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CVR Medical Research Council University of Glasgow Centre for Virus Research

Molecular evolution of vampire bats and rabies virus

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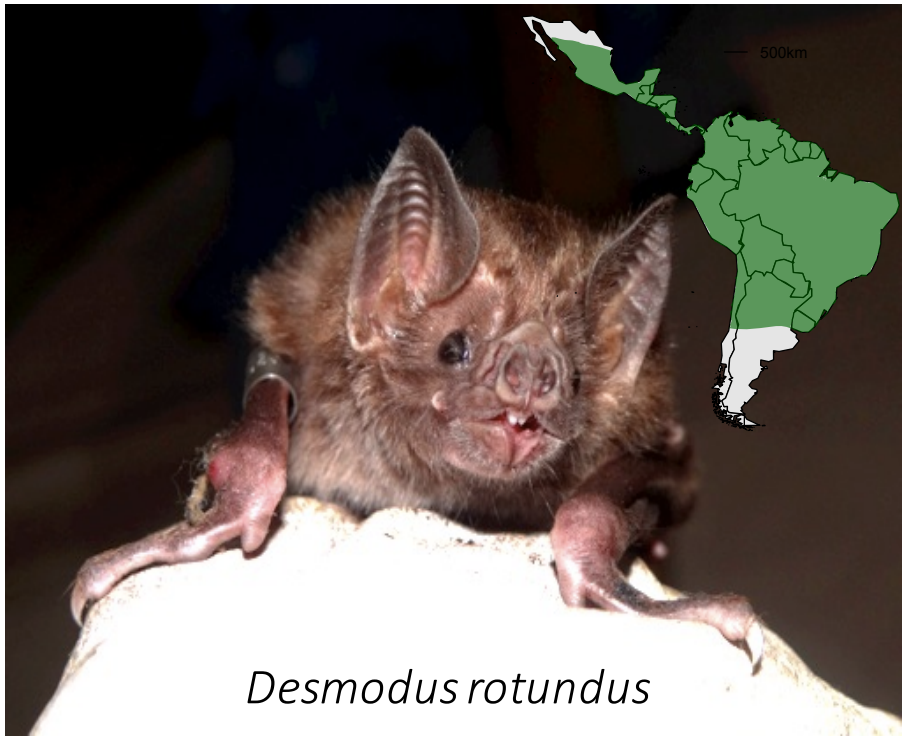
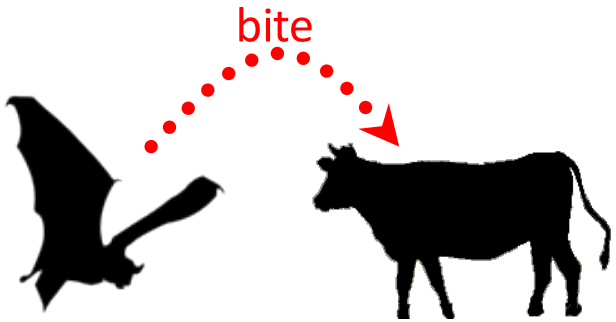
www.streickergroup.wordpress.com

