

# Why taxonomic splits matter for bat biodiversity and viral risk analyses

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Jorrit H. Poelen, Connor Burgin

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*NASBR meeting, Guadalajara*

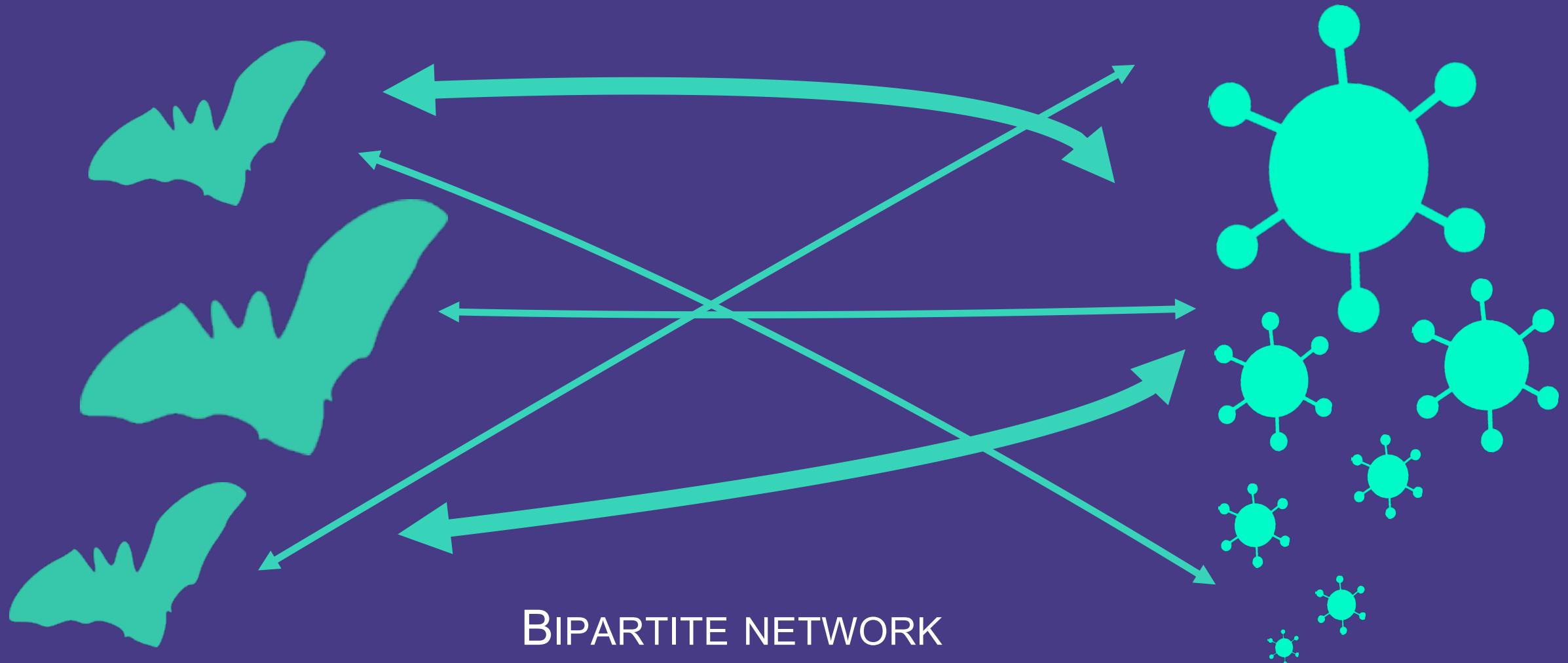


Viral  
spillover  
to humans

PHYLOGENY

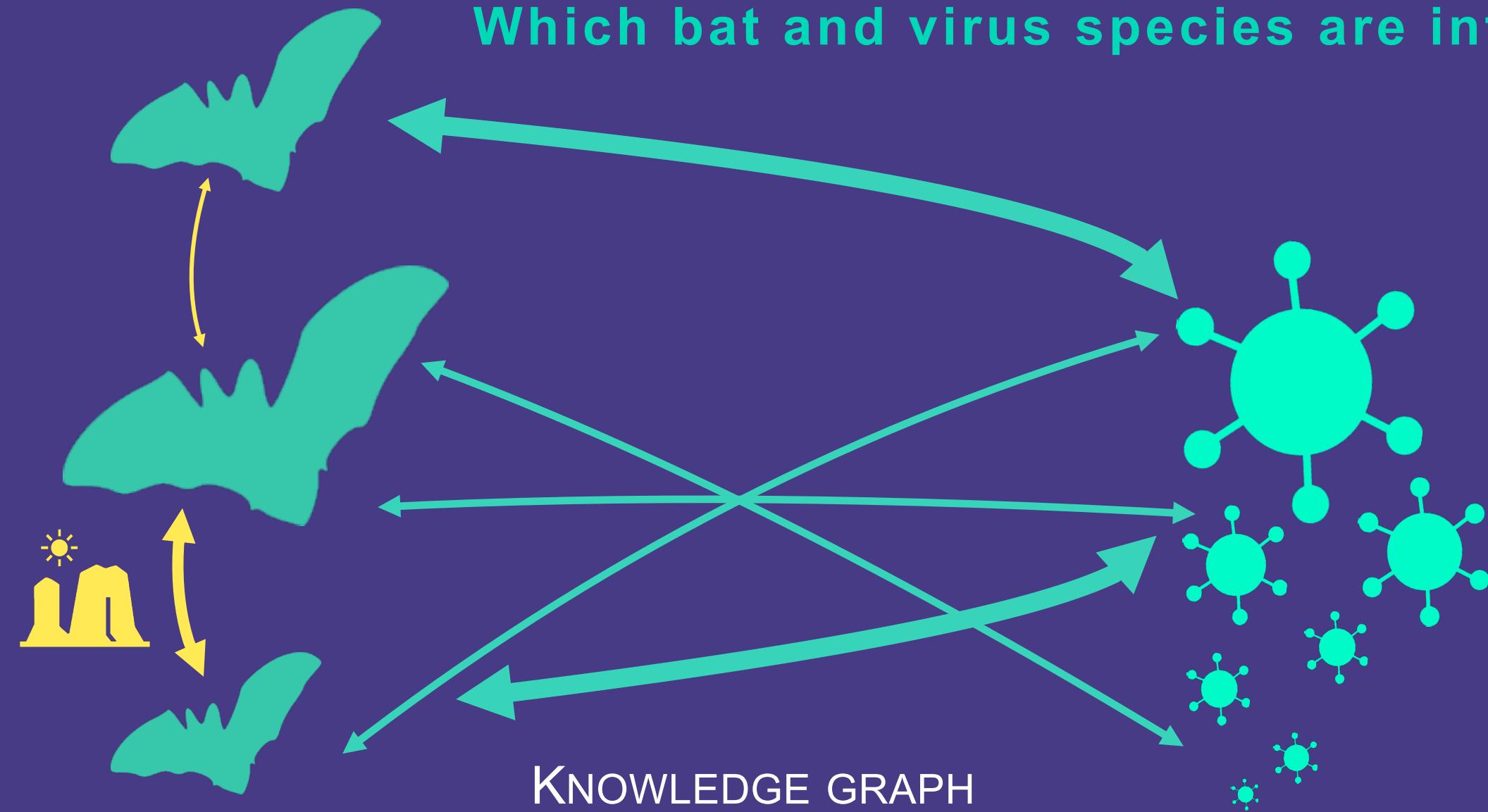


# Which bat and virus species are interacting?



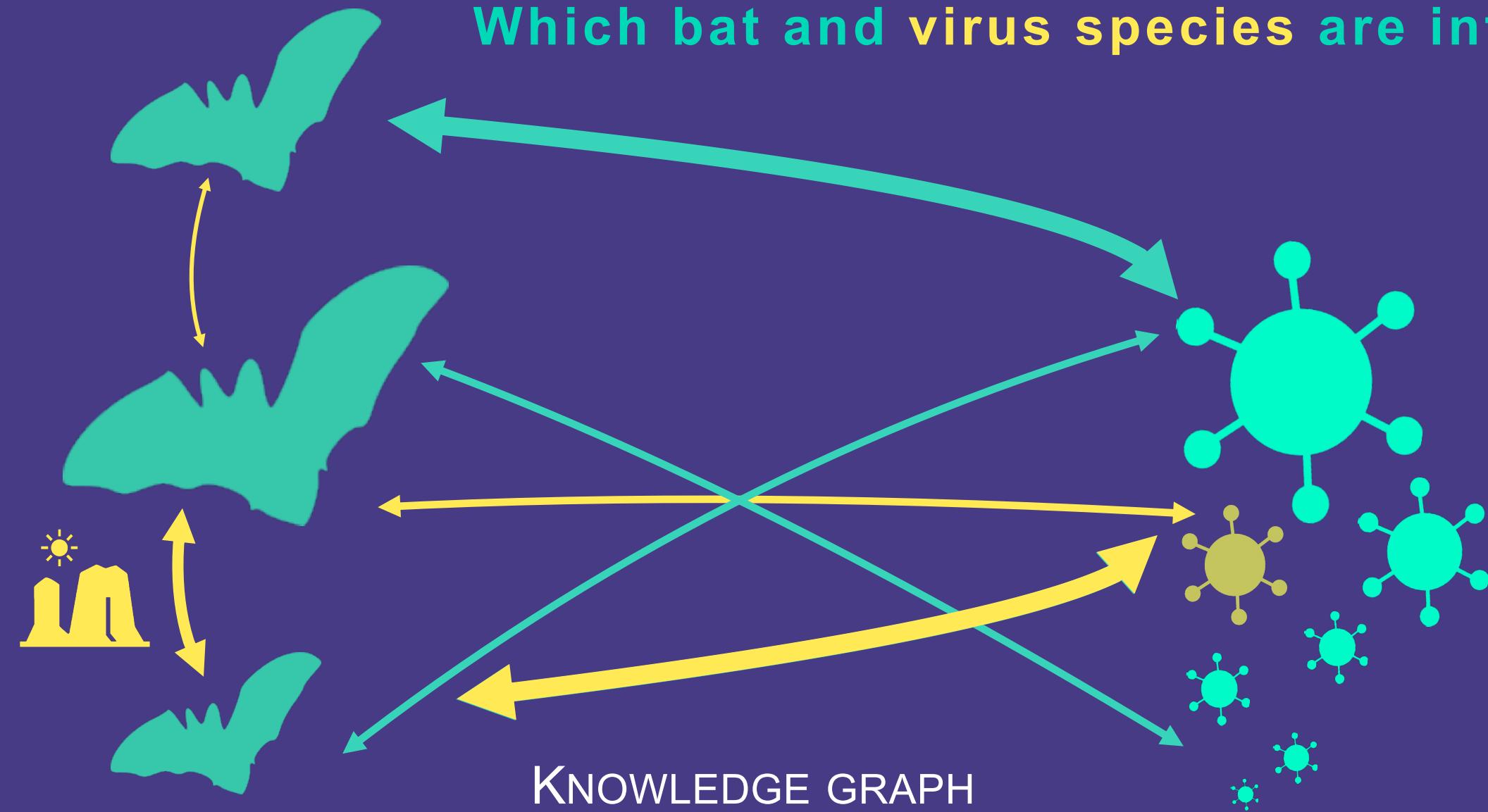
# Which bat species are interacting?

## Which bat and virus species are interacting?



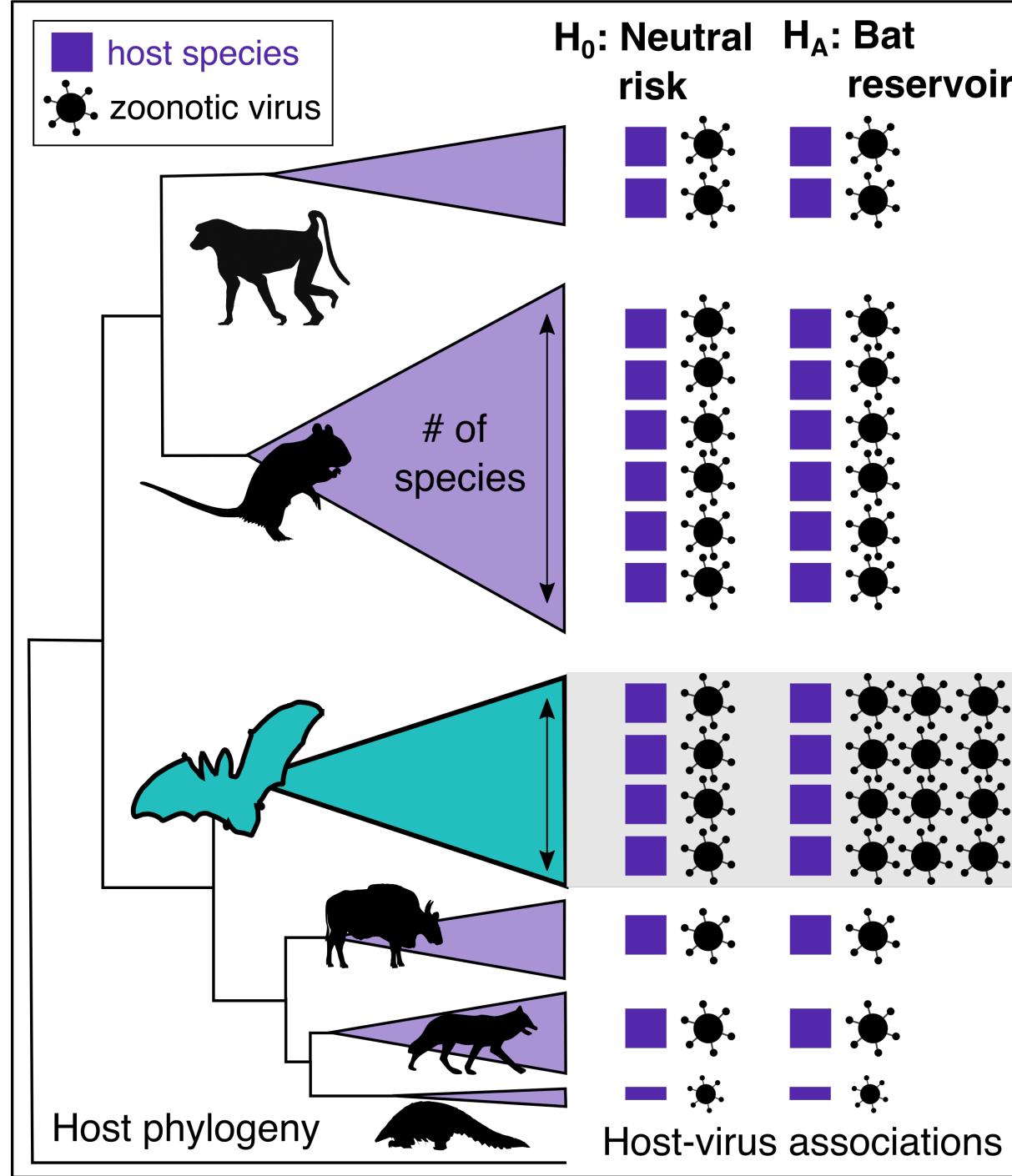
# Which bat species are interacting?

