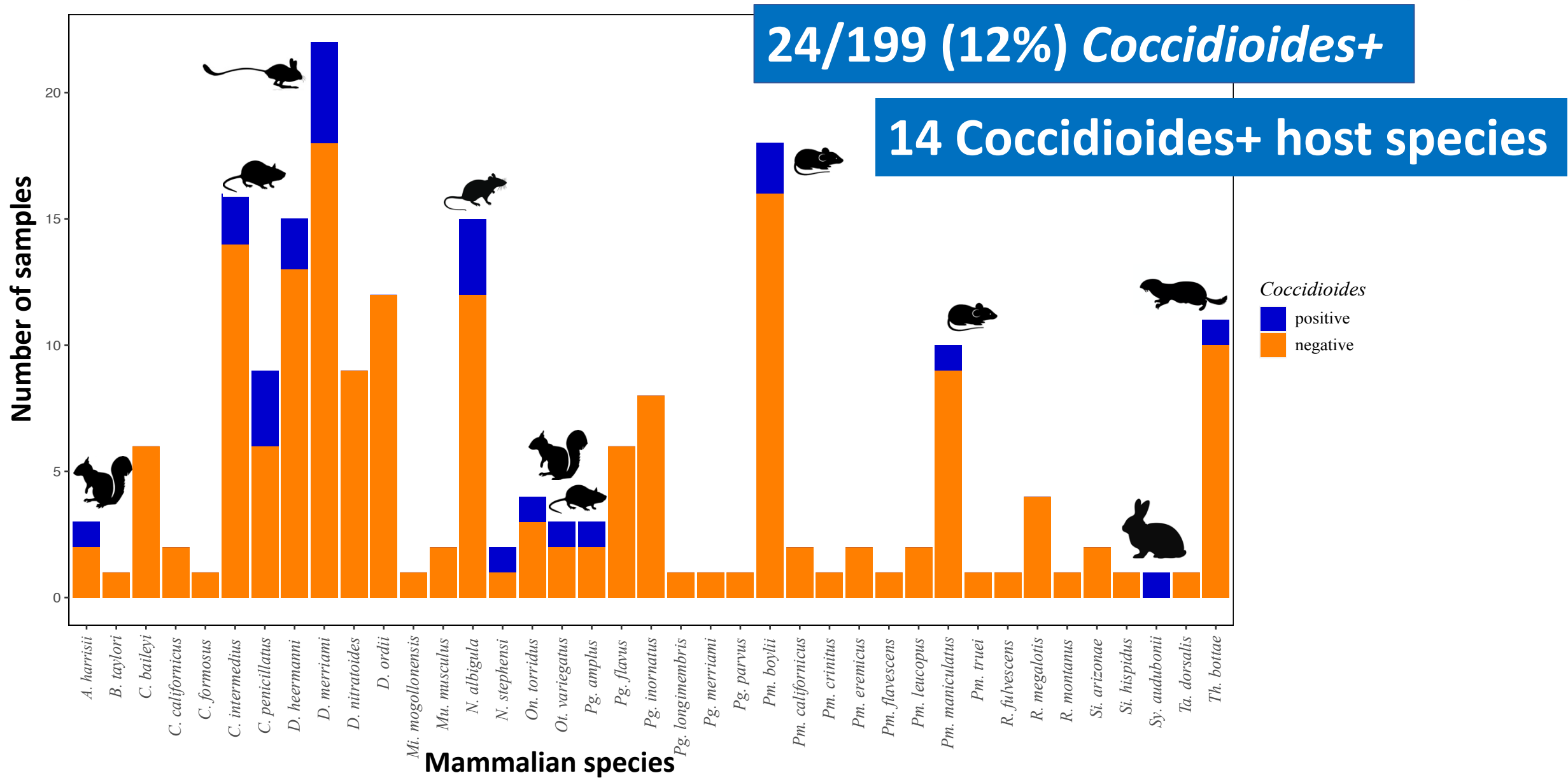
Time Period	Blue Bar (Cases)	Orange Bar (Cases)
before 1970	1	0
1970-1975	5	1
1976-1980	3	0
1981-1985	1	0
1986-1990	5	0
1991-1995	14	4
1996-2000	12	1
2001-2005	2	2
2006-2010	5	9
2011-2015	1	49