Vampire bat rabies in Latin America

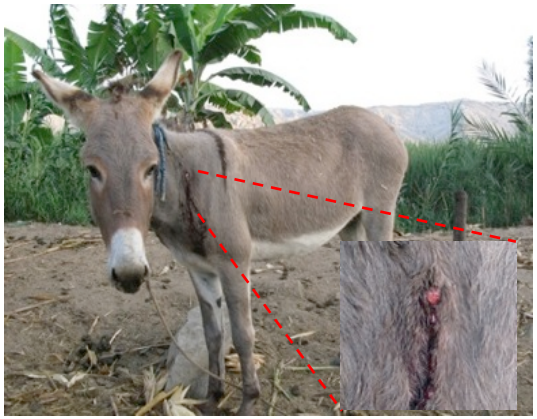
Maintenance host



Desmodus rotundus



Dead end hosts



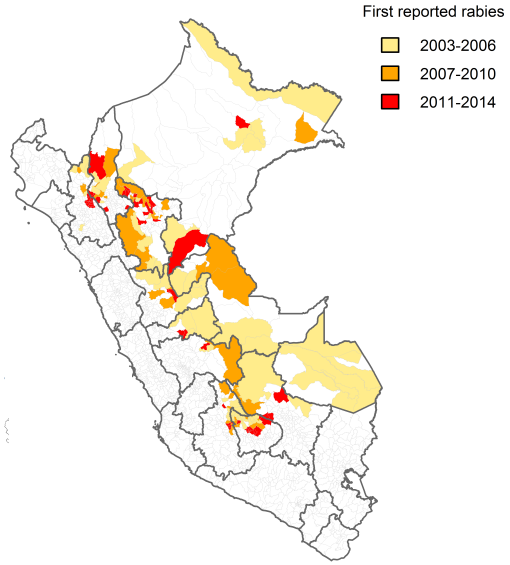
Livestock rabies

Thousands of lethal outbreaks every year

Human rabies

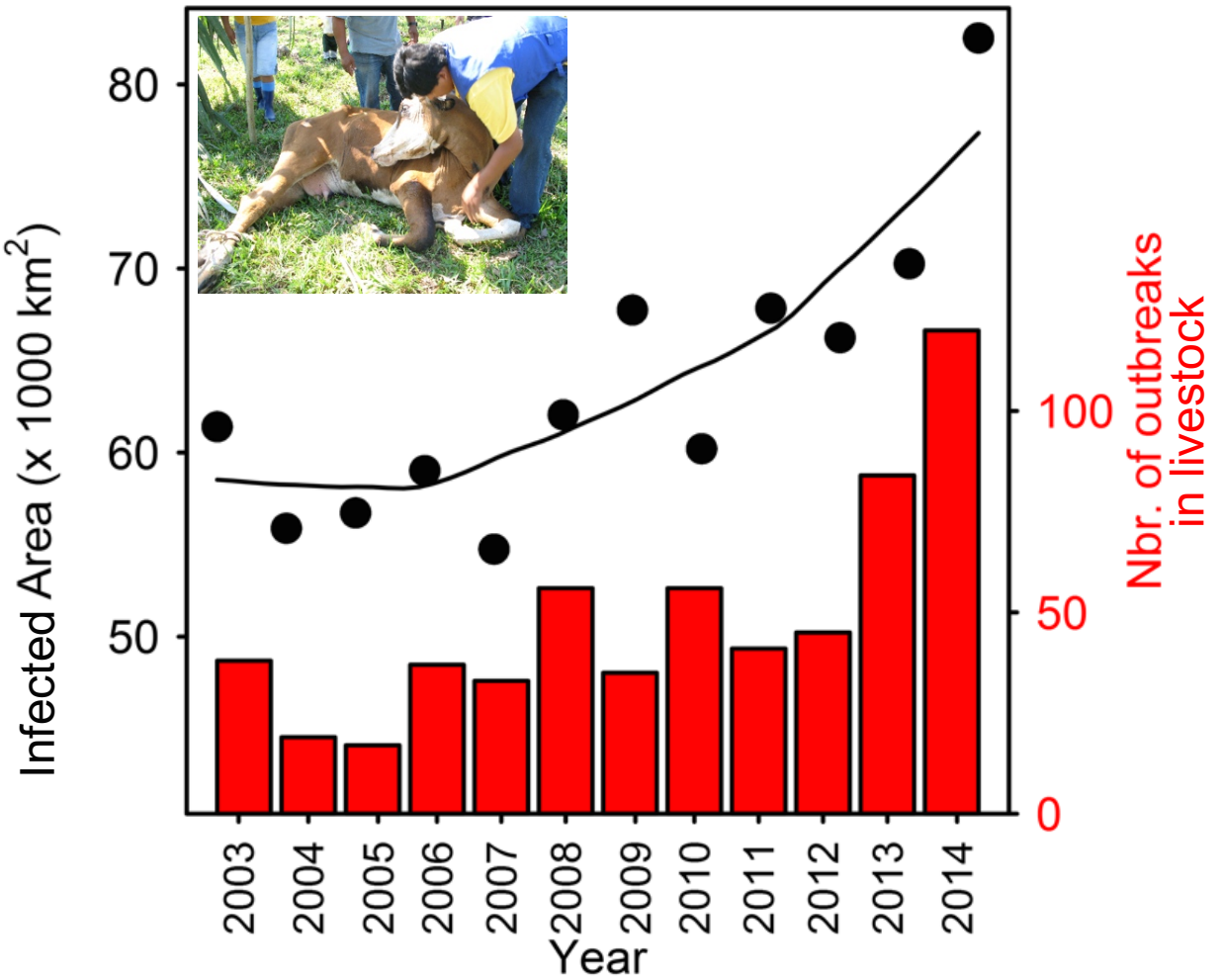
Increasing source (85% of 173 human rabies cases since 1996 in Peru)

Rabies expanding into previously rabies-free vampire bat populations



Data: SENASA Peru

Area infected and number of rabies outbreaks in livestock



Benavides, Valderrama & Streicker (2016) **Proc B**

Vampire bat dispersal

Anticipate outbreaks in enzootic areas

Forecast viral invasion to currently rabies-free areas

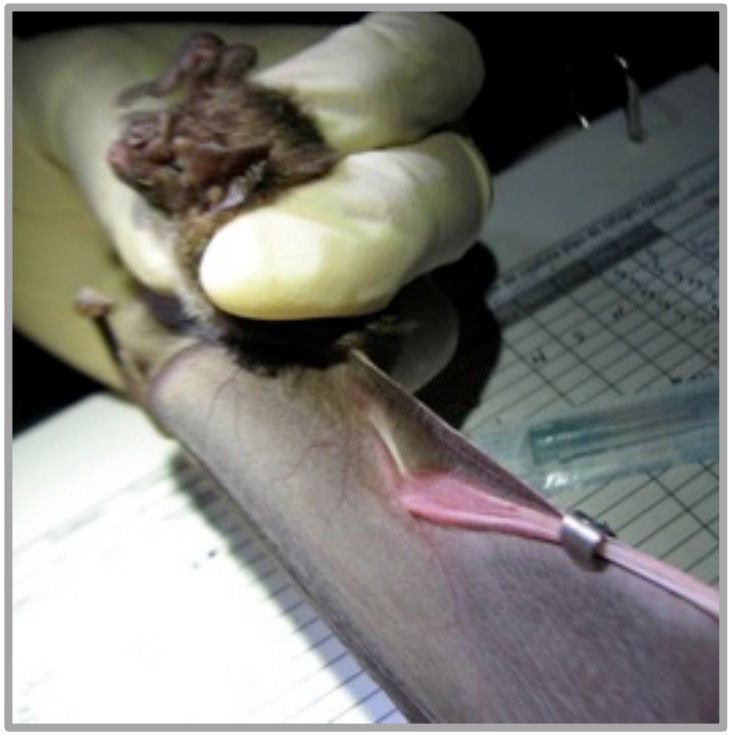
New opportunities for prevention and control

Field methods to study vampire bat dispersal

Radio-telemetry

Good on small spatial scales
Challenging to implement

Mark-recapture



Good on small to medium spatial scales
Requires recapture

Genetic approach to study bat and virus dispersal

Host genetics

Geographic barriers to bat flight

Identify connected populations

Sex-biased dispersal (♂ & ♀ inherited genetic markers)