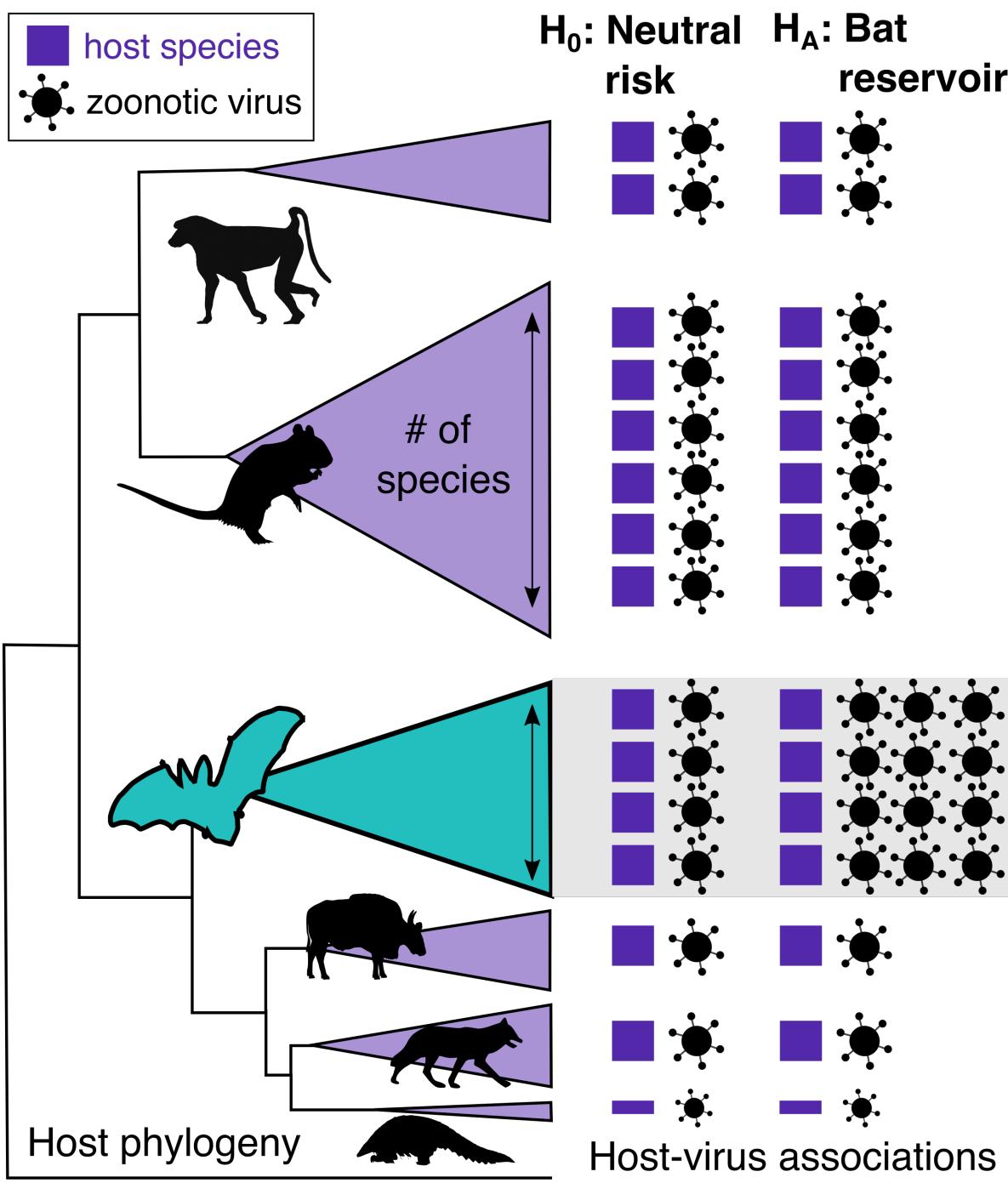
## Which bat and virus species are interacting?



# Taxon-specific zoonotic risk

Upham et al. (in prep)





Are bats ‘**special reservoirs**’ carrying more viruses than expected given their species richness?

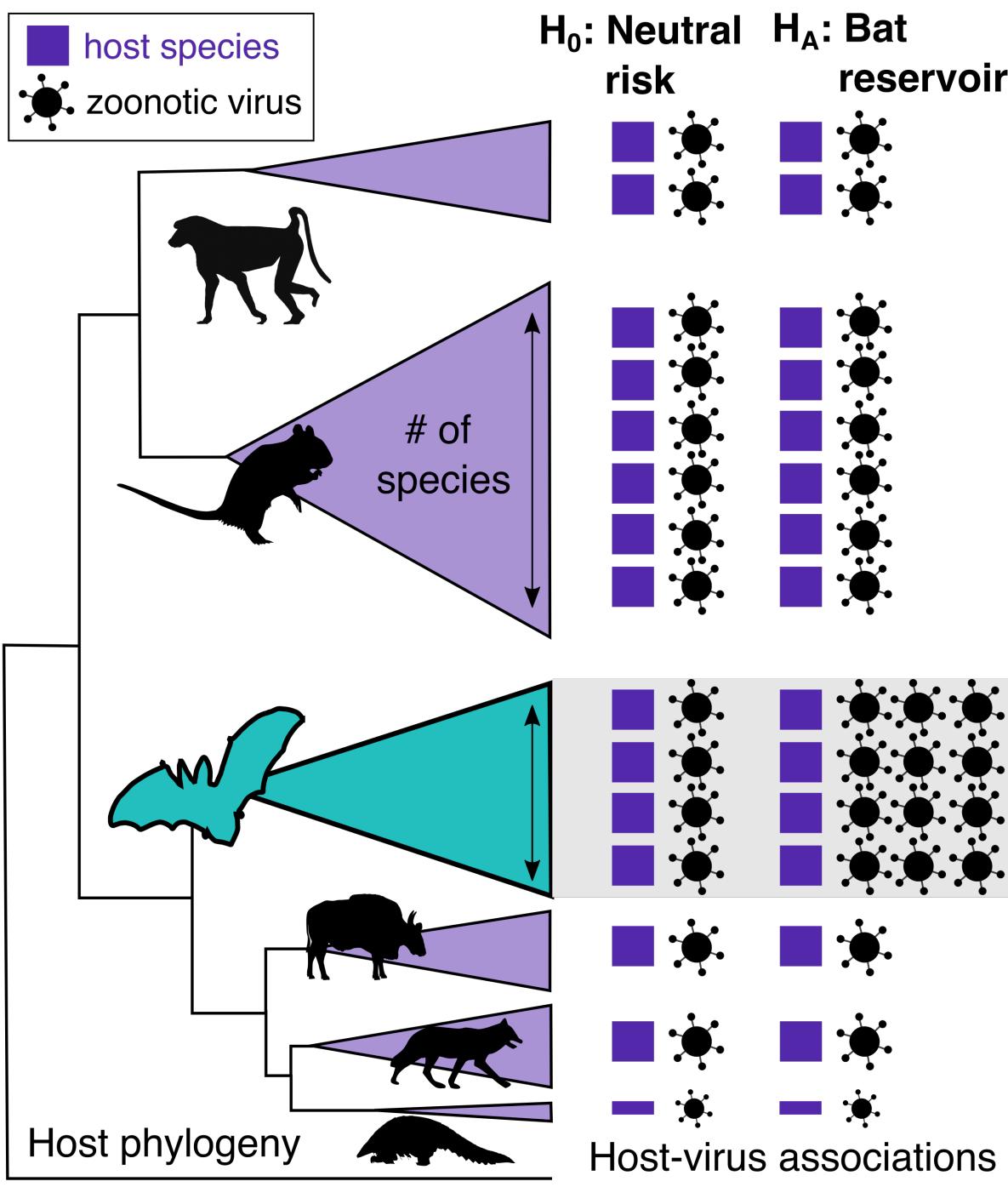
→ **Bat reservoir hypothesis**

Luis et al. (2013) *Proc B*,  
Hayman (2016) *Ann Rev Vir*

Or do all mammal groups carry viral diversity in proportion to their species diversity?

→ **Neutral risk hypothesis**

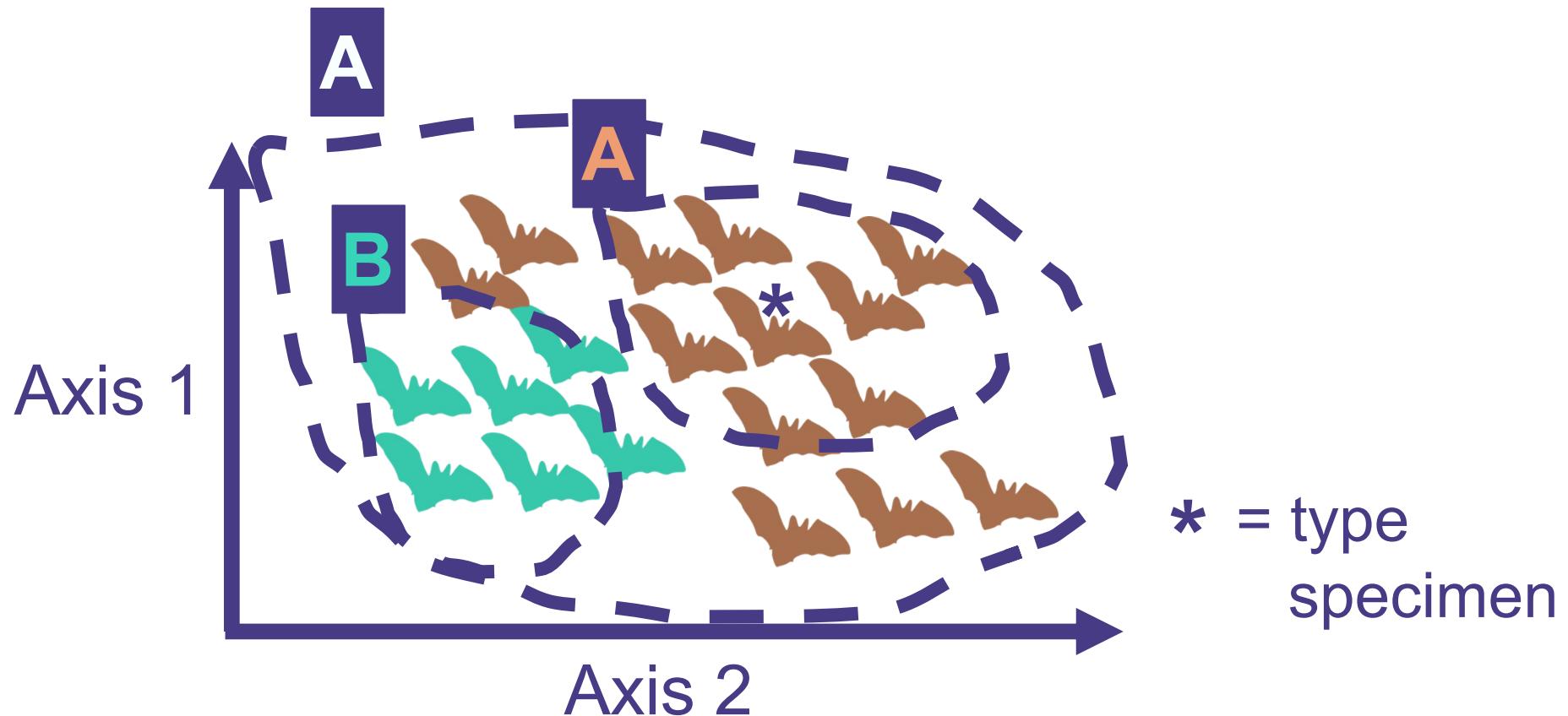
Mollentze and Streicker (2020) *PNAS*



Viral interaction data is  
not yet resolved enough  
to answer this question.