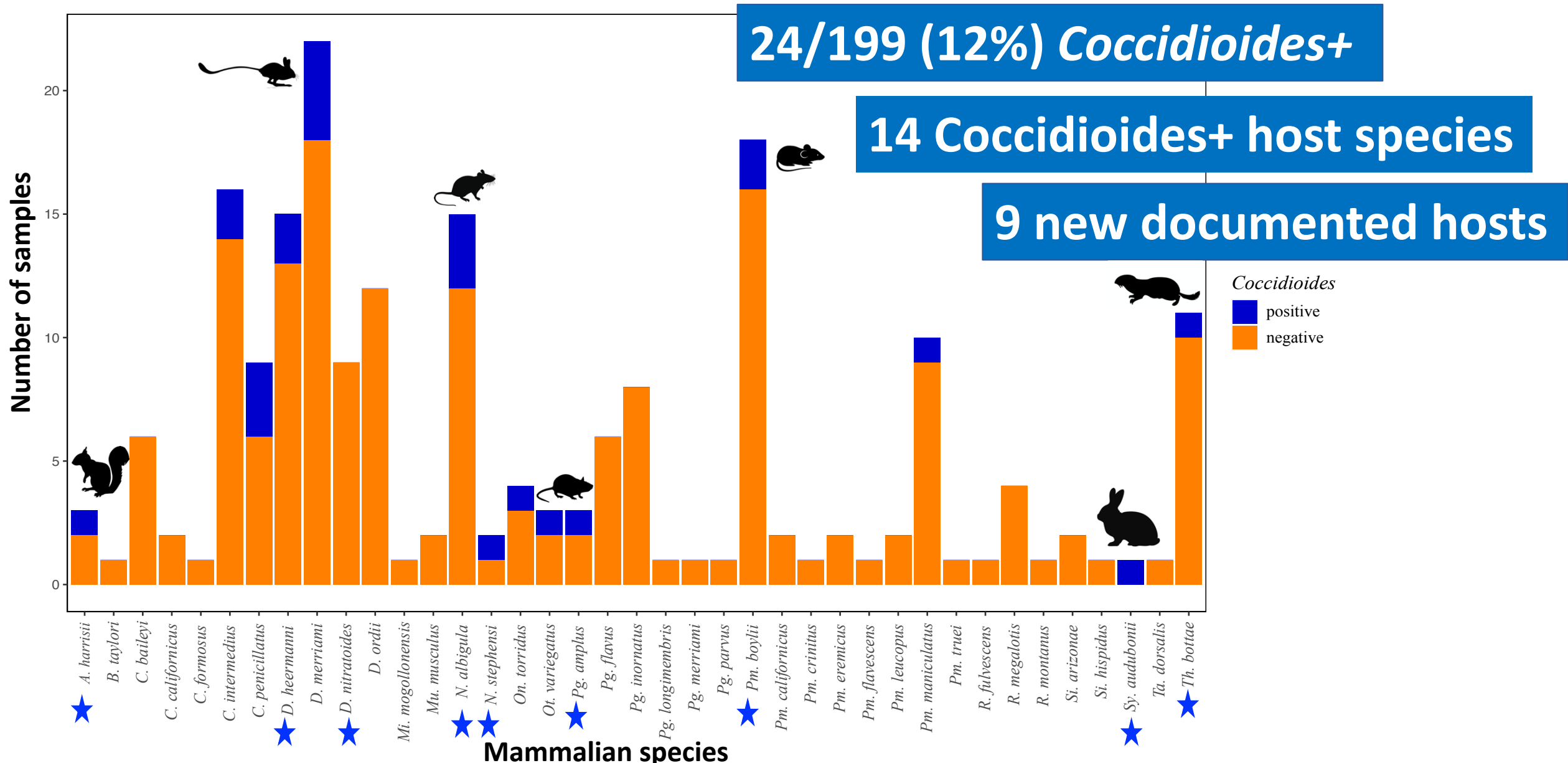
Coccidioides presence in small mammals



Coccidioides presence in small mammals

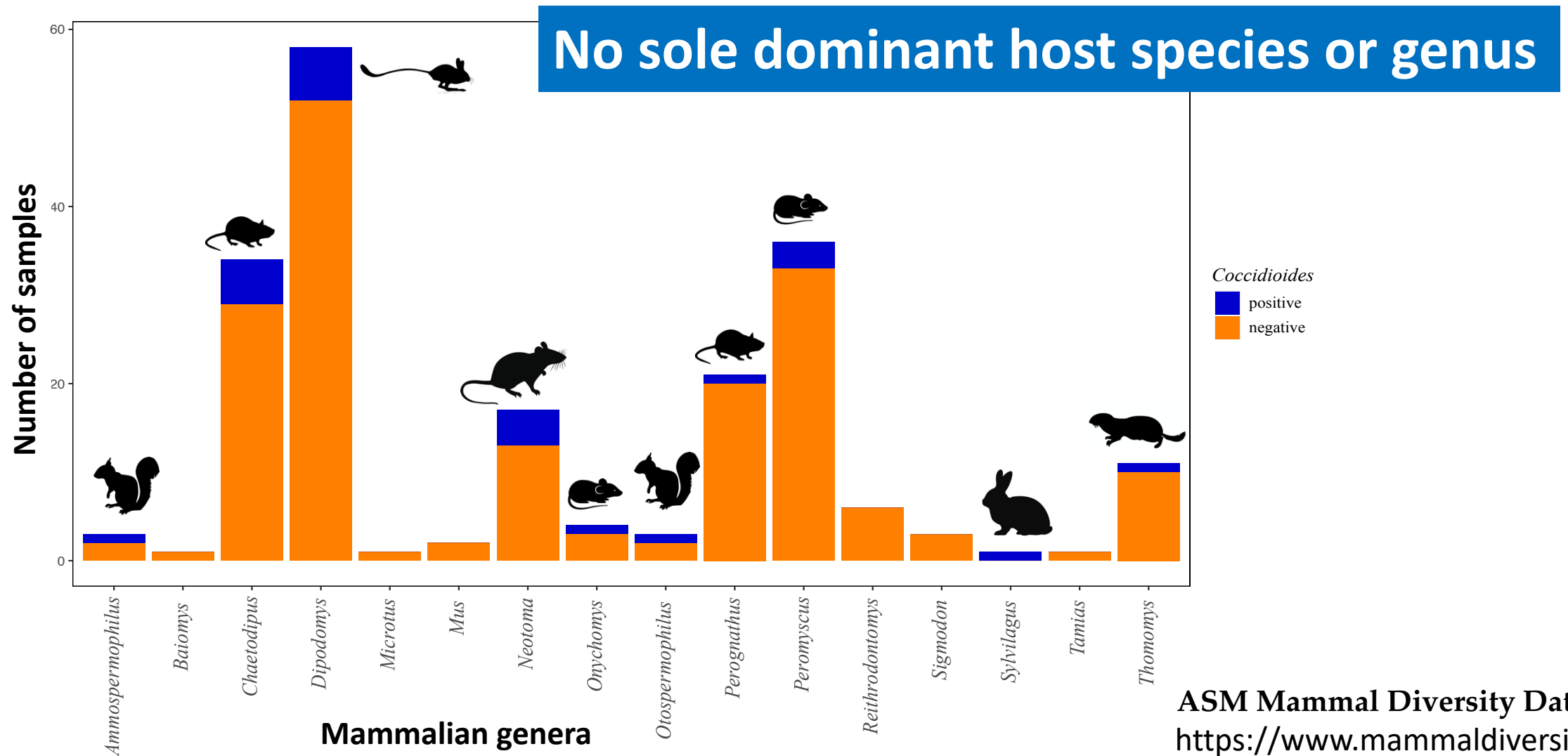