Geographic routes and mechanisms for future virus spread

Virus sequences

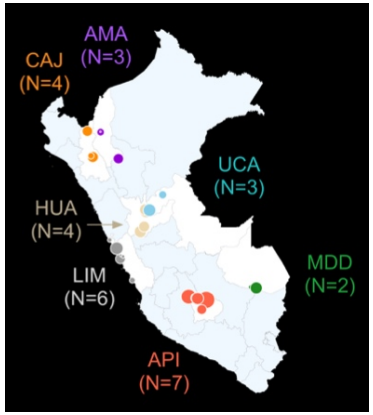
Quantify speed of viral invasion

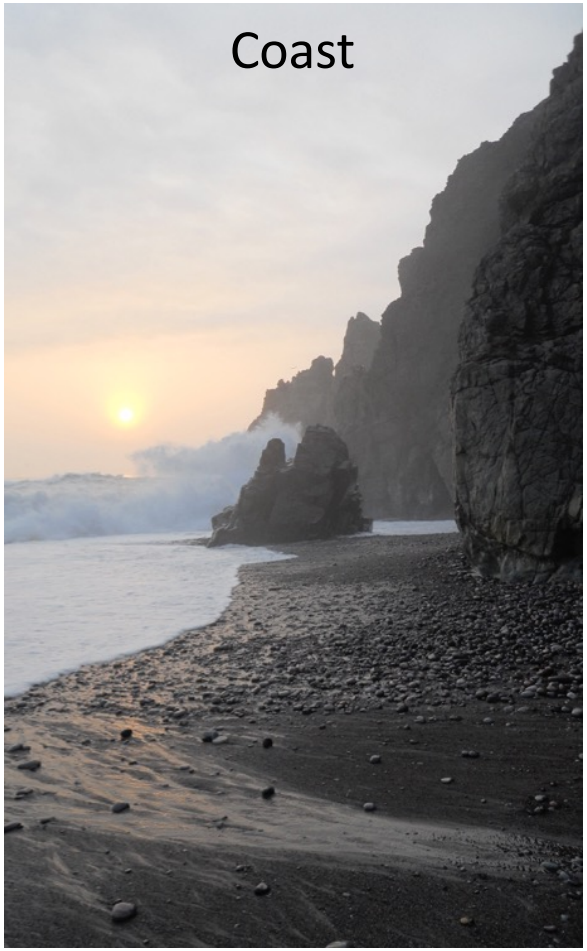
Speed of viral spread

Predict routes and timing of future viral invasions to rabies free-areas

Capture and sampling of vampire bats in Peru

29 colonies of *Desmodus*





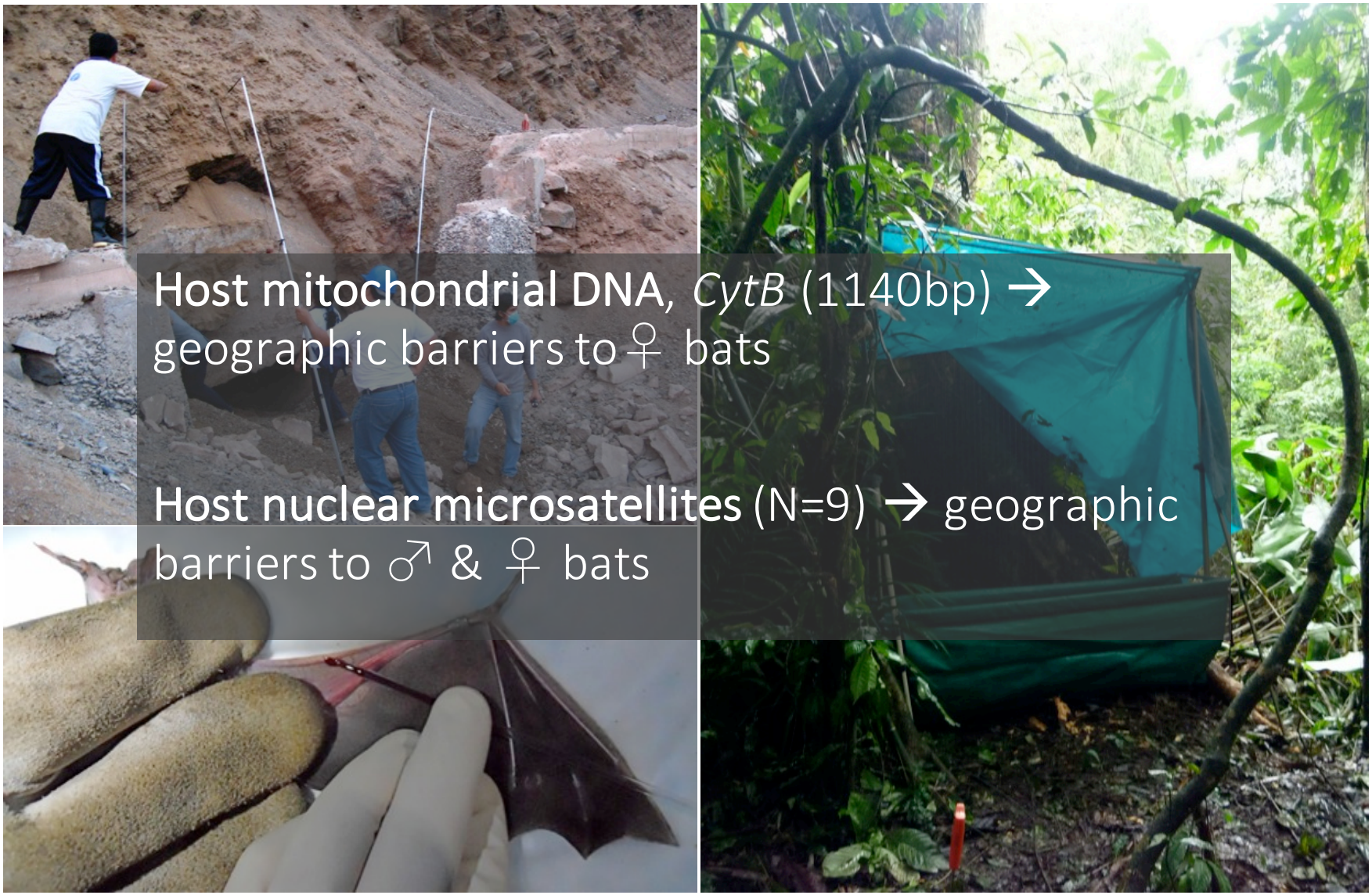
Vampire bat rabies free

Vampire bat rabies enzootic

Vampire bat rabies enzootic

Collection of DNA from vampire bats