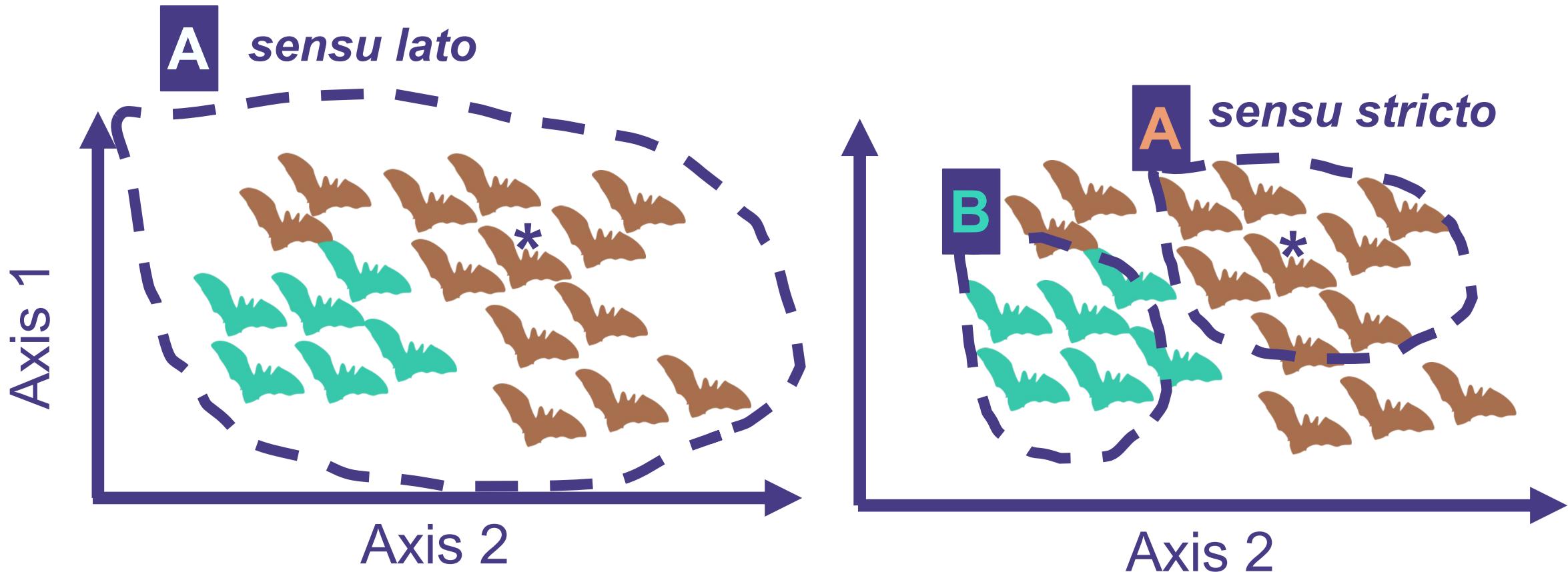
TAXONOMY → BIODIVERSITY → RISK

## Observations of species according to who?



# TAXONOMY → BIODIVERSITY → RISK

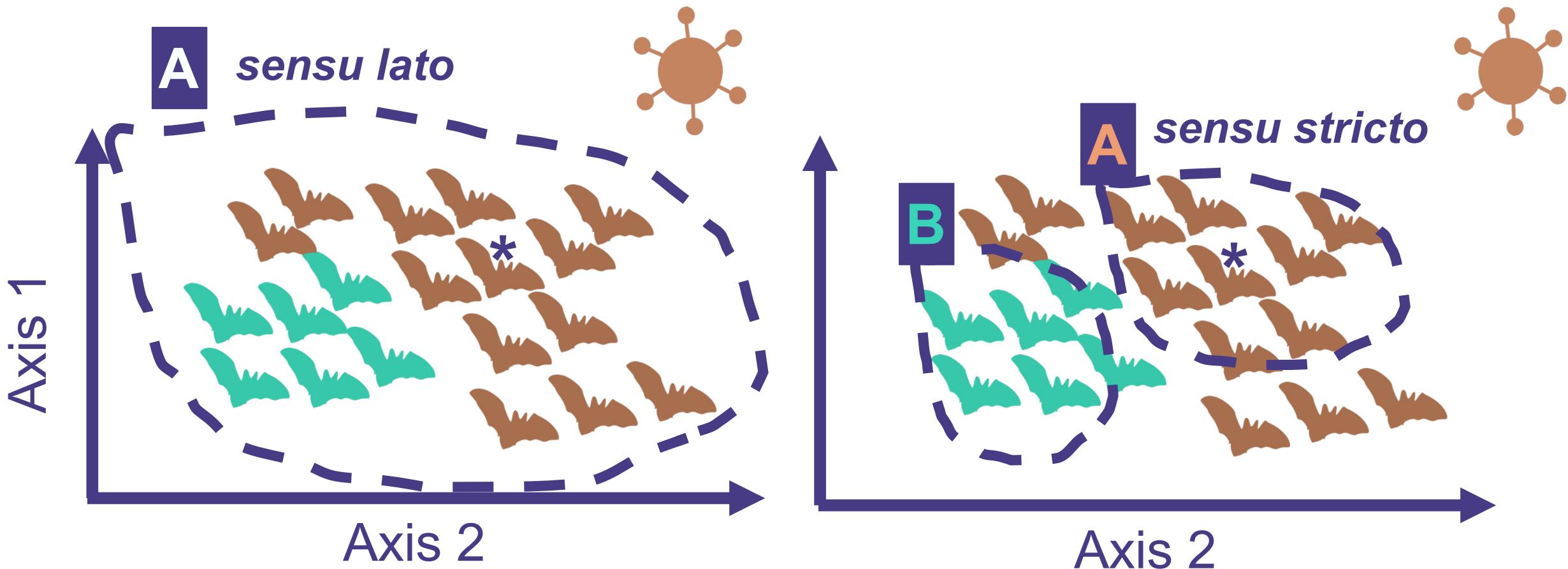
**Common problem:** Same name “A” used with different taxonomic meanings



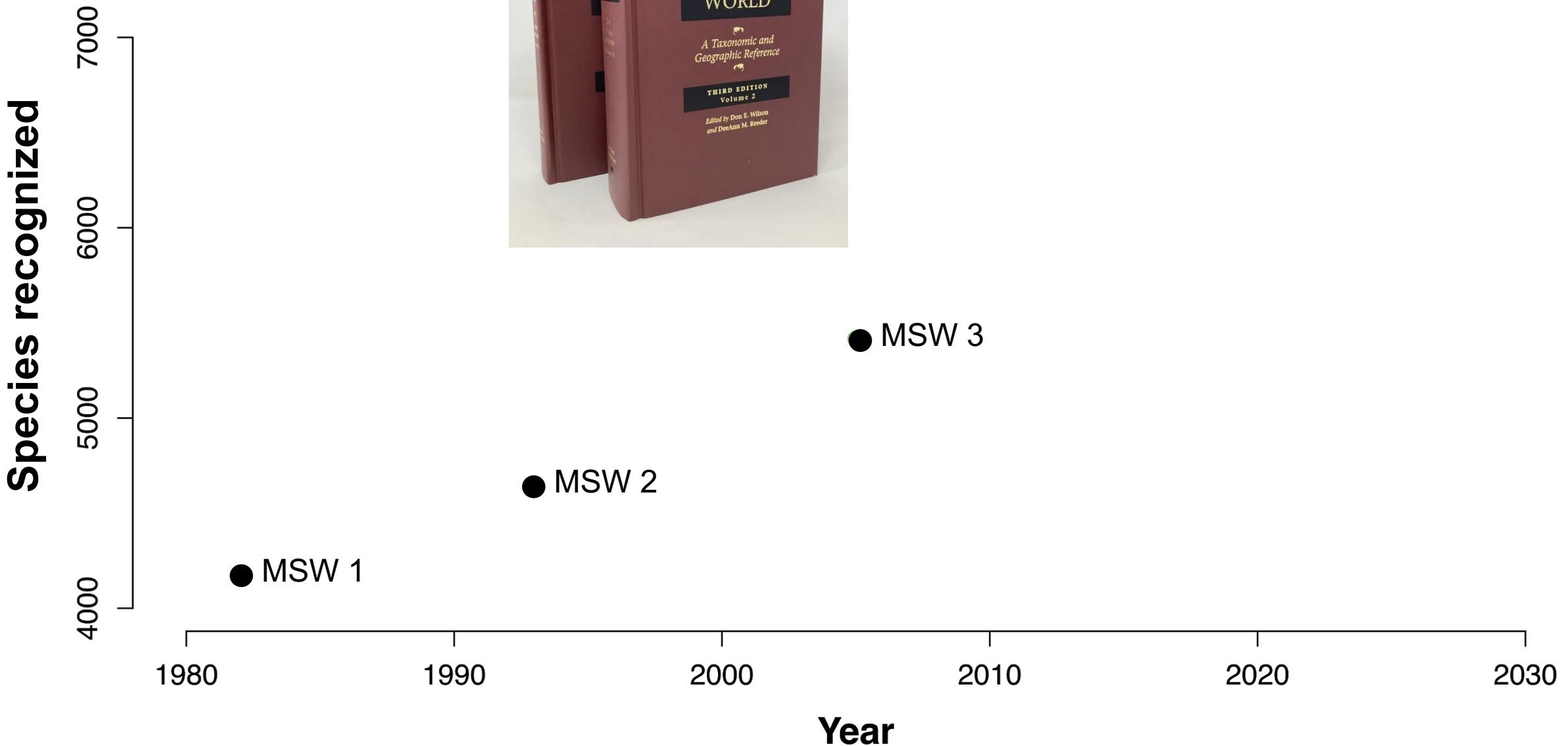
# TAXONOMY → BIODIVERSITY → RISK

**Question for today:**

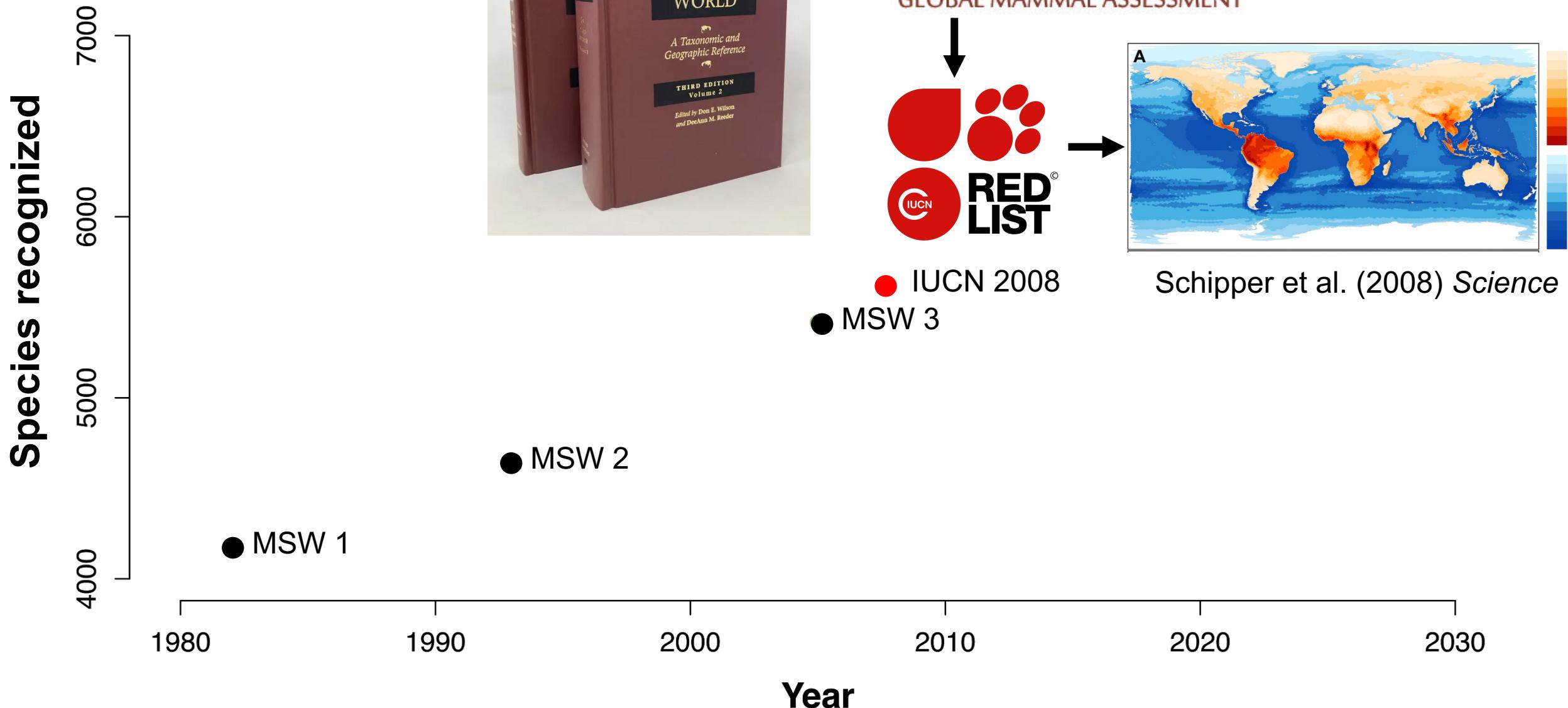
When do **taxonomic splits** change viral risk estimates?