Coccidioides presence in small mammals





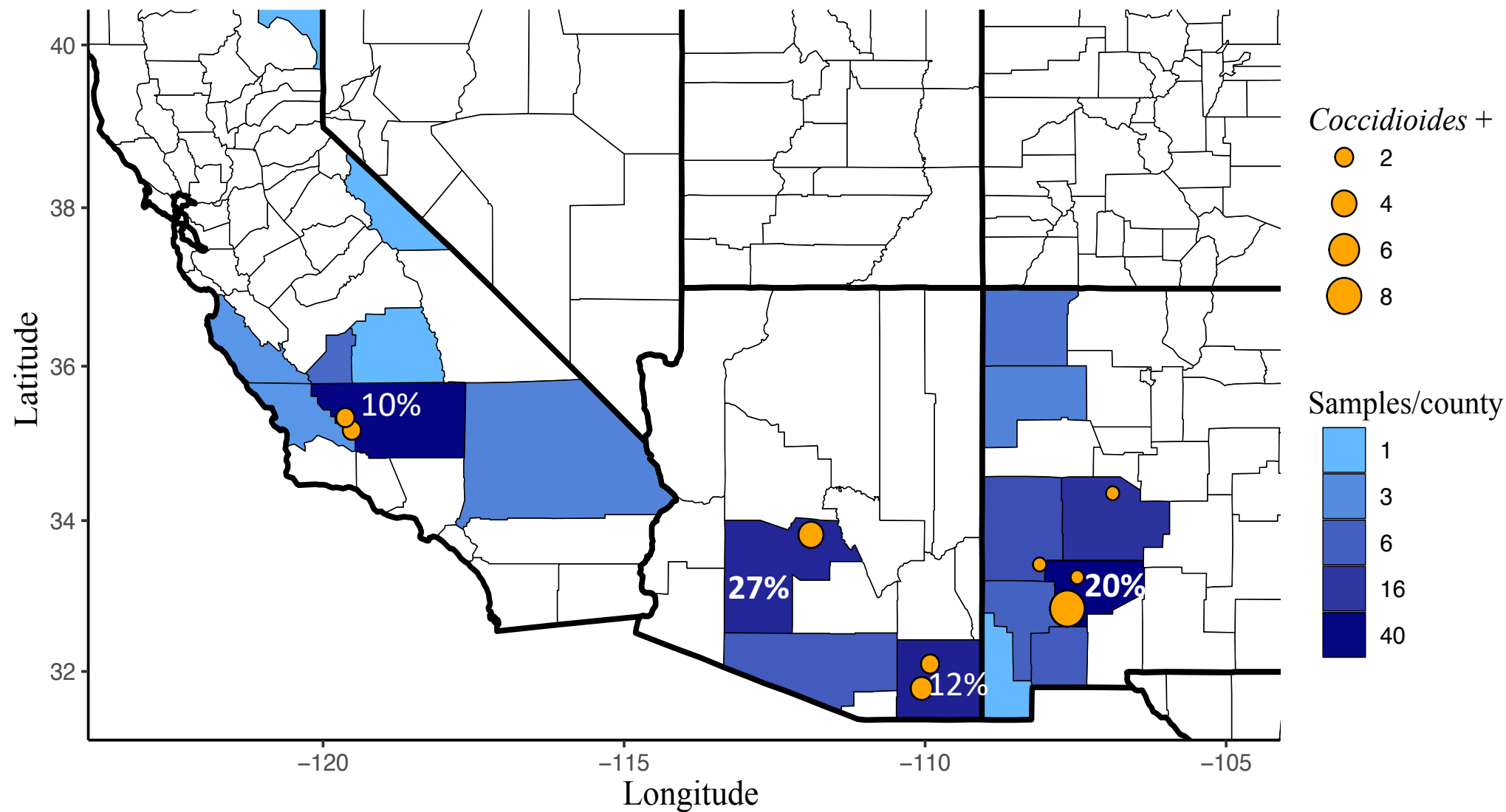
Coccidioides presence in small mammals



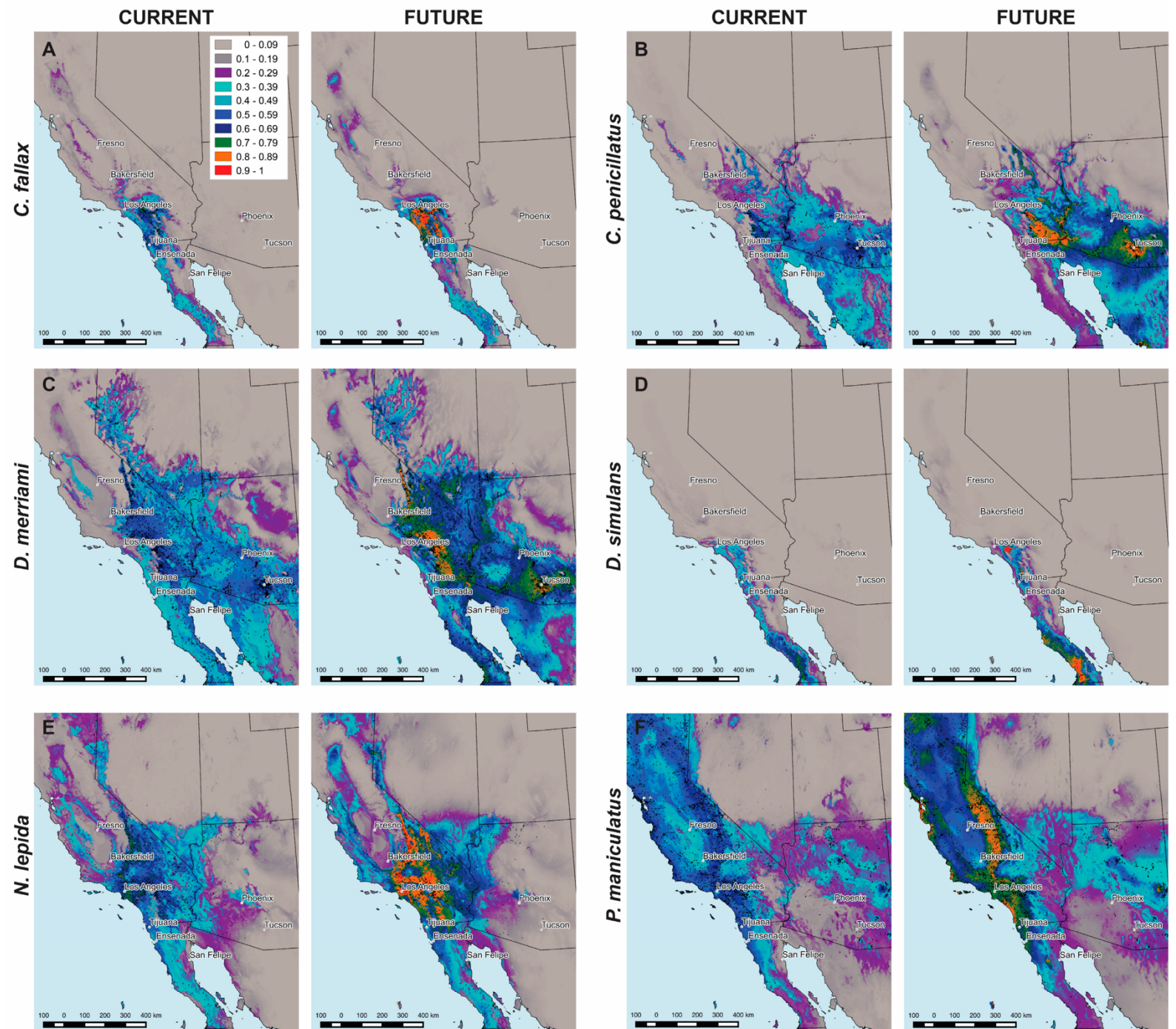