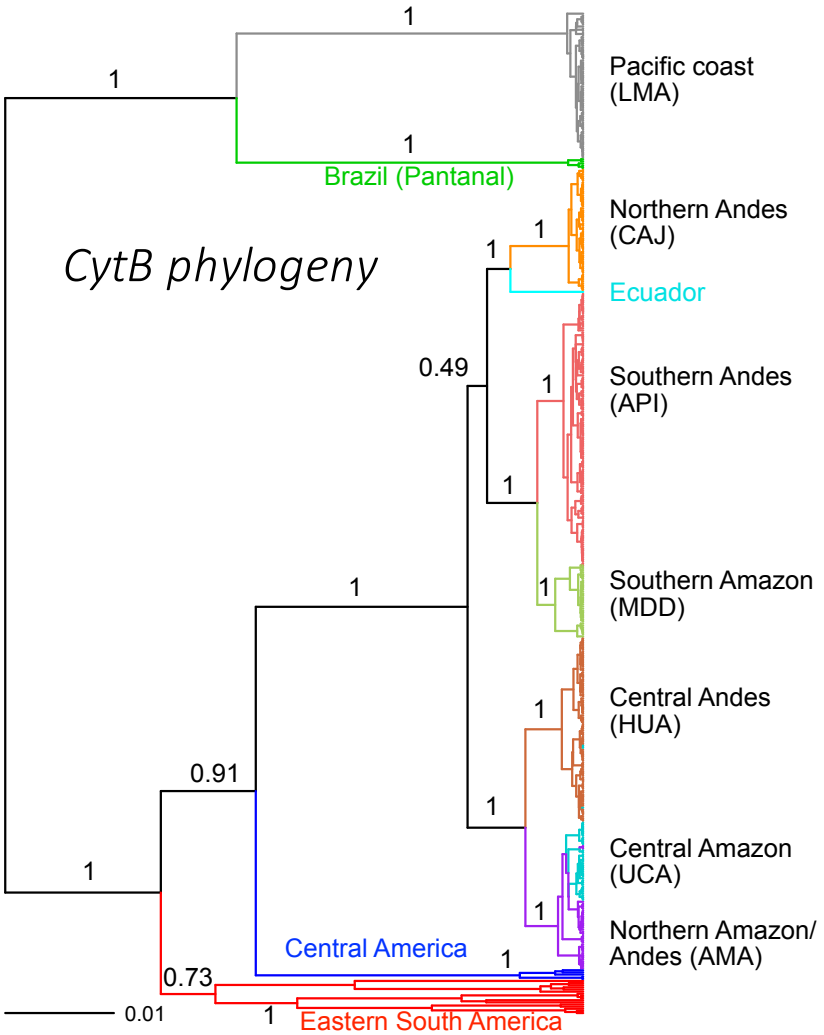
> 480 bats

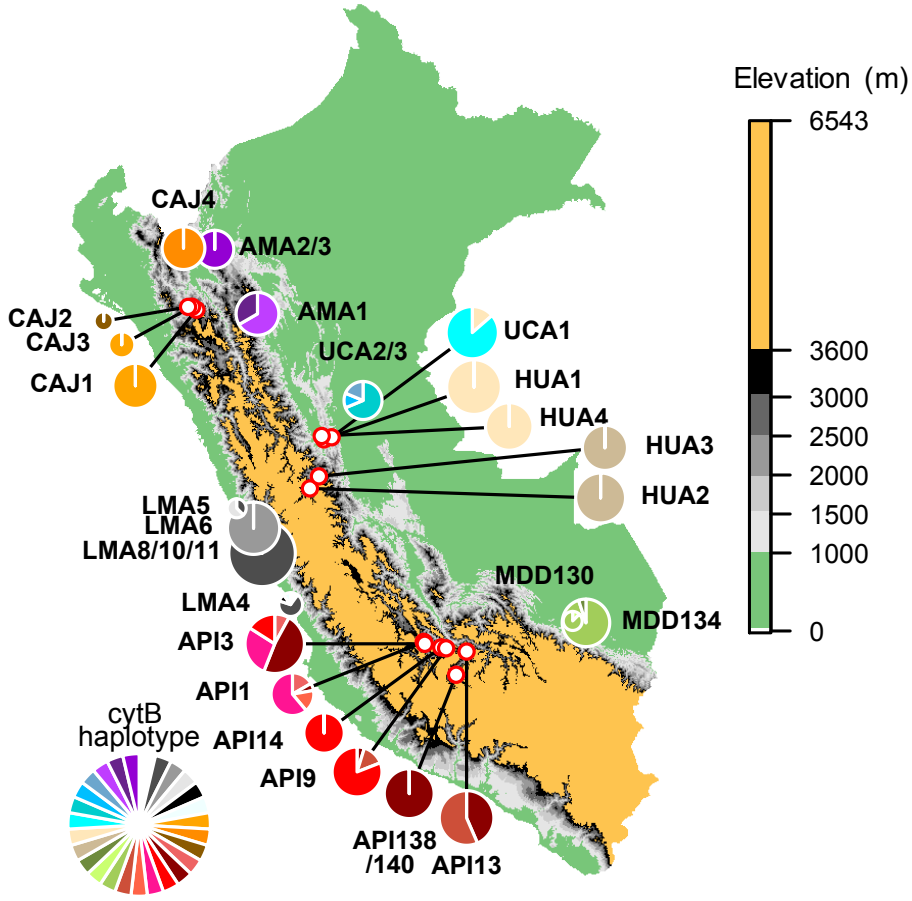


Host mitochondrial DNA, *CytB* (1140bp) → geographic barriers to ♀ bats

Host nuclear microsatellites (N=9) → geographic barriers to ♂ & ♀ bats

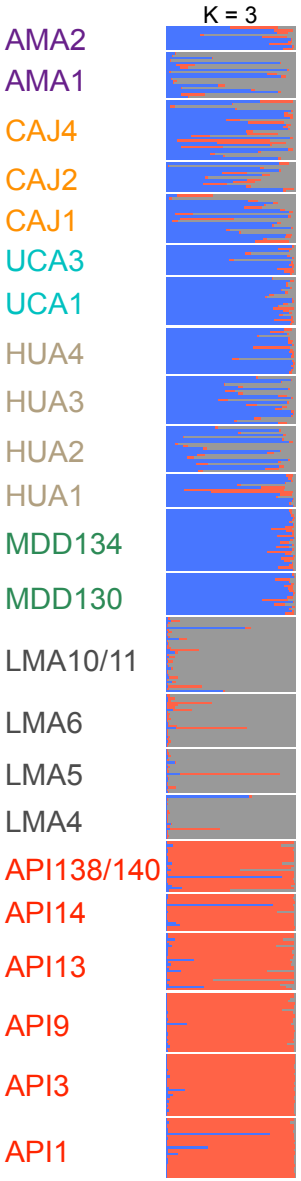
Bat mitochondrial DNA: females are sedentary



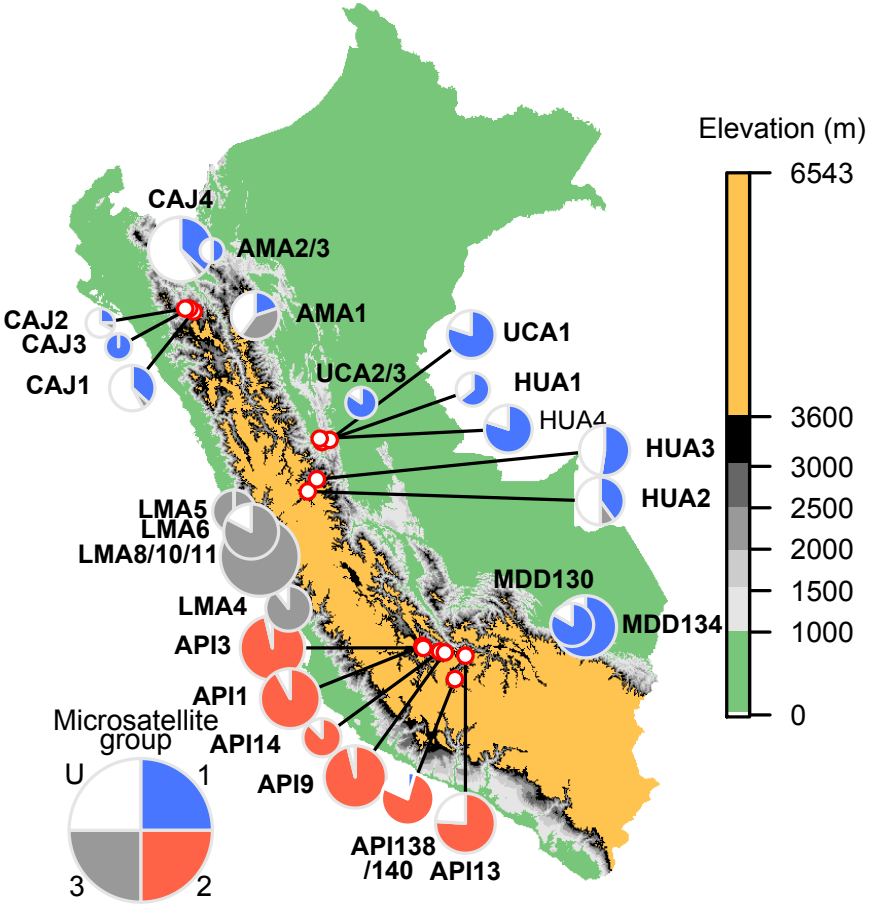


Streicker *et al.* (2016) **PNAS**

Bat nuclear microsatellites: gene flow over larger distances



Analyses using **STRUCTURE** and **DAPC** support 3 genetic groups of vampire bats