# What are the mammal species?



# What are the mammal species?

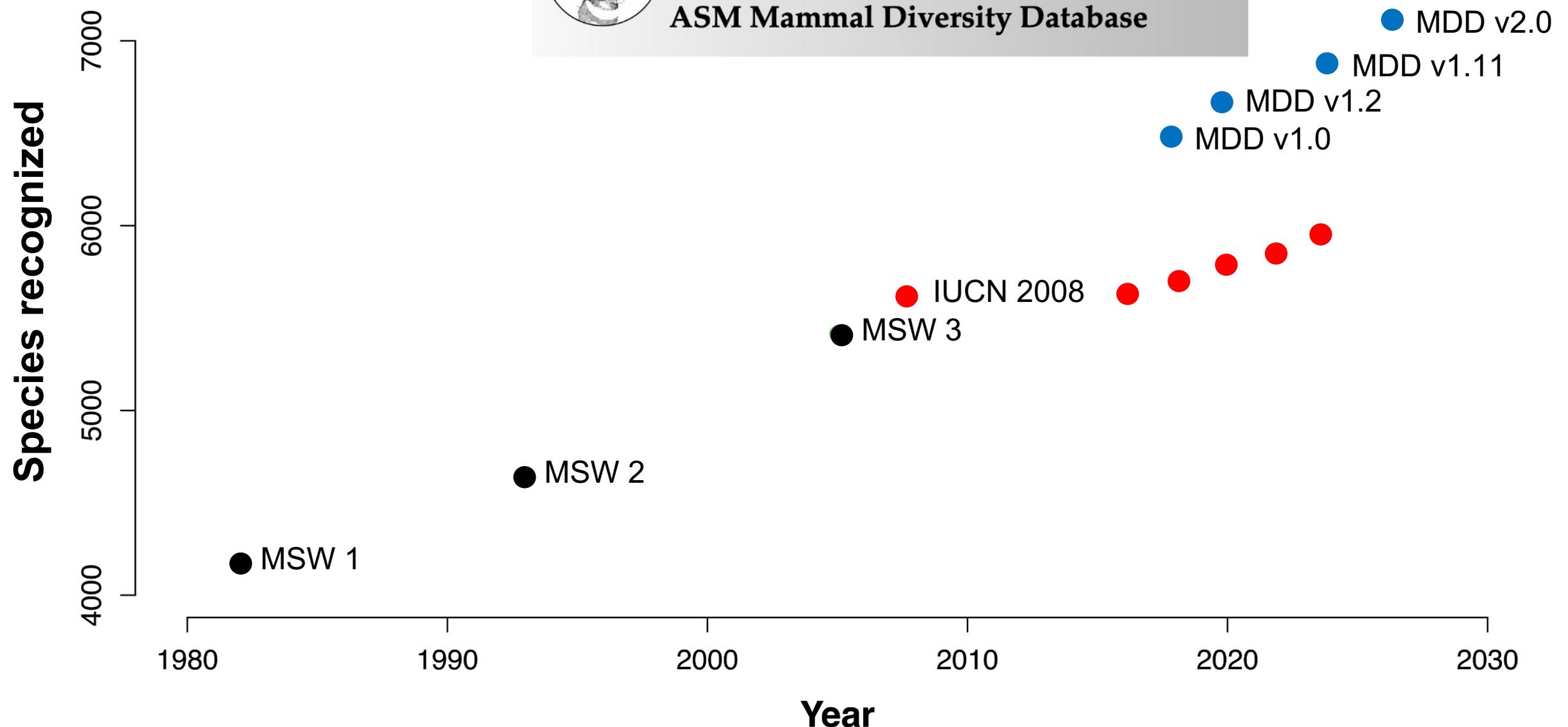


# What are the mammal species?



<https://mammaldiversity.org>

ASM Mammal Diversity Database

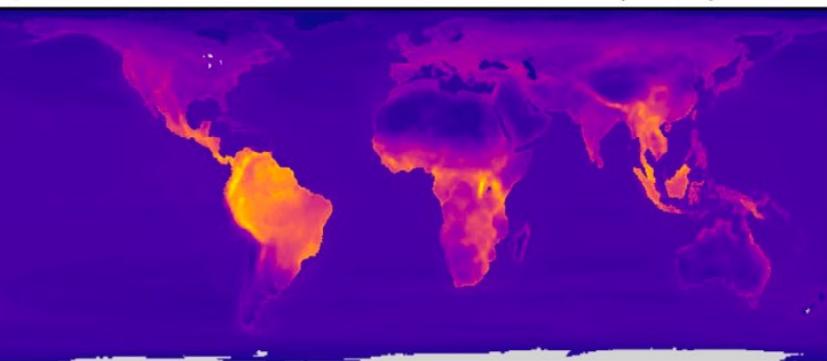


# Expert range maps of global mammal distributions harmonised to three taxonomic authorities

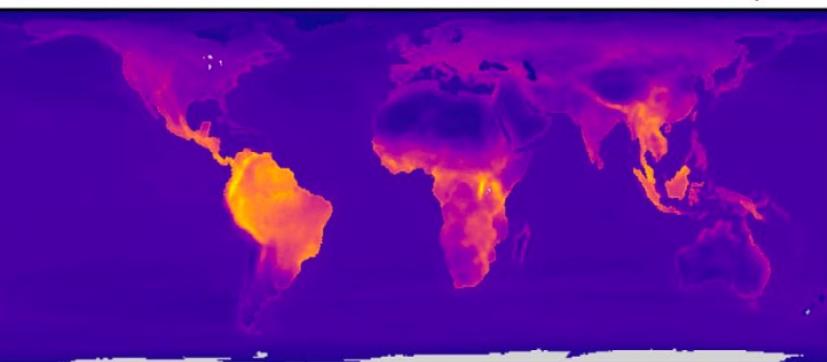
Charles J. Marsh<sup>1,2</sup>  | Yanina V. Sica<sup>1,2</sup>  | Connor J. Burgin<sup>3</sup> | Wendy A. Dorman<sup>1,2</sup> | Robert C. Anderson<sup>1,2</sup> | Isabel del Toro Mijares<sup>1,2</sup> | Jessica G. Vigneron<sup>1,2</sup> | Vijay Barve<sup>4</sup> | Victoria L. Dombrowik<sup>1,2</sup> | Michelle Duong<sup>1,2</sup> | Robert Guralnick<sup>4</sup> | Julie A. Hart<sup>1,2,5</sup> | J. Krish Maypole<sup>1,2</sup> | Kira McCall<sup>1,2</sup> | Ajay Ranipeta<sup>1,2</sup> | Anna Schuerkmann<sup>1,2</sup> | Michael A. Torselli<sup>1,2</sup> | Thomas Lacher Jr<sup>6,7</sup> | Russell A. Mittermeier<sup>7</sup> | Anthony B. Rylands<sup>7</sup> | Wes Sechrest<sup>7</sup> | Don E. Wilson<sup>8</sup> | Agustín M. Abba<sup>9</sup> | Luis F. Aguirre<sup>10</sup> | Joaquín Arroyo-Cabral<sup>11</sup> | Diego Astúa<sup>12</sup> | Andrew M. Baker<sup>13,14</sup> |

Marsh et al. Upham, Jetz  
(2022) *J Biogeogr*

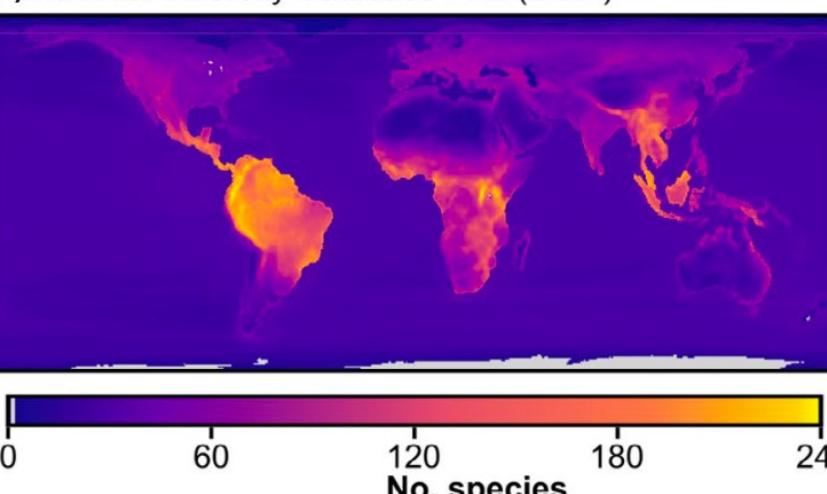
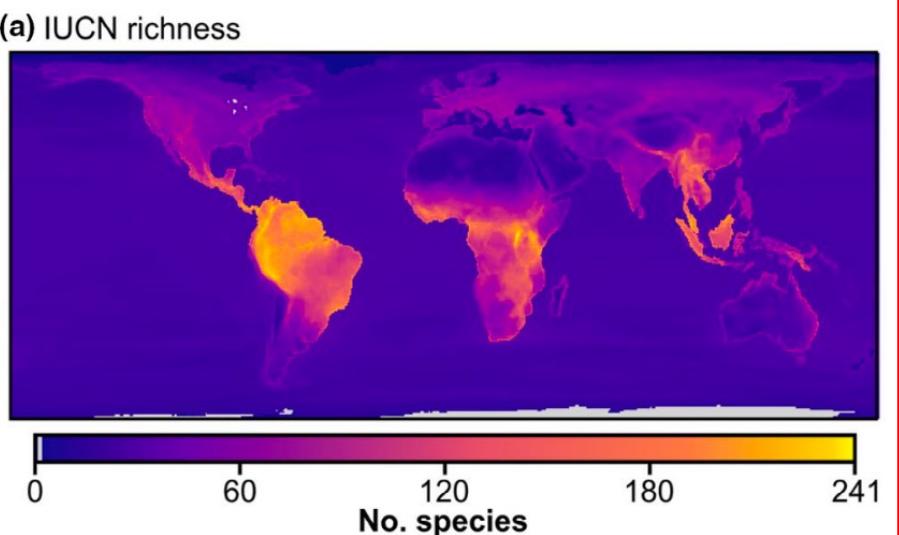
(a) Handbook of the Mammals of the World (HMW)



(b) Illustrated Checklist of the Mammals of the World (CMW)



(c) Mammal Diversity Database v1.2 (MDD)

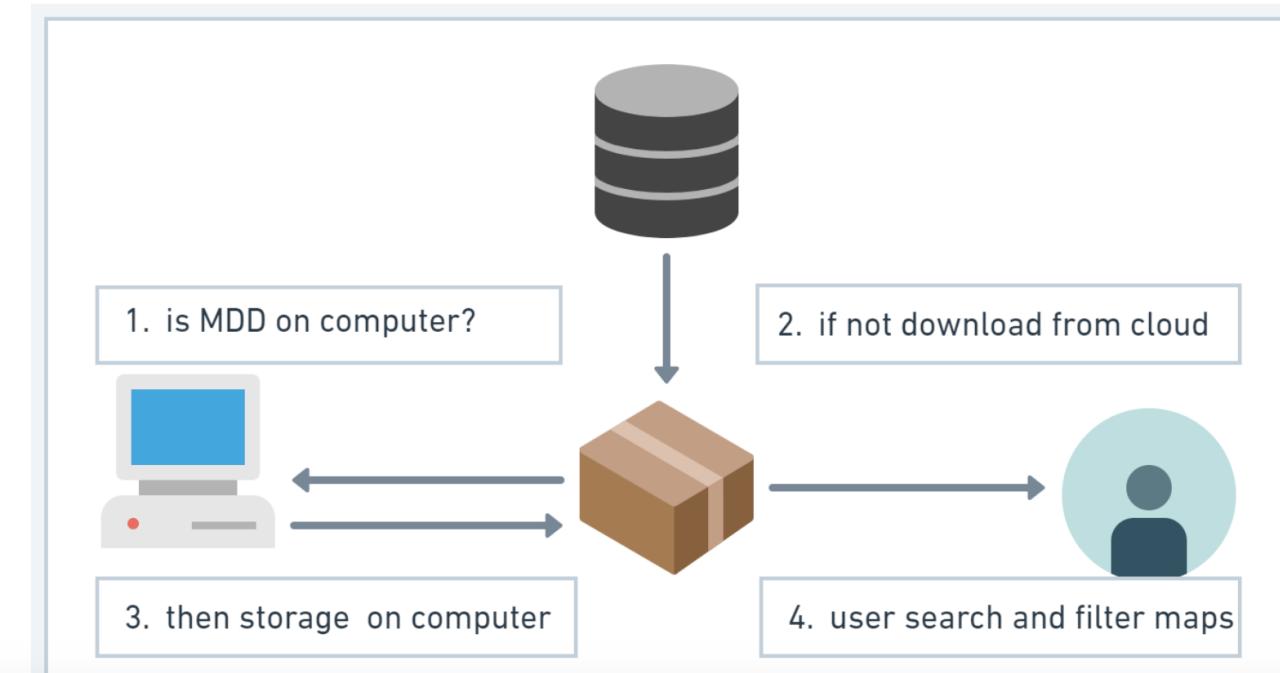


# mddmaps R package: maps for v1.2 → v1.11

<https://alrobles.github.io/mddmaps/index.html>

## mddmaps

The goal of mddmaps is to provide an interface to download and manipulate spatial range maps for mammals according with Mammal Diversity Database taxonomy. Currently the map version is related to MDD v1.9. See below for further details



### Links

[Browse source code](#)

[Report a bug](#)

### License

[Full license](#)

GPL (>= 3)

### Citation

[Citing mddmaps](#)