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Coccidioides detected in small mammal lungs



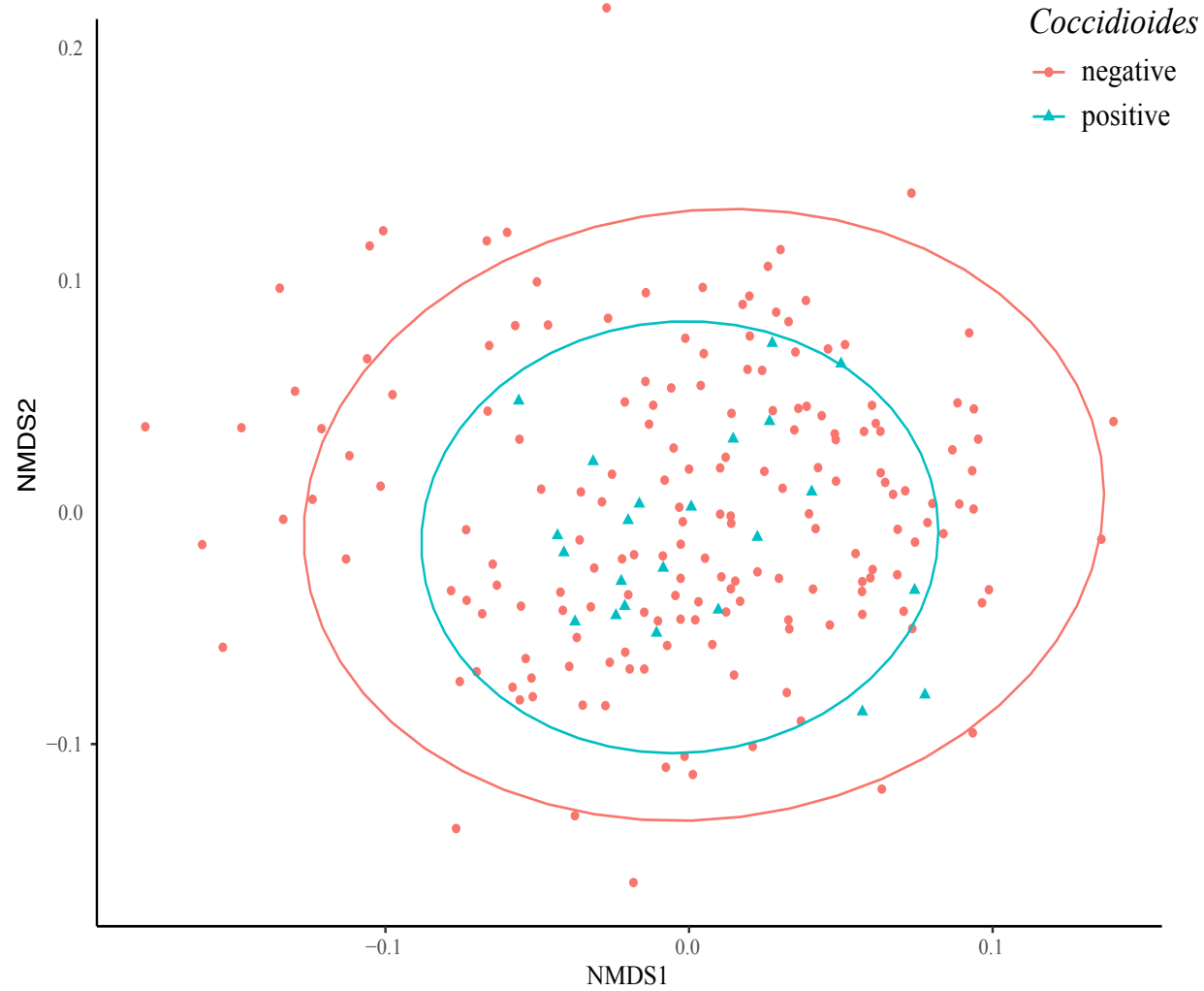
Rodent distribution maps to compare to Valley fever incidence