Less genetic structure in bi-parentally inherited marker than in maternally-inherited maker suggests male-biased dispersal

Streicker *et al.* (2016) **PNAS**

Virus samples from national surveillance system of Peru (SENASA)

***Rabies virus* sequences**

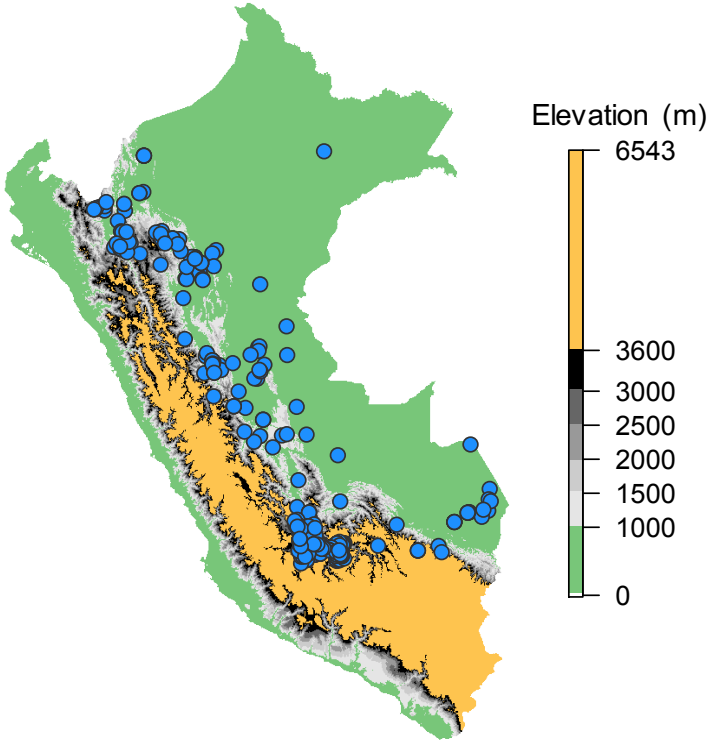
Nucleoprotein (1350bp)

G-L (519bp)

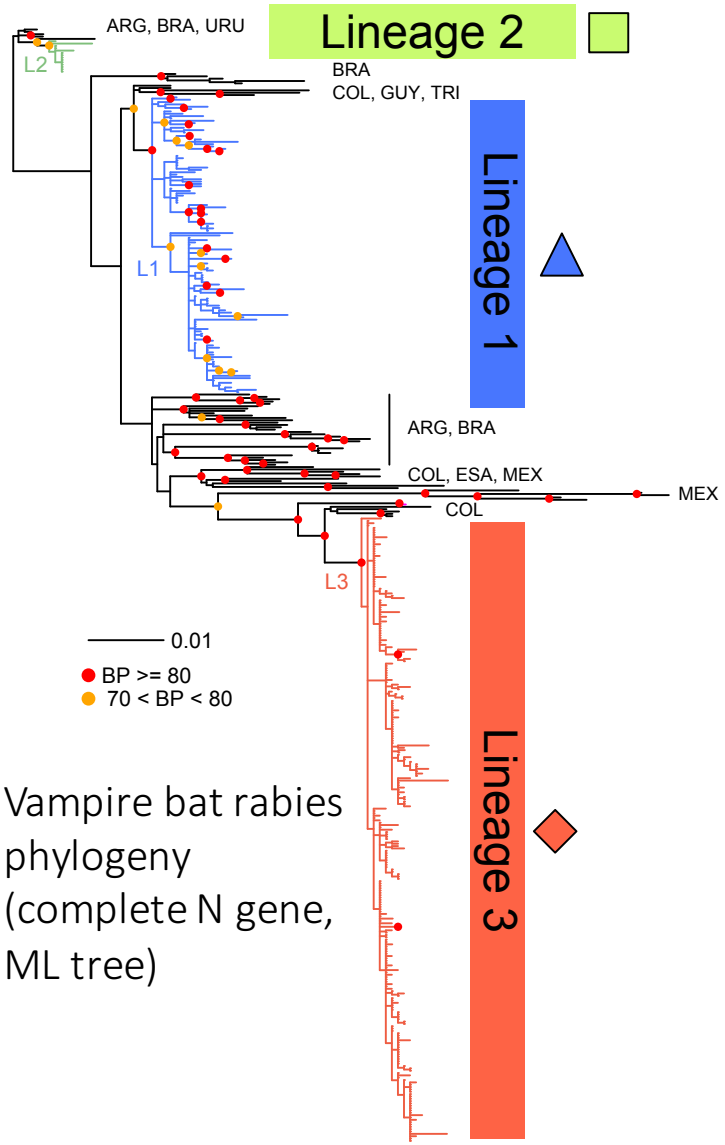
N=264 isolates

1997-2012

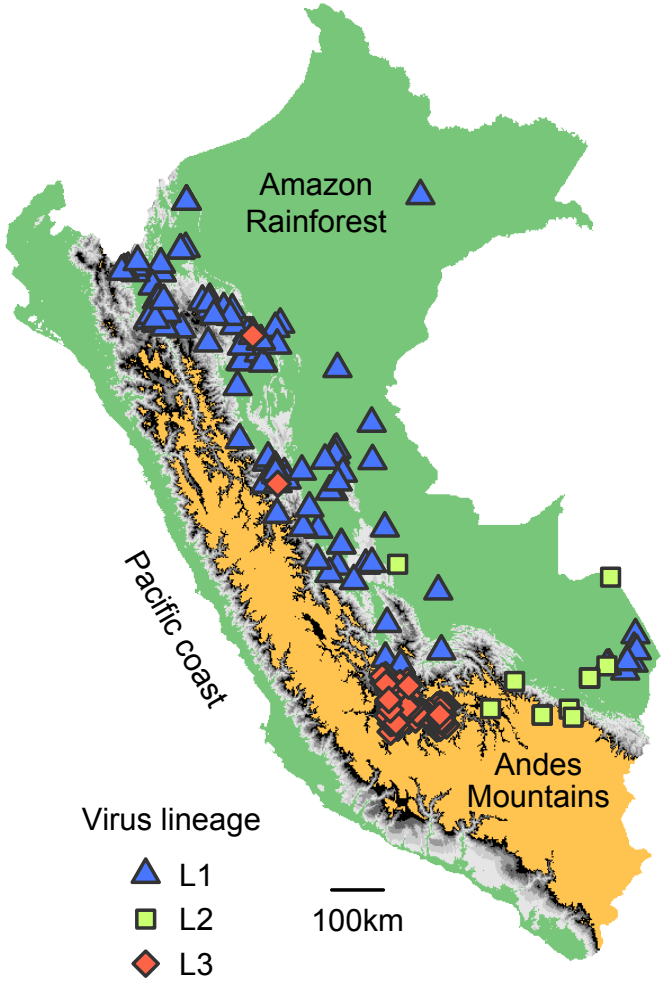
Rabies cases in Peruvian livestock



Rabies virus sequences: 3 independent lineages with different geographic associations