### Developers

Angel Robles

Author, maintainer

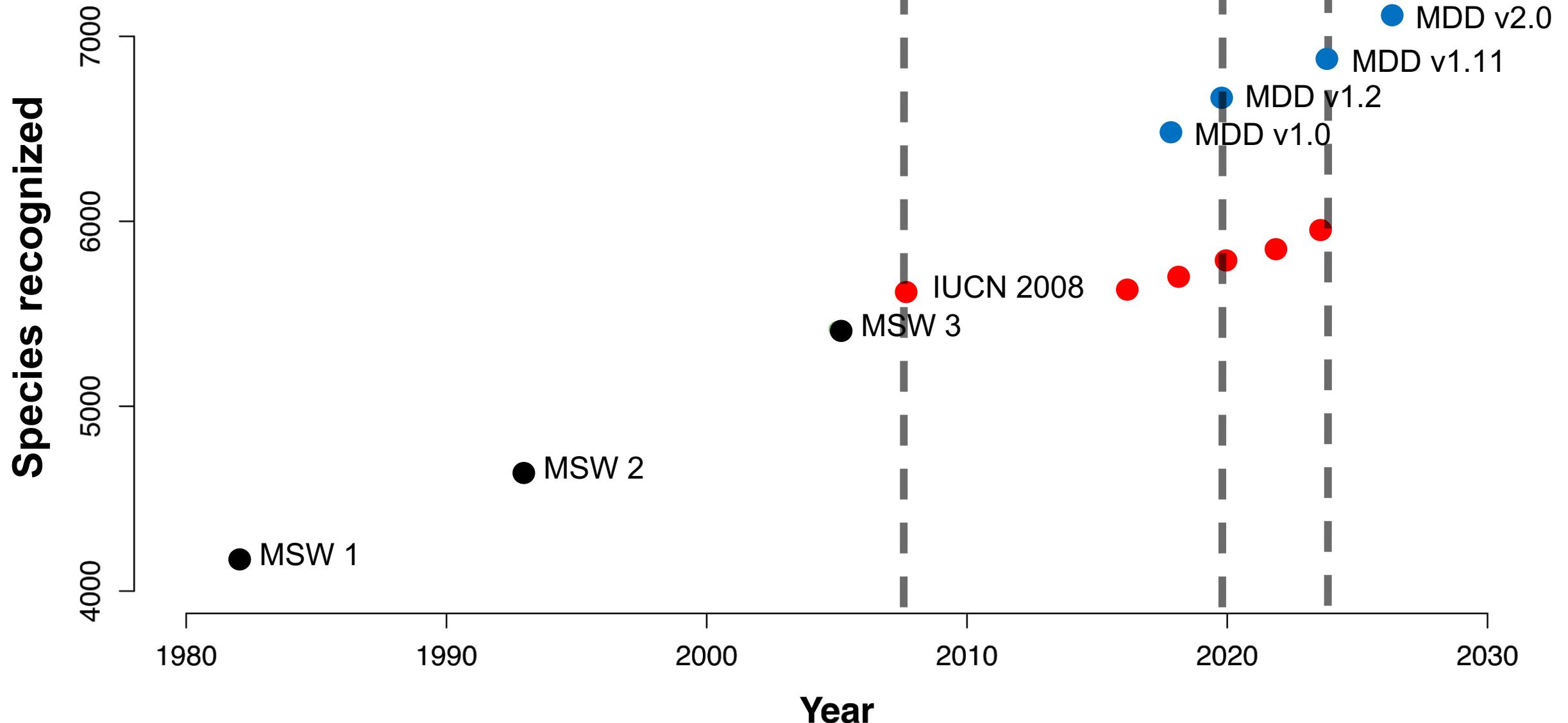


**Ángel L. Robles Fernández**  
ASU PhD student



**Norma A. Hernández Hernández**  
Visiting Scholar

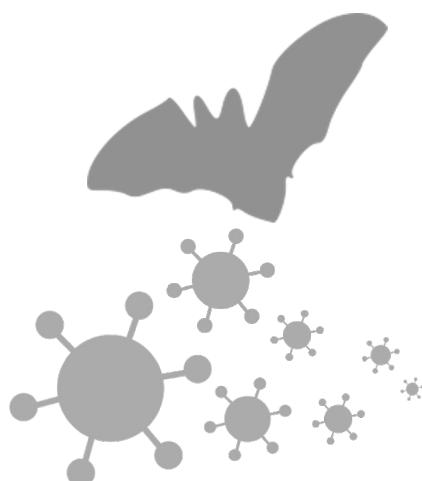
# Periods of taxonomic change: with range maps



1

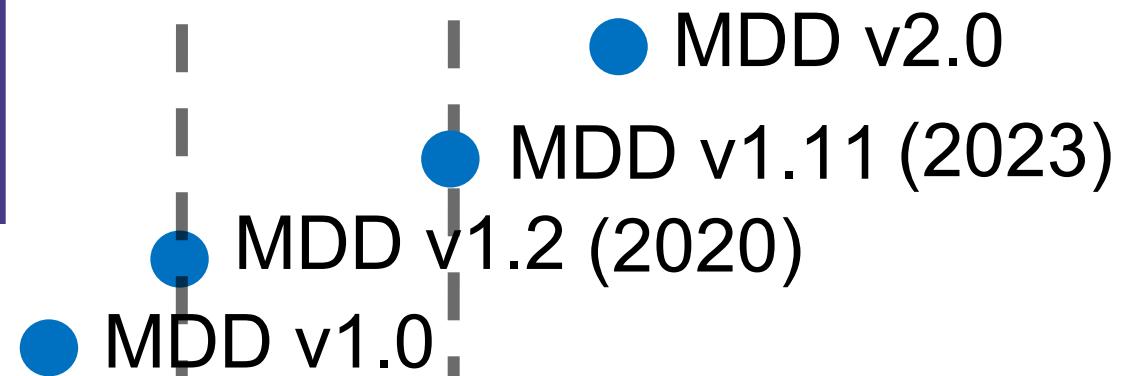
2

How do period 1 and 2  
**range map changes**  
(taxonomic splits and lumps)  
impact **bat-virus interactions?**



MSW 3

IUCN 2008



MDD v2.0

MDD v1.11 (2023)

MDD v1.2 (2020)

MDD v1.0

IUCN 2008

MSW 3

## Taxonomic splits

1

2

Bat species	Periods of change	
	2008-2020	2020-2023
<i>de novo</i> new	67	
<b>Split new</b>	111	
<b>Existing affected</b>	74	
<b>Total affected by splits</b>	185	
<b>% of bats globally</b>	12.6%	

## Taxonomic splits

1

2

Bat species	Periods of change		<b>Total change</b>
	<b>2008-2020</b>	<b>2020-2023</b>	
<i>de novo</i> new	67	22	89
<b>Split new</b>	111	35	146
<b>Existing affected</b>	74	25	99
<b>Total affected by splits</b>	185	60	<b>245</b>
<b>% of bats globally</b>	12.6%	4.1%	16.7%

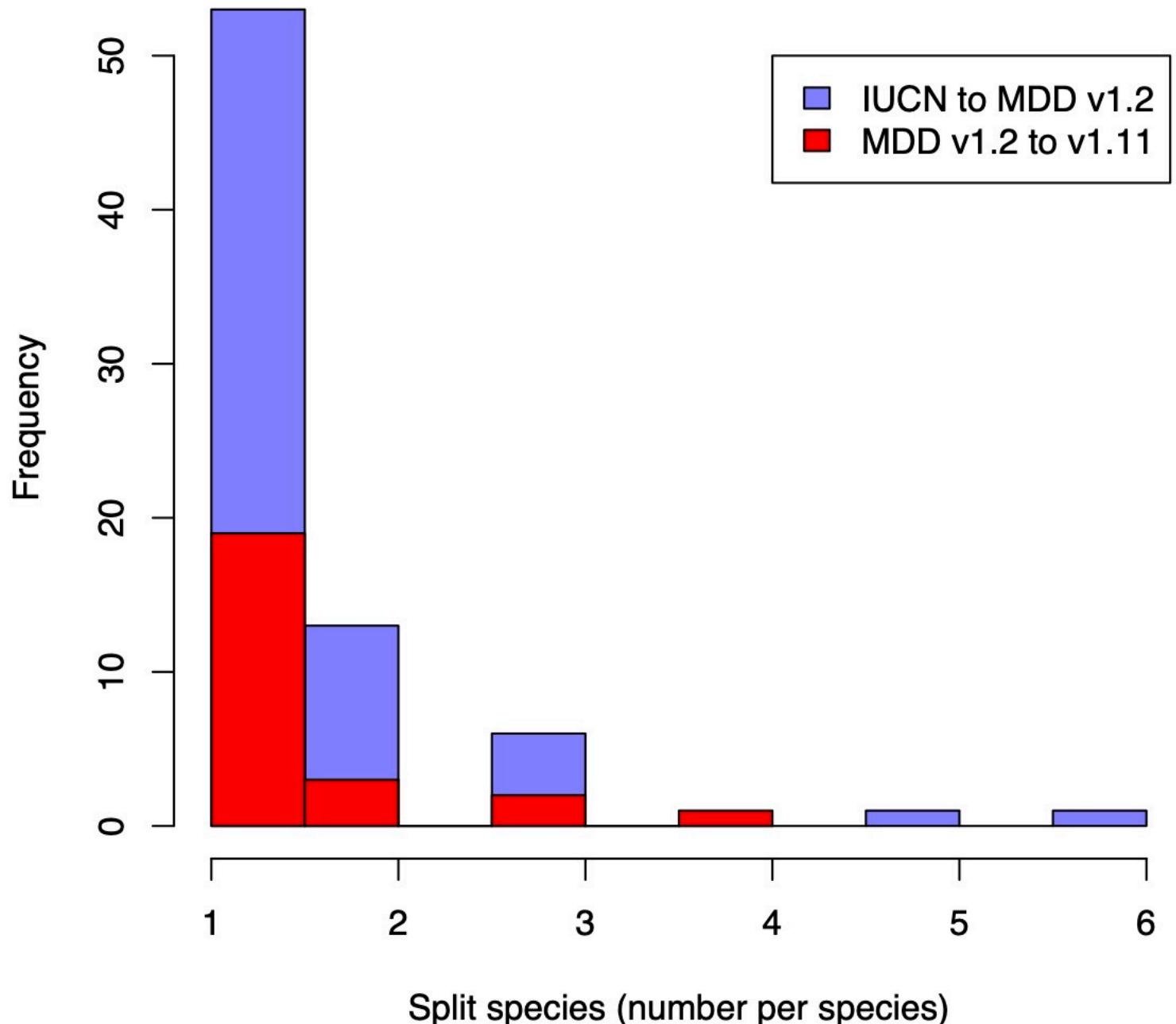
= 1 in 6 bat species was affected by  
a taxonomic split since 2008 !!!

# Taxonomic splits

n = 245

Most splits divide  
1 or 2 species  
from an existing  
species

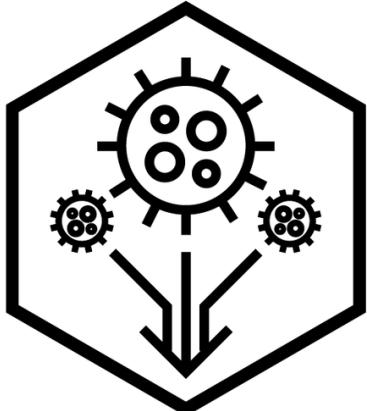
But some splits  
divide out 3, 4, 5,  
6 species...



## Taxonomic splits



## Viral interactions



# The Global Virome, in One Network (VIRION)

Carlson et al. (2022) *mBio*

“Host names were harmonized to the NCBI taxonomy using the R package taxize...” → synonyms

VIRION fields	Number of observations	% of total
<b>Included datasets</b>		
GenBank	350,743	82%
EID2	47,017	11%
GLOBI (unique portion)	17,018	4%
Shaw	5,822	1%
HP3	2,802	1%
PREDICT	2,729	1%
GMPD2	1,765	0%
<b>Detection methods</b>		
PCR/sequencing	382,379	89%
Not specified	36,896	9%
Antibodies	4,731	1%
Isolation/observation	3,890	1%