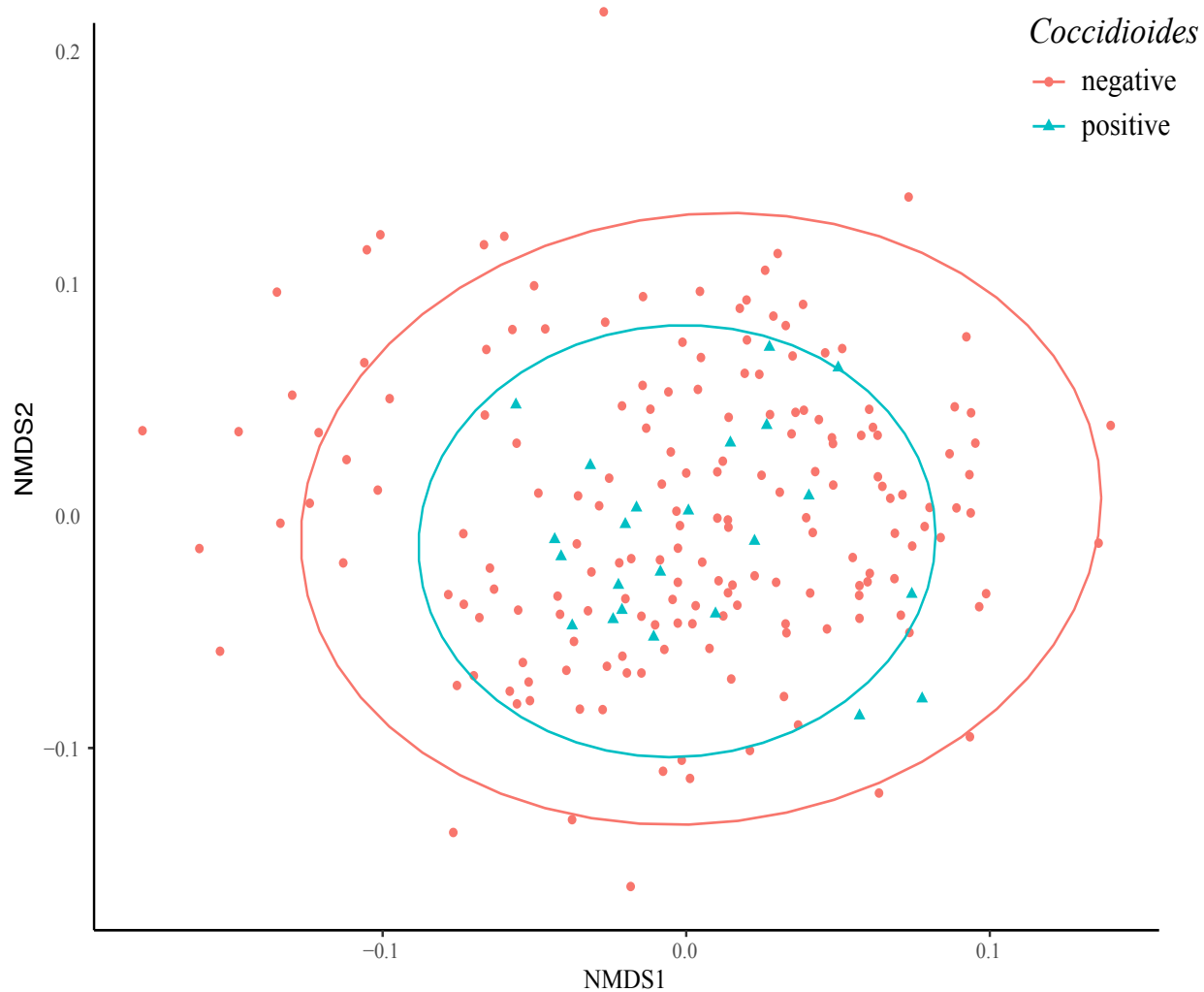
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Fungal community does not alter with presence of *Coccidioides*