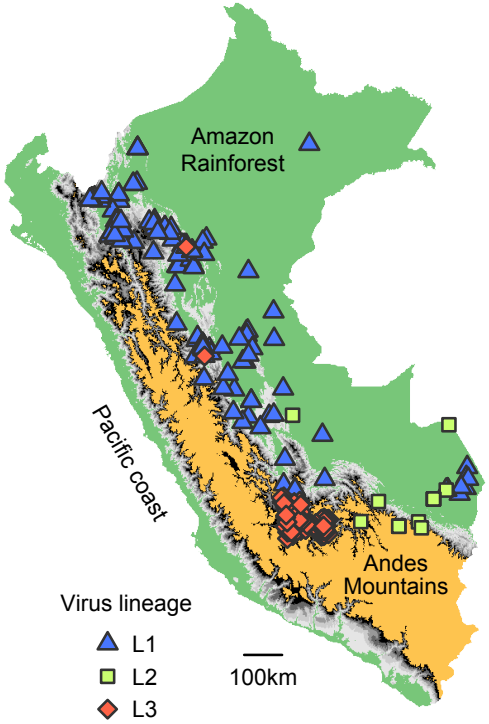
Vampire bat rabies phylogeny (complete N gene, ML tree)



Streicker *et al.* (2016) **PNAS**

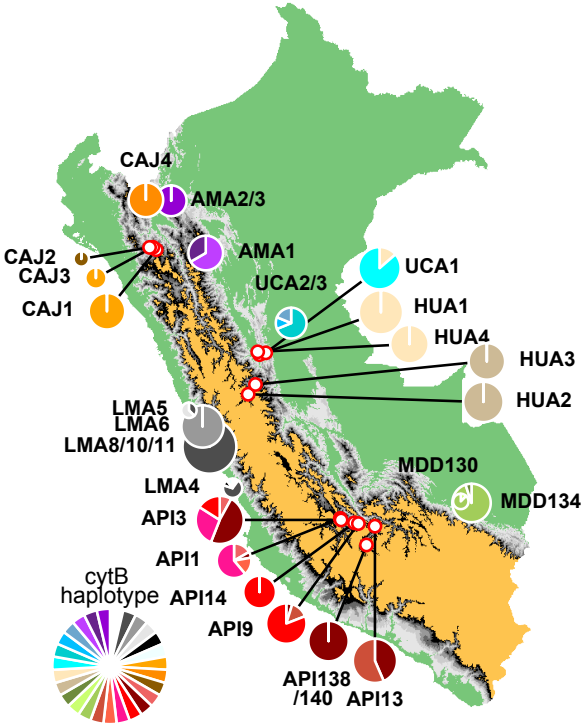
Contrasting patterns of population structure in bat and virus

Rabies virus



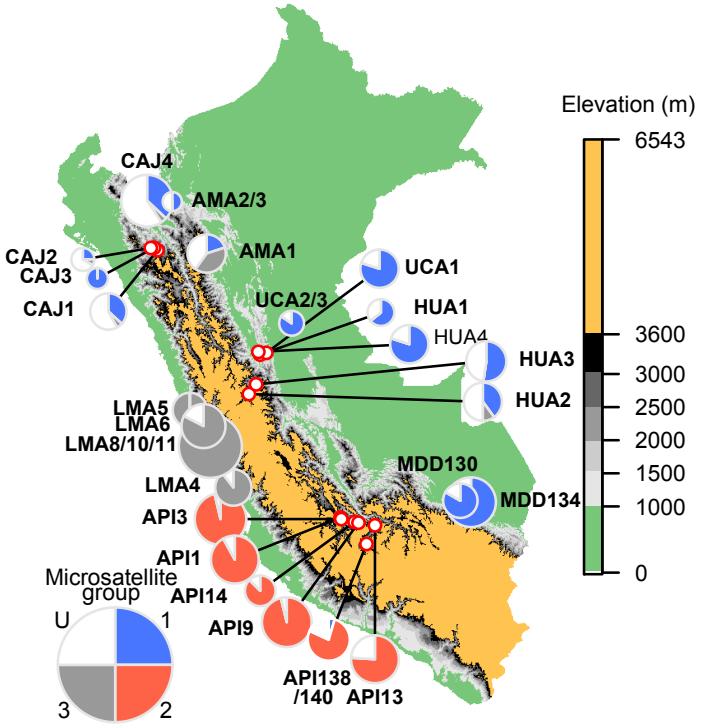
Isolation of coast & southern Andes
Gene flow east of Andes

Bat mtDNA (♀ inherited)



Isolation of all regions
No gene flow east of Andes

Bat Microsats (♂ & ♀ inherited)