Taxonomic splits

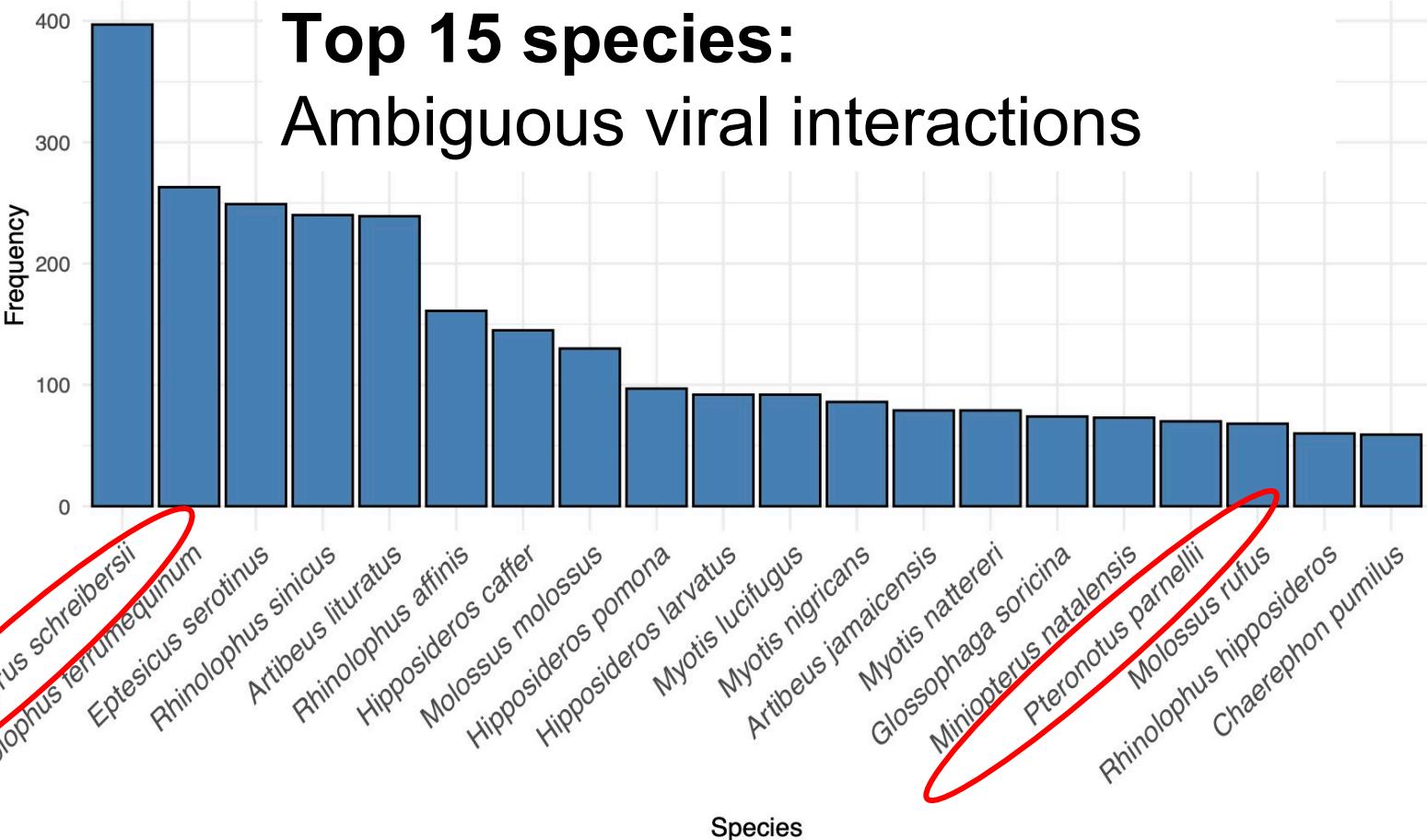


Viral interactions

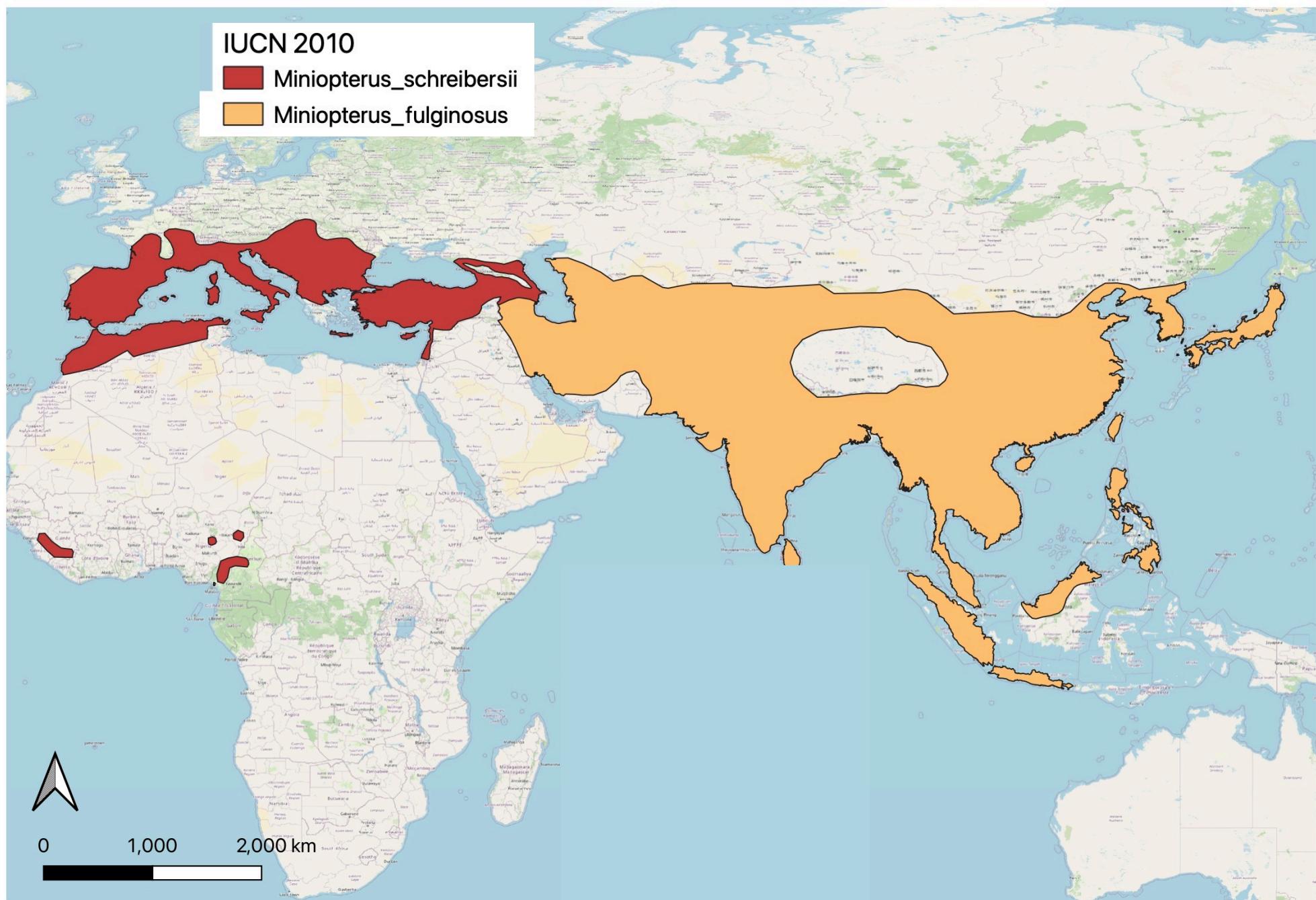
245 bat species affected (16.7% of total)

...impacting...

**3,343 bat-virus interactions (22.5% of total)**



# Example: *Miniopterus schreibersii* / *fulginosus*

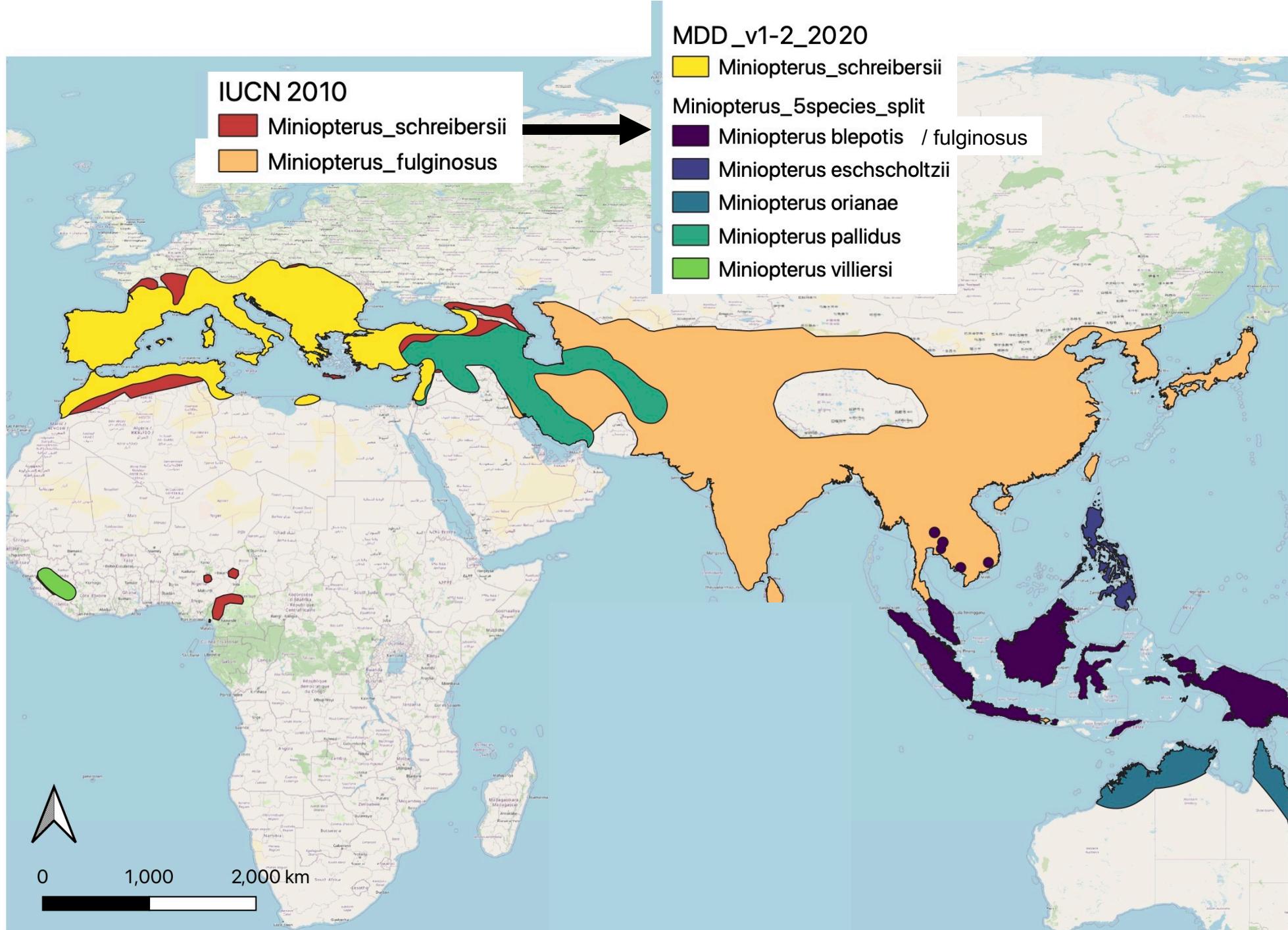


# Example: *Miniopterus schreibersii* / *fulginosus*

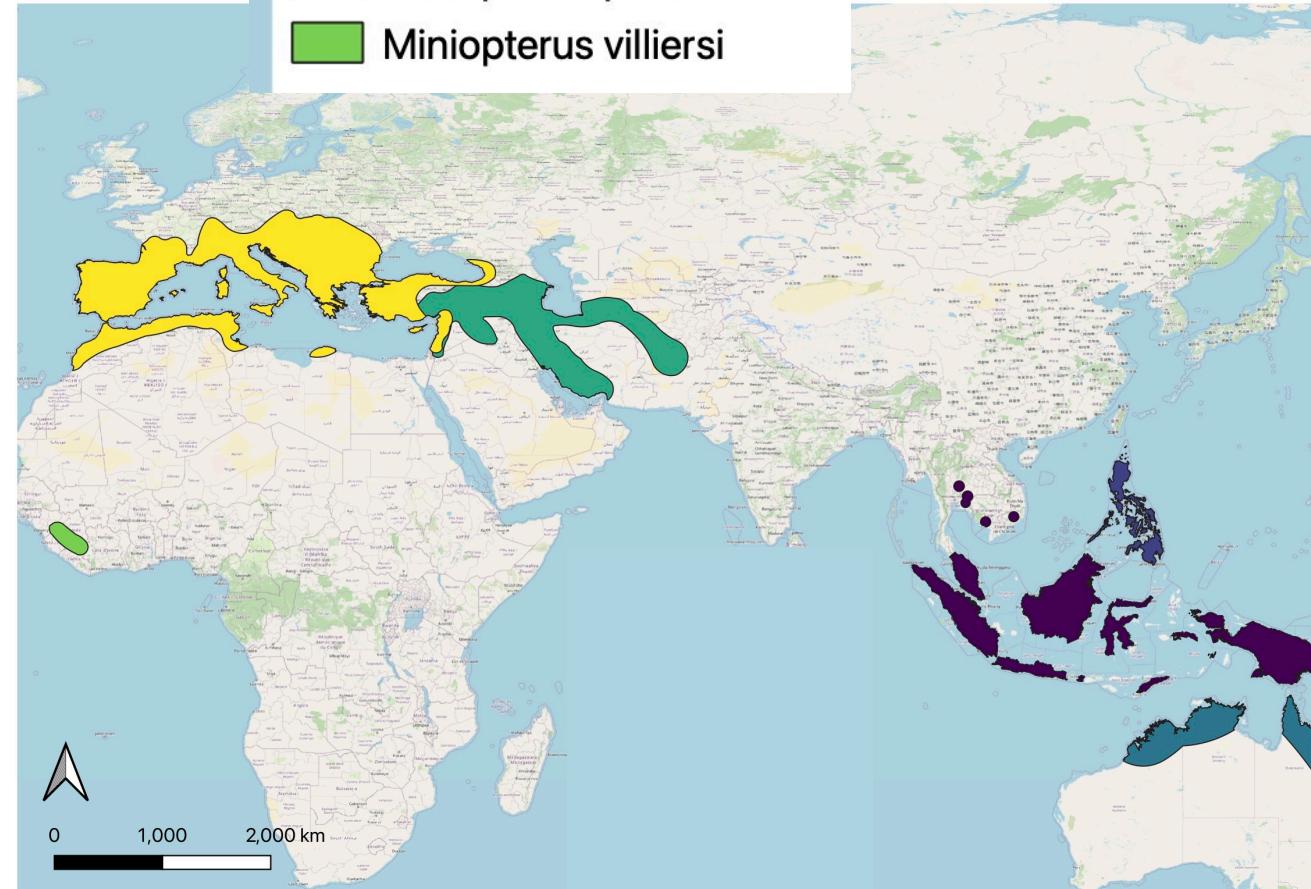
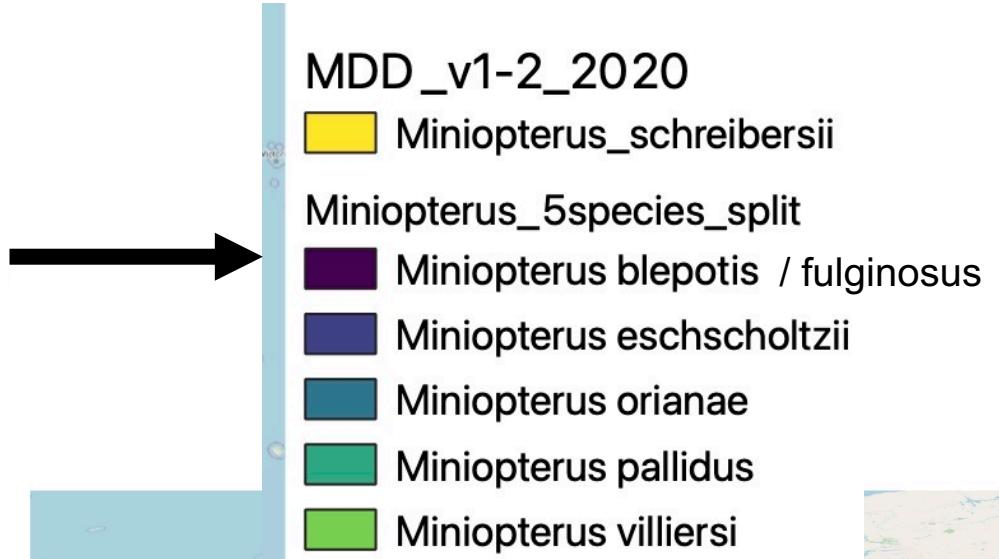
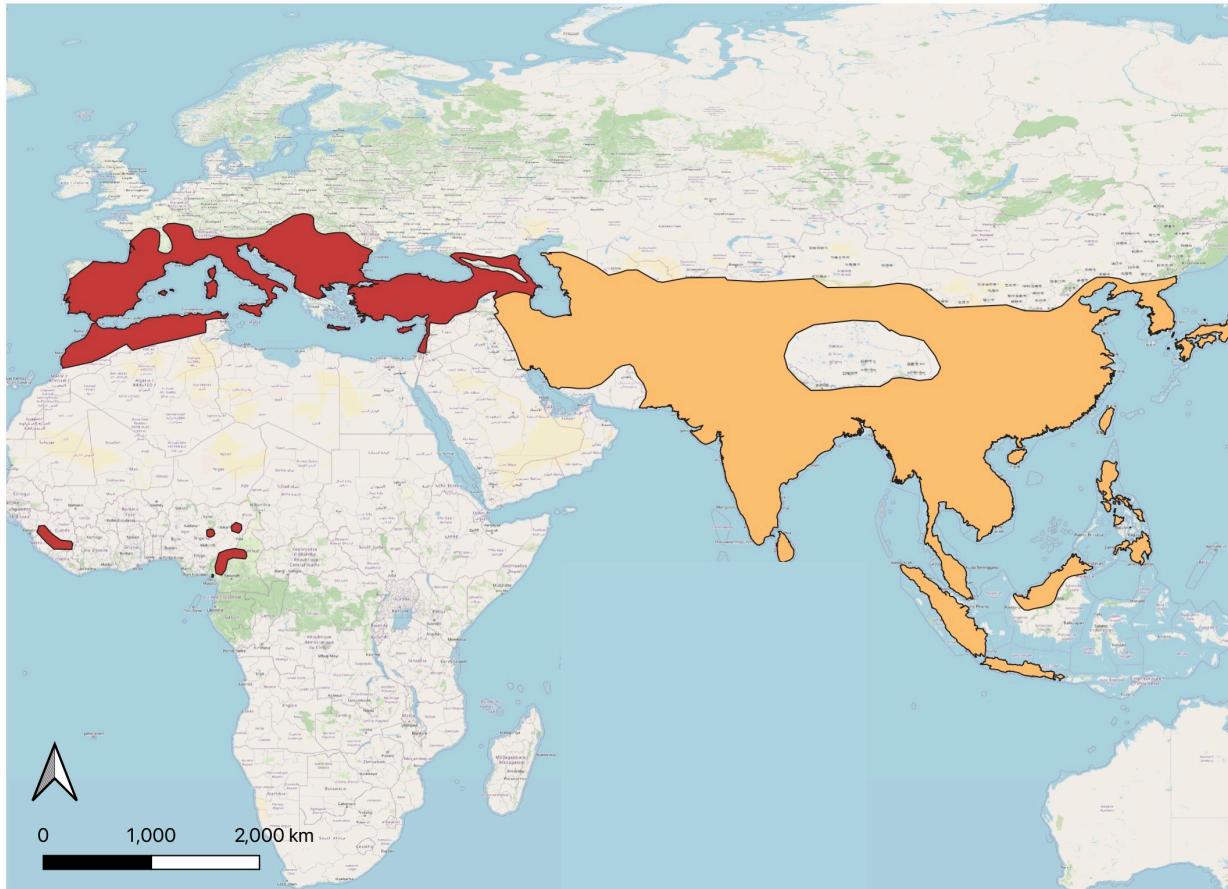
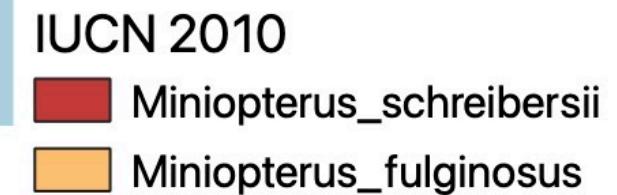