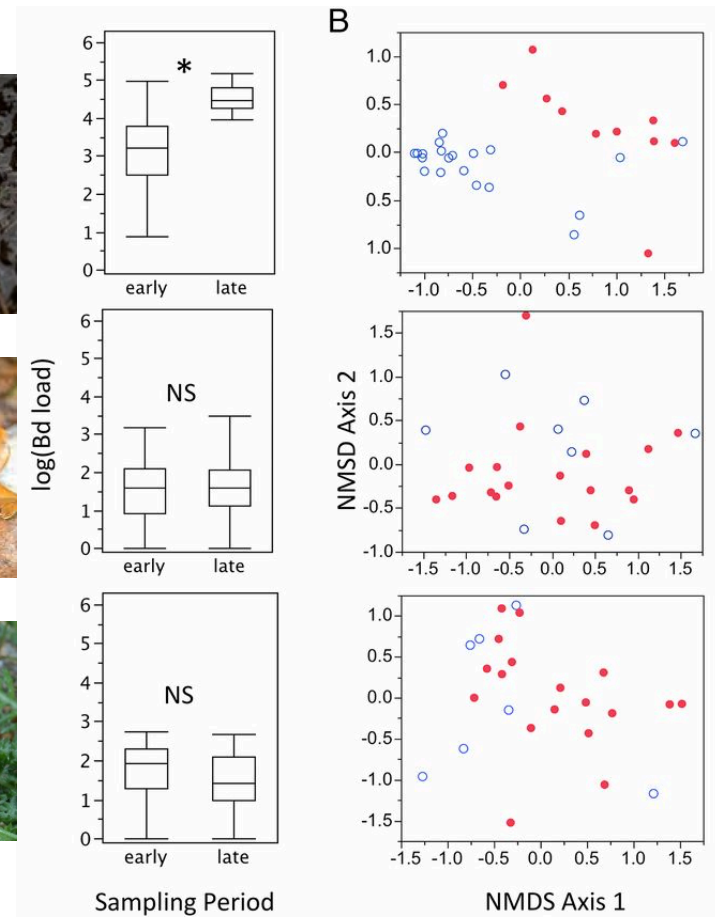
Fungal community does not alter with presence of *Coccidioides*



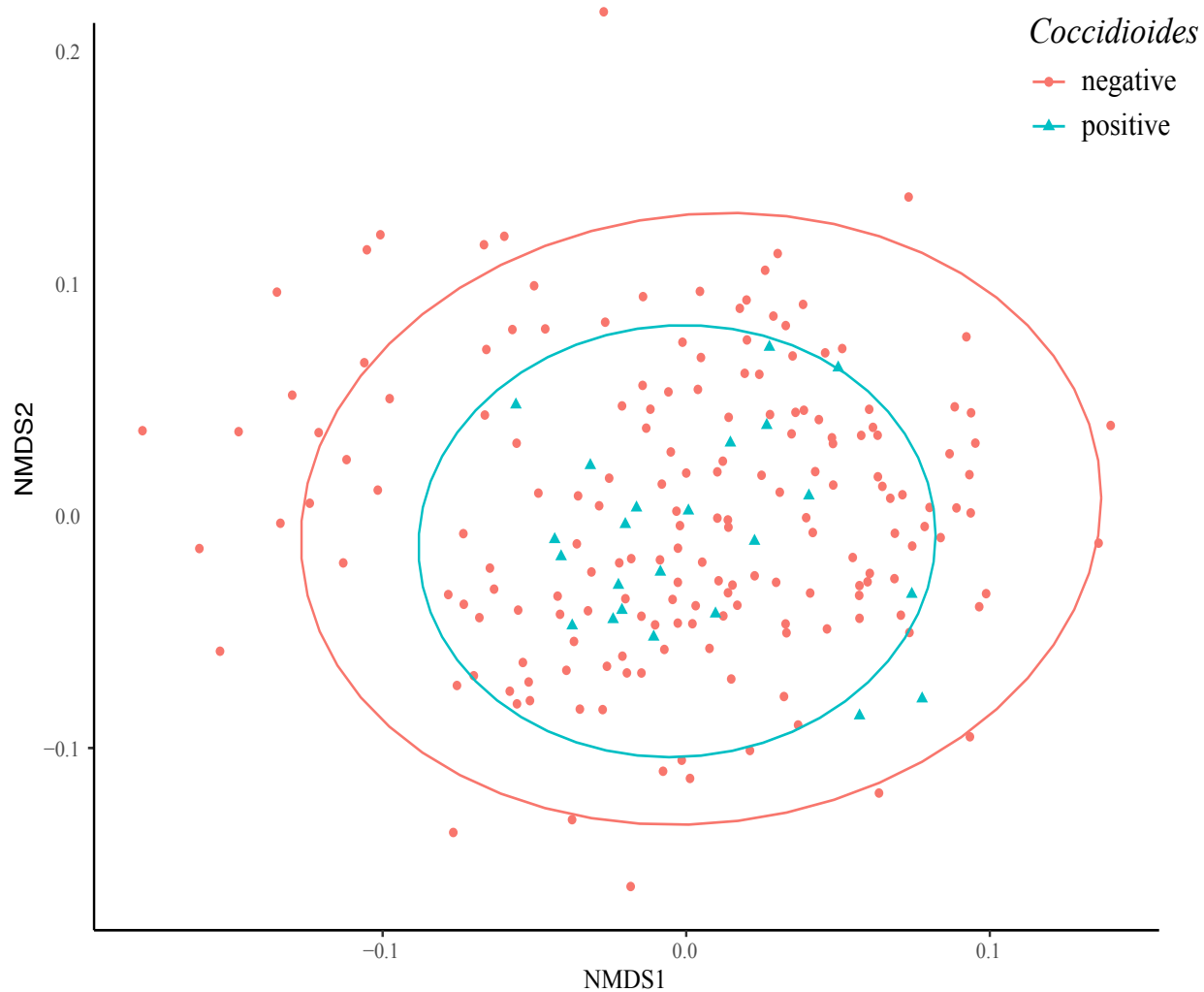
Chytridiomycosis in frogs causes community shift