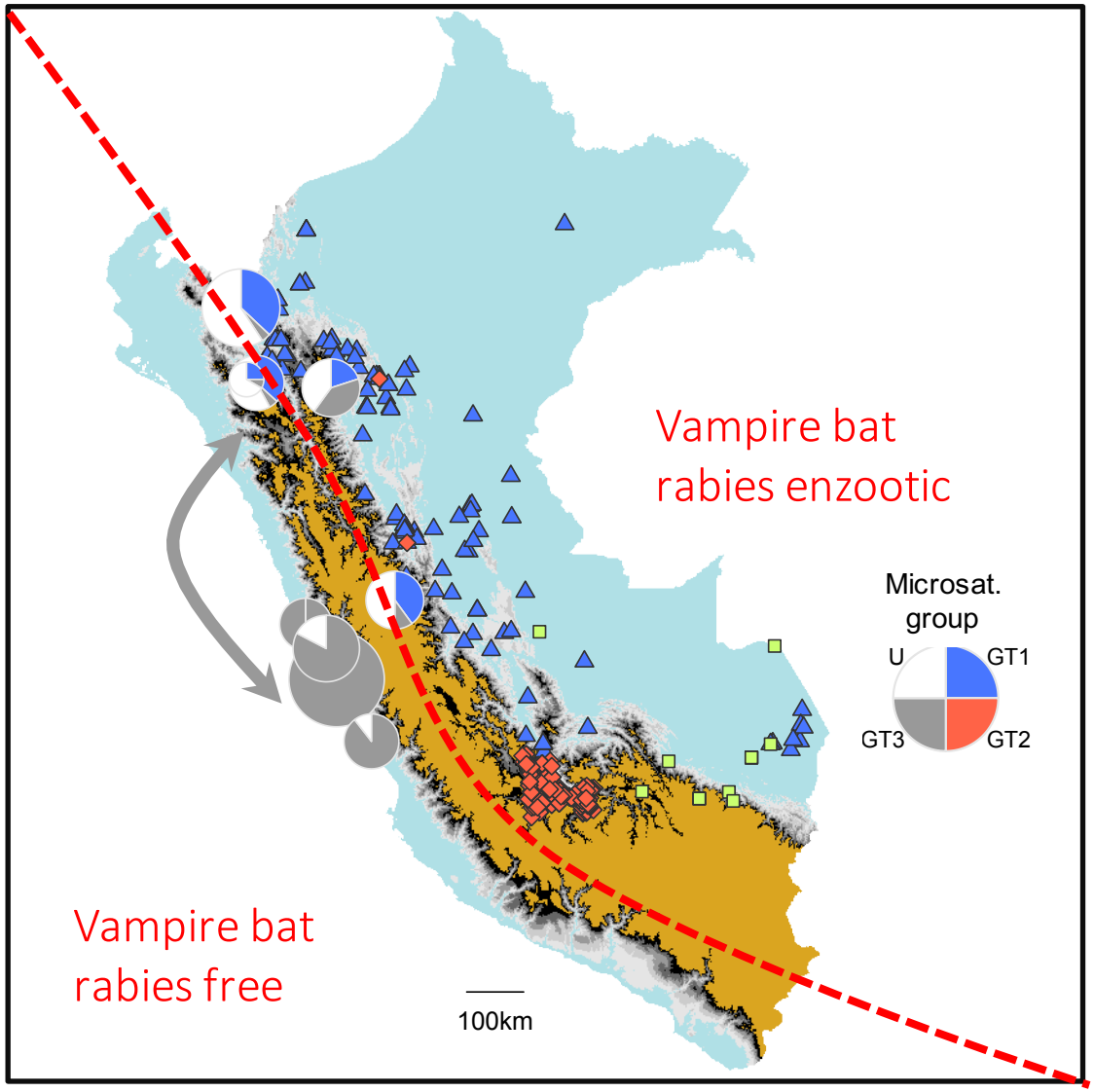
Isolation of coast & southern Andes
Gene flow east of Andes

Greater population structure of mtDNA indicates male-biased dispersal
Similarity of virus and microsatellites suggests male bats are key to viral spread