Jackson, S. M., & Groves, C. (2015). Taxonomy of Australian mammals.

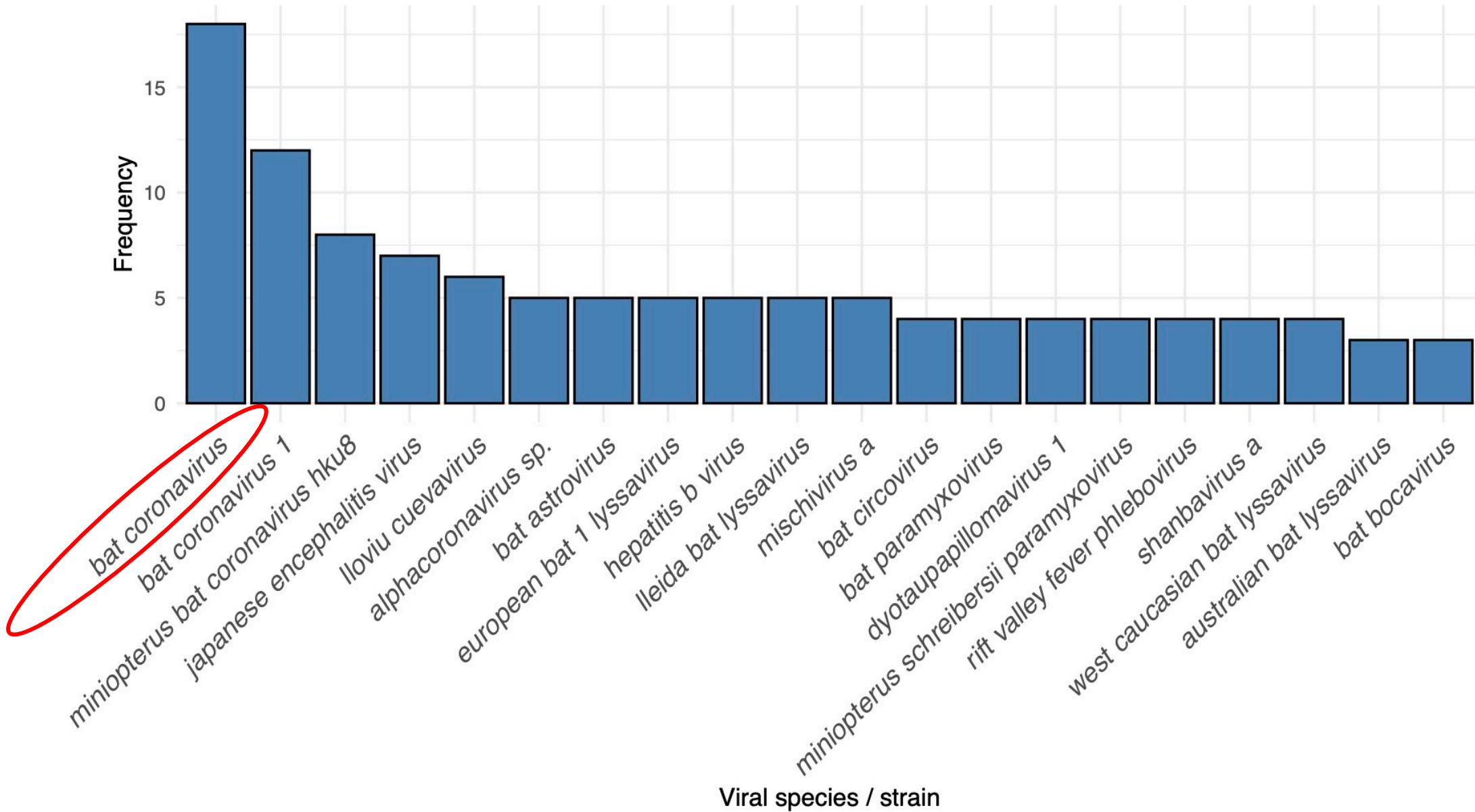
Miller-Butterworth, et al. (2007). Molecular Biology and Evolution



# Example: *Miniopterus schreibersii* / *fulginosus*



# Split of *Miniopterus schreibersii / fulginosus* → top 20 viruses affected



# Bat coronavirus isolate Anlong-3 RNA-dependent RNA polymerase gene, partial cds

GenBank: KF294268.1

[FASTA](#) [Graphics](#) [PopSet](#)

Go to:

LOCUS KF294268 2780 bp RNA linear VRL 16-MAR-2020  
DEFINITION Bat coronavirus isolate Anlong-3 RNA-dependent RNA polymerase gene, partial cds.

ACCESSION KF294268  
VERSION KF294268.1  
KEYWORDS .  
SOURCE Bat coronavirus  
ORGANISM [Bat coronavirus](#)

Viruses; Riboviria; Orthornavirae; Pisuviricota; Pis Nidovirales; Cornidovirinae; Coronaviridae; Coronav 1 (bases 1 to 2780)

REFERENCE AUTHORS Lin,X.D., Wang,W., Hao,Z.Y., Wang,Z.X., Guo,W.P., Gu Wang,M.R., Wang,H.W., Zhou,R.H., Li,M.H., Tang,G.P., Holmes,E.C. and Zhang,Y.Z.

TITLE Extensive diversity of coronaviruses in bats from Ch JOURNAL Virology 507, 1-10 (2017)  
PUBMED [28384506](#)

REFERENCE AUTHORS Wang,W., Lin,X.-D., Zhou,R.-H., Guo,W.-P. and Zhang,J.

TITLE Direct Submission JOURNAL Submitted (23-JUN-2013) Department of Zoonoses, National of Communicable Disease Control and Prevention, China Disease Control and Prevention, Changping Liuzi 5, Beijing, China

FEATURES source Location/Qualifiers  
1..2780  
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/host="Miniopterus schreibersii"

FEATURES  
source

CHINA

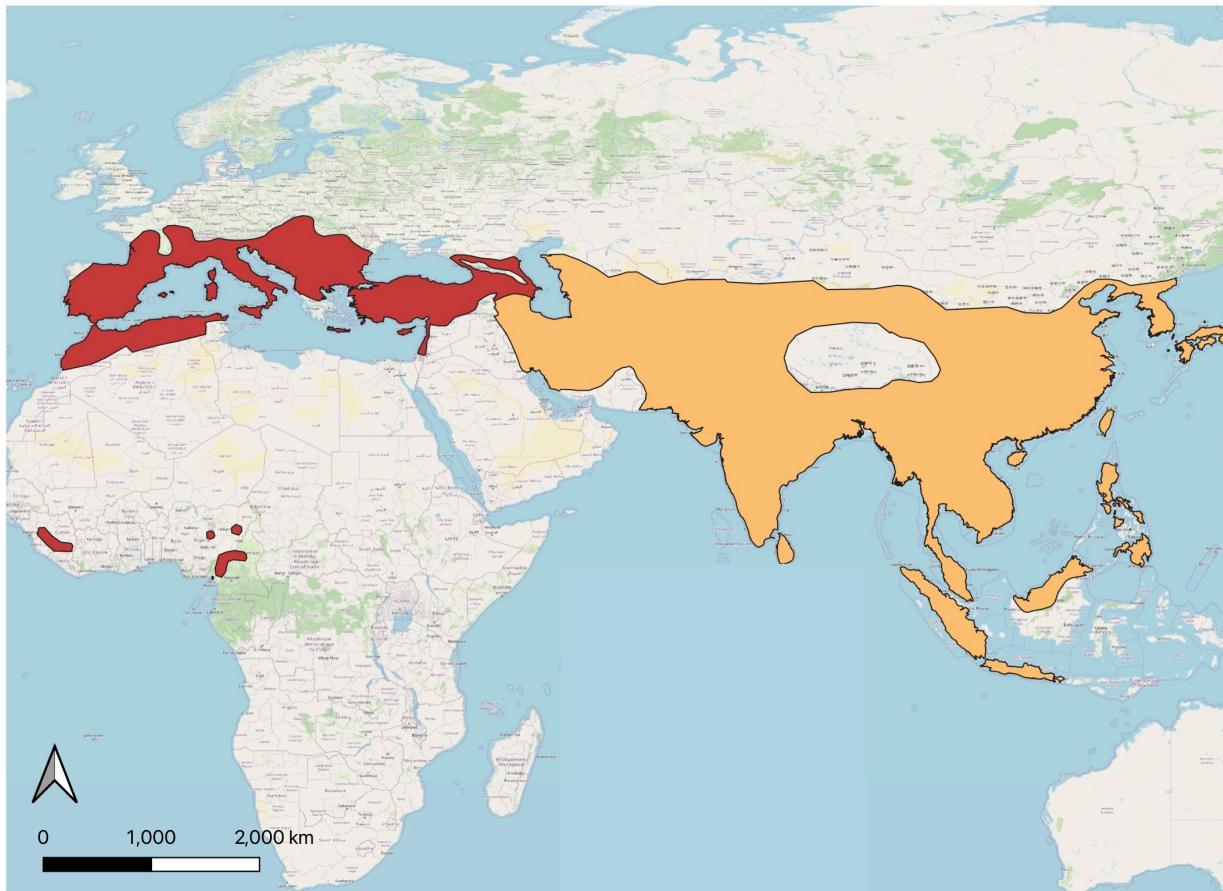
CDS

Location/Qualifiers  
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# Example: *Miniopterus schreibersii* / *fulginosus*