Jani and Briggs 2014



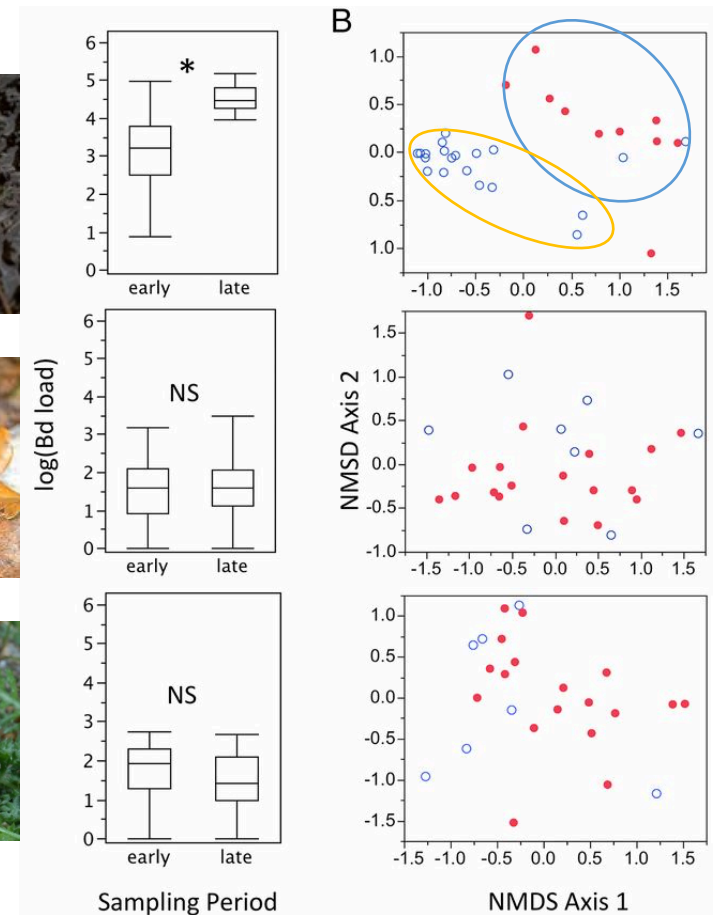
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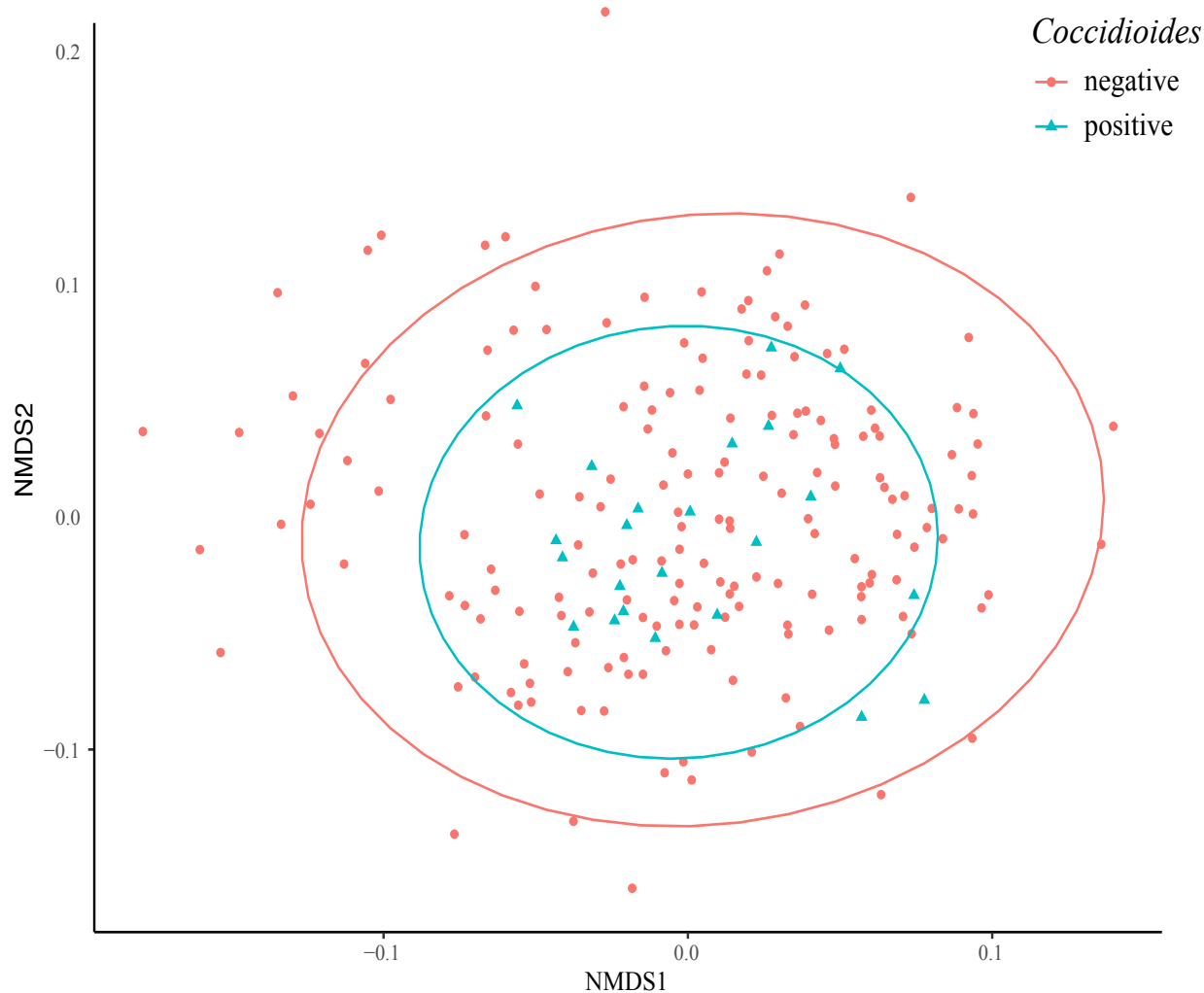
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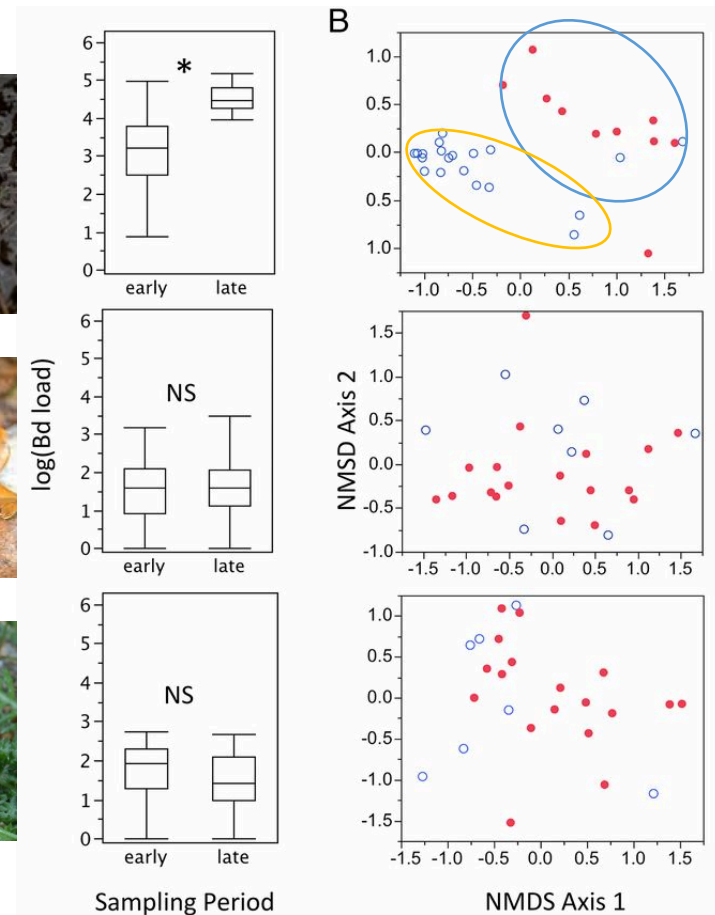
Fungal community does not alter with presence of *Coccidioides*