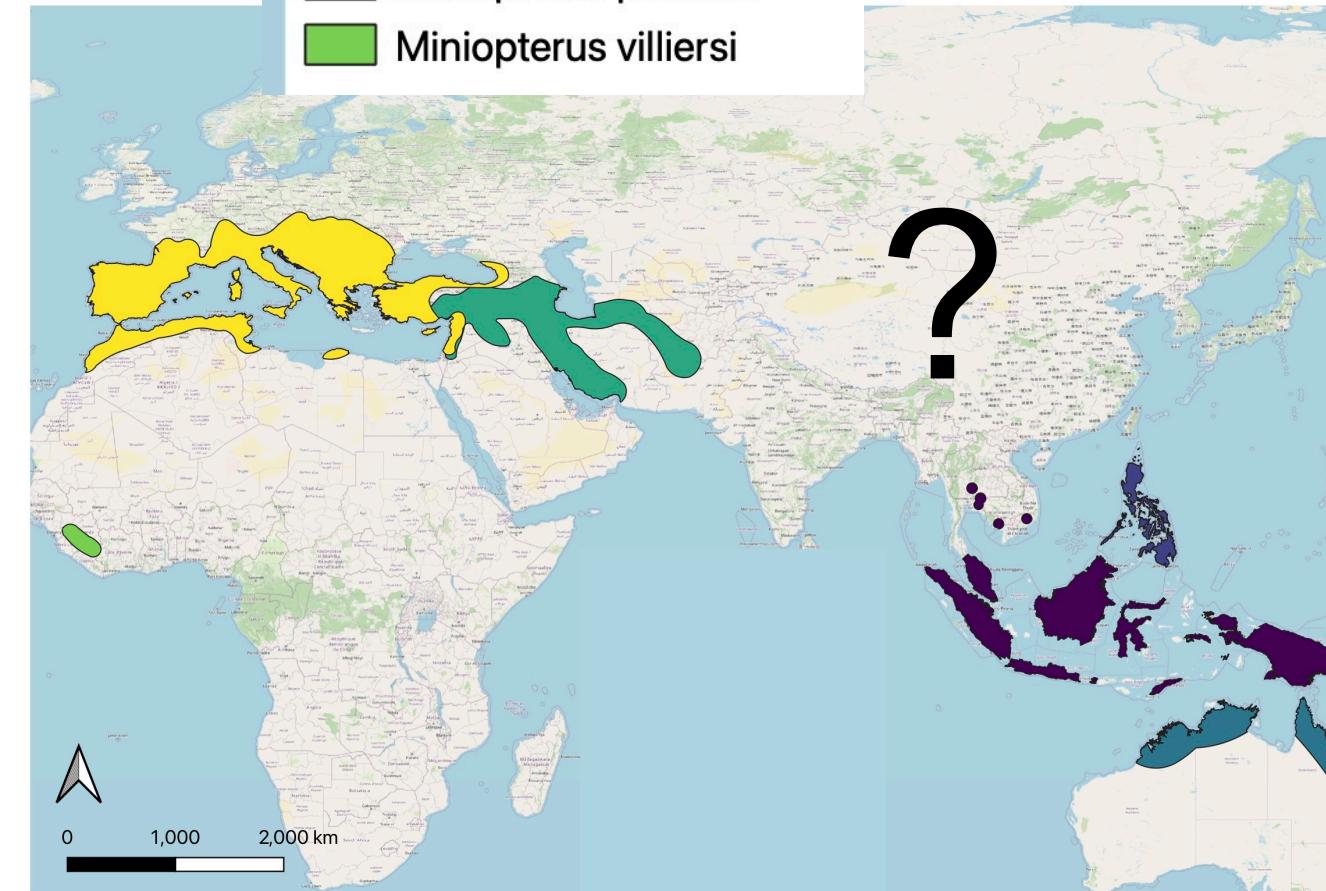
IUCN 2010

- Miniopterus\_schreibersii
- Miniopterus\_fulginosus



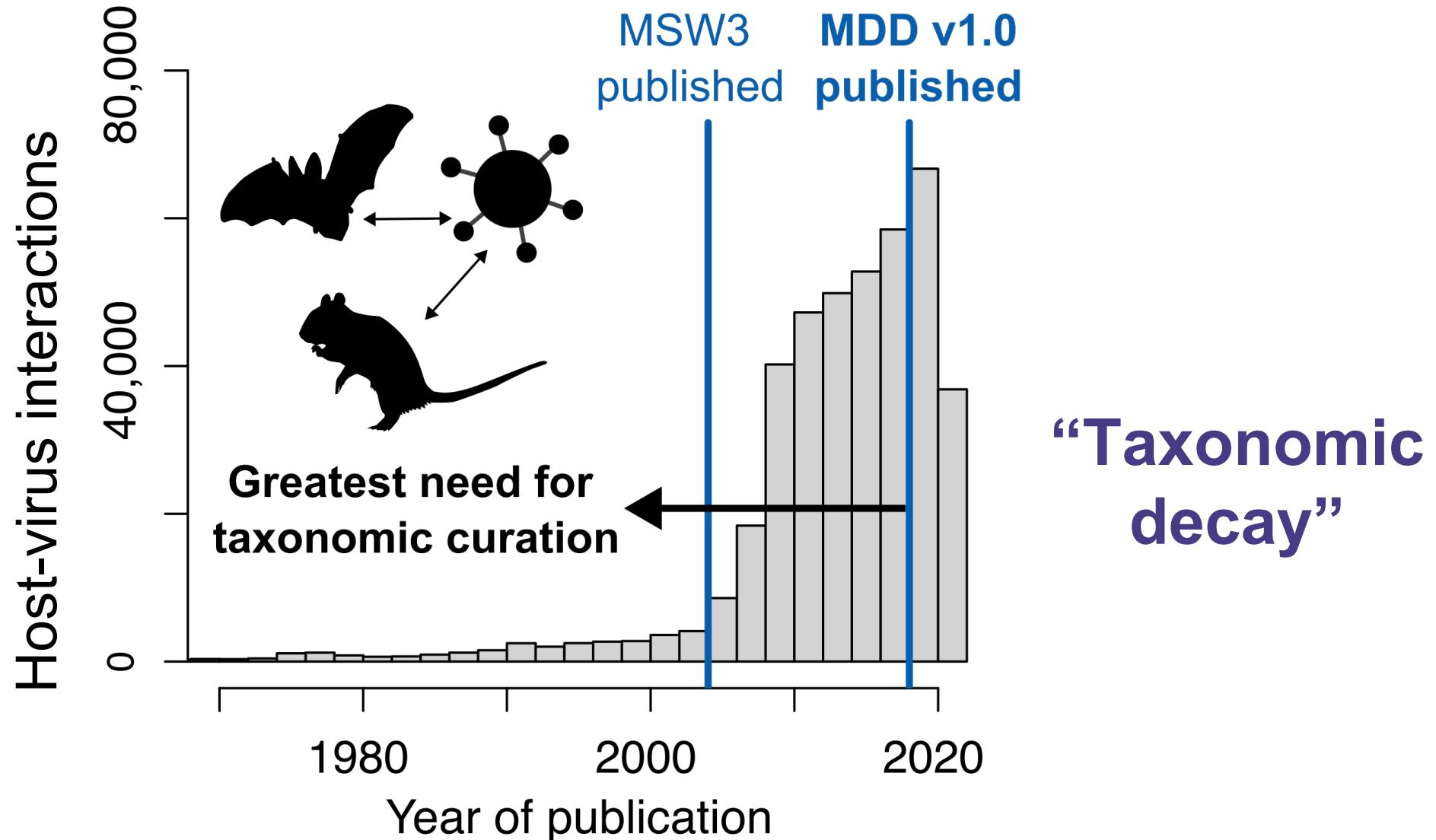
MDD\_v1-2\_2020

- Miniopterus\_schreibersii
- Miniopterus\_5species\_split
- Miniopterus\_blepotis / fulginosus
- Miniopterus\_eschscholtzii
- Miniopterus\_orianae
- Miniopterus\_pallidus
- Miniopterus\_villiersi



**Conclusion 1:**

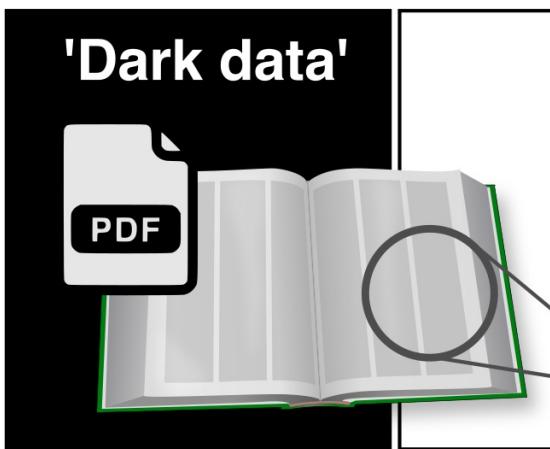
**Broader issue for all mammal-virus data**  
→ Taxonomic curation tools are badly needed



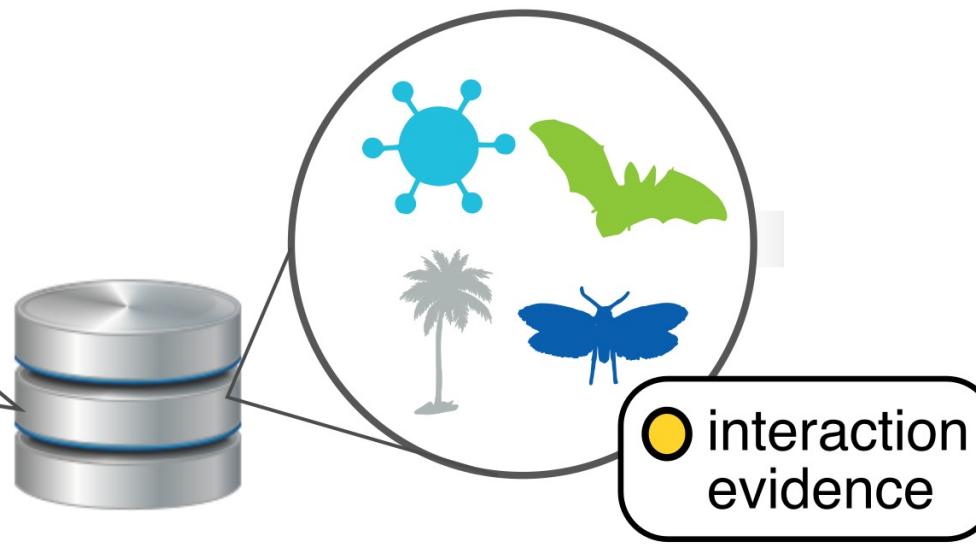
## Conclusion 2:

**Literature context of viral interactions is key**  
→ Location of sampling → taxonomic change

Written knowledge



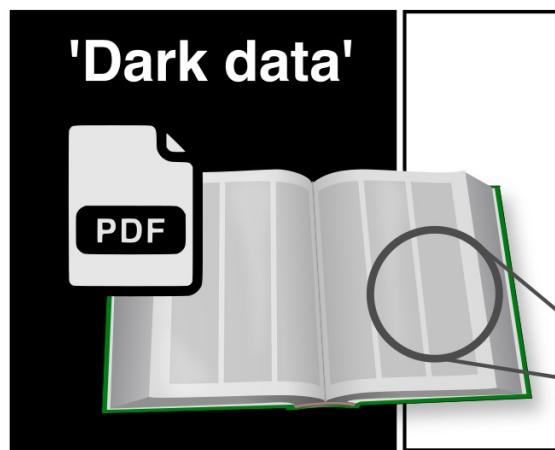
Digital data



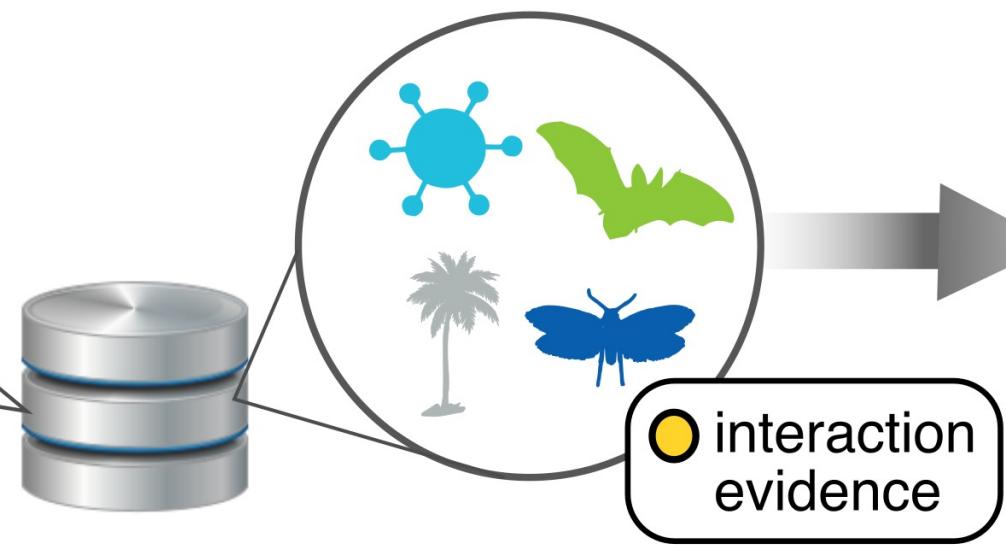
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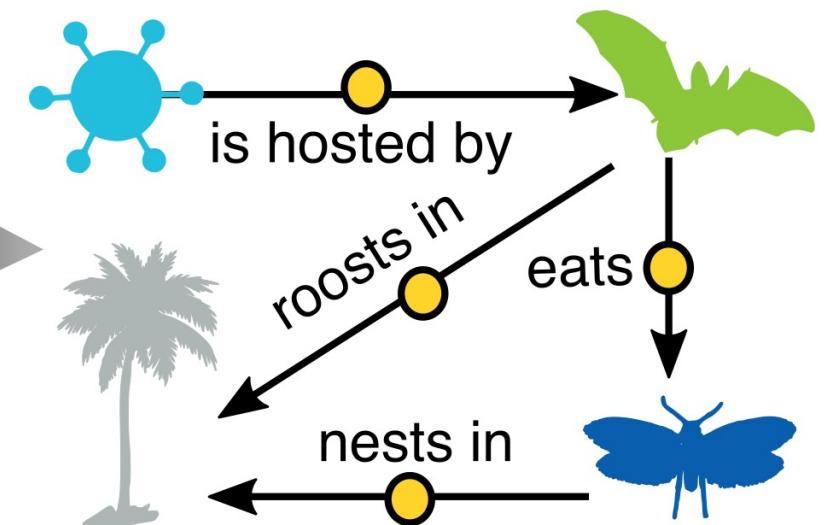
Written knowledge



Digital data



Host-virus knowledge graph





# Bat Eco-Interactions Working Group



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Bat Eco-Interaction Project



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EcoHealth Alliance



**Donat Agosti**

Plazi



**Anna Willoughby**

Univ Georgia

**Arizona State  
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## Upham Lab:

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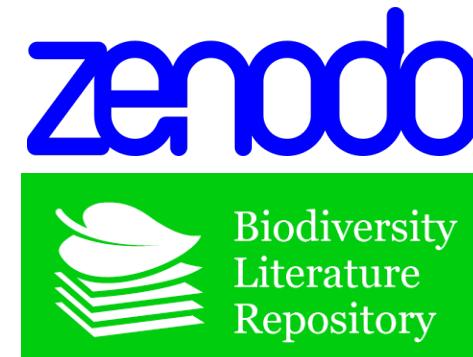
## Arizona State Univ:

Nico Franz, Beckett Sterner, Atriya Sen, Prashant Gupta, Nicole Veeder, Dakota Rowsey, Laura Steger, Jonathan Rees, Andrew Johnston, Laura Prado, Ángel Robles, Caleb Powell, Sharon Hall



## CETAF-DiSSCo Taskforce:

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# Questions?

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