Chytridiomycosis in frogs causes community shift



Jani and Briggs 2014



Sea star wasting disease, Lloyd *et al.* 2018



Snake fungal disease, Allender *et al.* 2018

The diagram features a central horizontal blue arrow pointing from left to right. The left half of the arrow is a lighter shade of blue and contains the word 'Healthy'. The right half is a darker shade of blue and contains the words 'Severe Disease'. Above the arrow, the text 'Environmental factors' is followed by a bulleted list: 'Climactic variables', 'Nutrient availability', and 'Spore load'. Below the arrow, on the left side, the text 'Host factors' is followed by a bulleted list: 'Genetics', 'General health', and 'Microbiome'. On the right side, below the arrow, the text 'Pathogen factors' is followed by a bulleted list: 'Host evasion', 'Survival efficiency', and 'Antimicrobial resistance'. At the bottom center, the text '*Coccidioides* on a continuum from commensal to pathogenic' is written in a blue, italicized font. The background consists of several interlocking puzzle pieces in light gray, some of which are slightly offset to create a layered effect.

Environmental factors

- Climactic variables
- Nutrient availability
- Spore load

Healthy

Severe Disease

Host factors

- Genetics
- General health
- Microbiome

Pathogen factors

- Host evasion
- Survival efficiency
- Antimicrobial resistance

Coccidioides on a continuum from
commensal to pathogenic

Conclusions

1. *Coccidioides* was detected in 14 species of small mammals in 12% of the samples.
2. Collections can suggest locally acquired *Coccidioides* in Kern (CA), Maricopa (AZ), Cochise (AZ), Sierra (NM), Socorro (NM), and Catron (NM) counties.
3. *Coccidioides* was in low relative abundance and its presence doesn't disrupt the normal lung mycobiome suggesting it could be commensal.

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