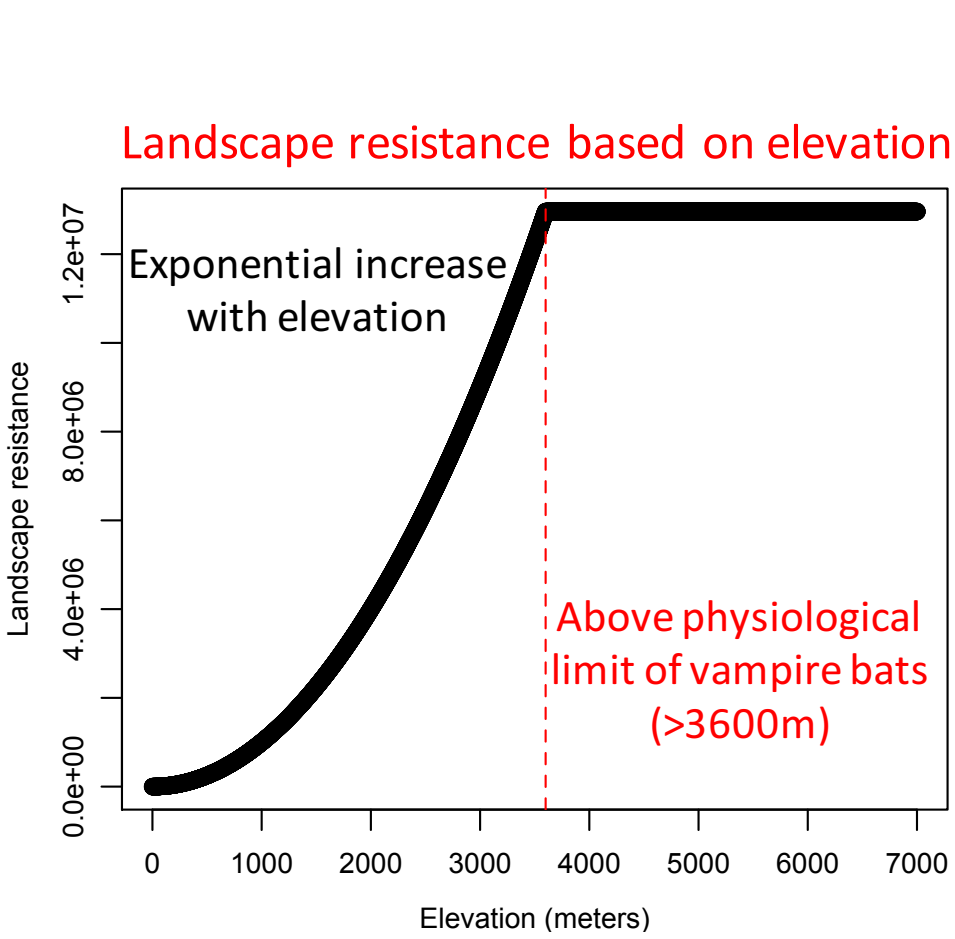
Gene flow across the Andes

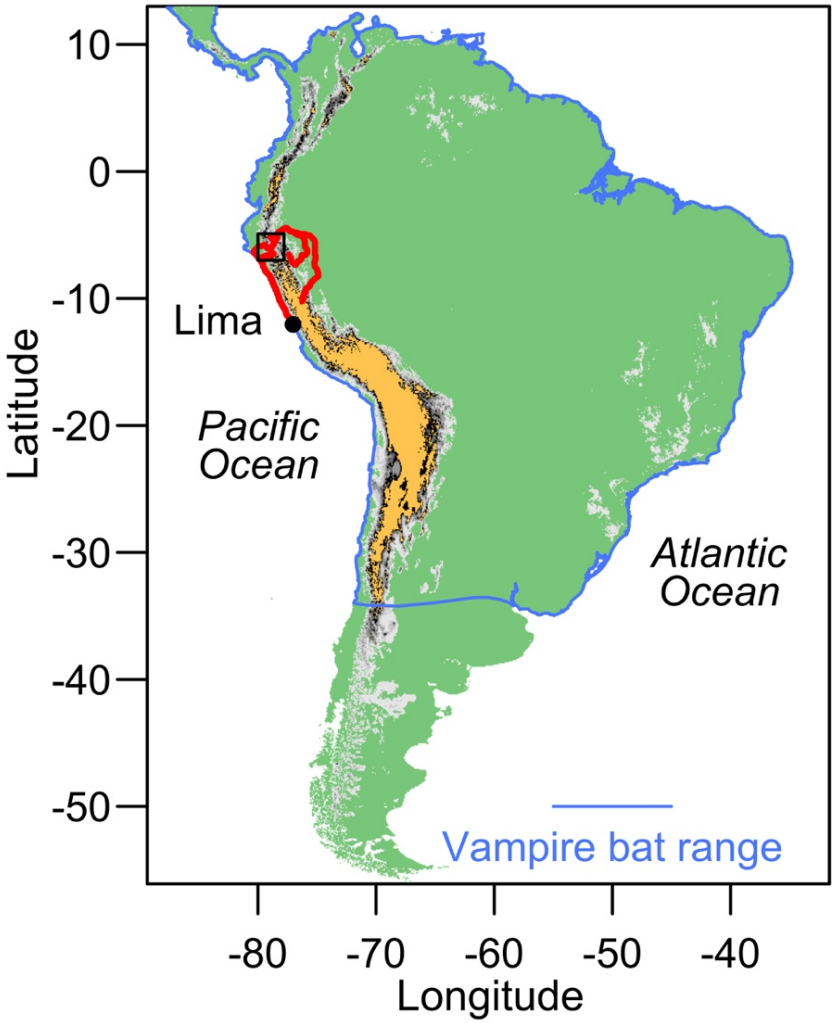
What routes might the virus follow to invade the coast?

Is rabies already spreading to the coast?



Simple landscape model of bat dispersal and viral spread

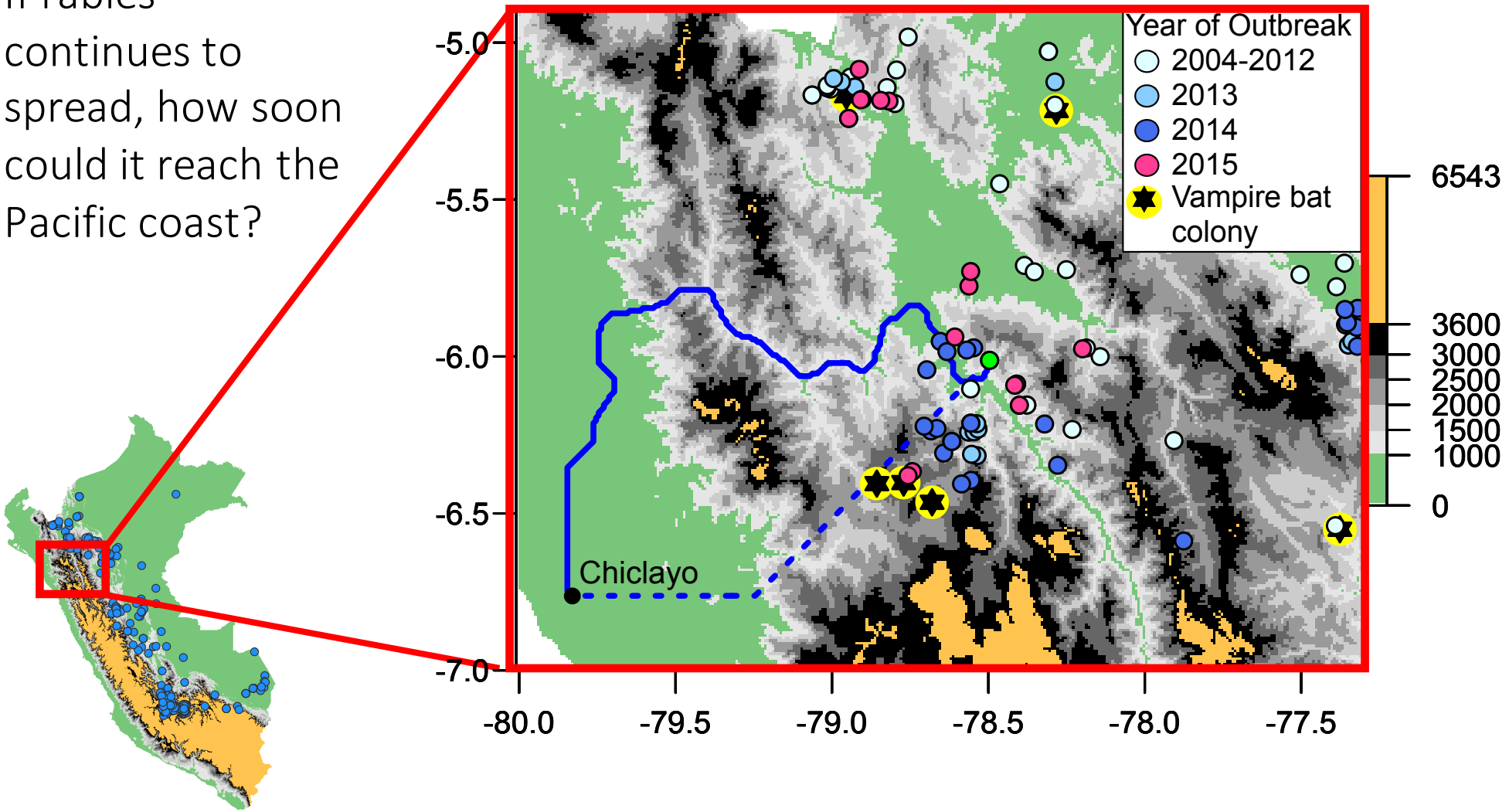




Most likely routes of viral invasion pass through Northern Peru

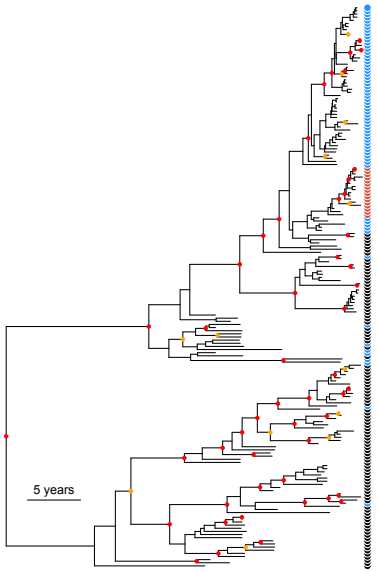
Recent viral invasion on projected routes to Pacific coast?

If rabies continues to spread, how soon could it reach the Pacific coast?

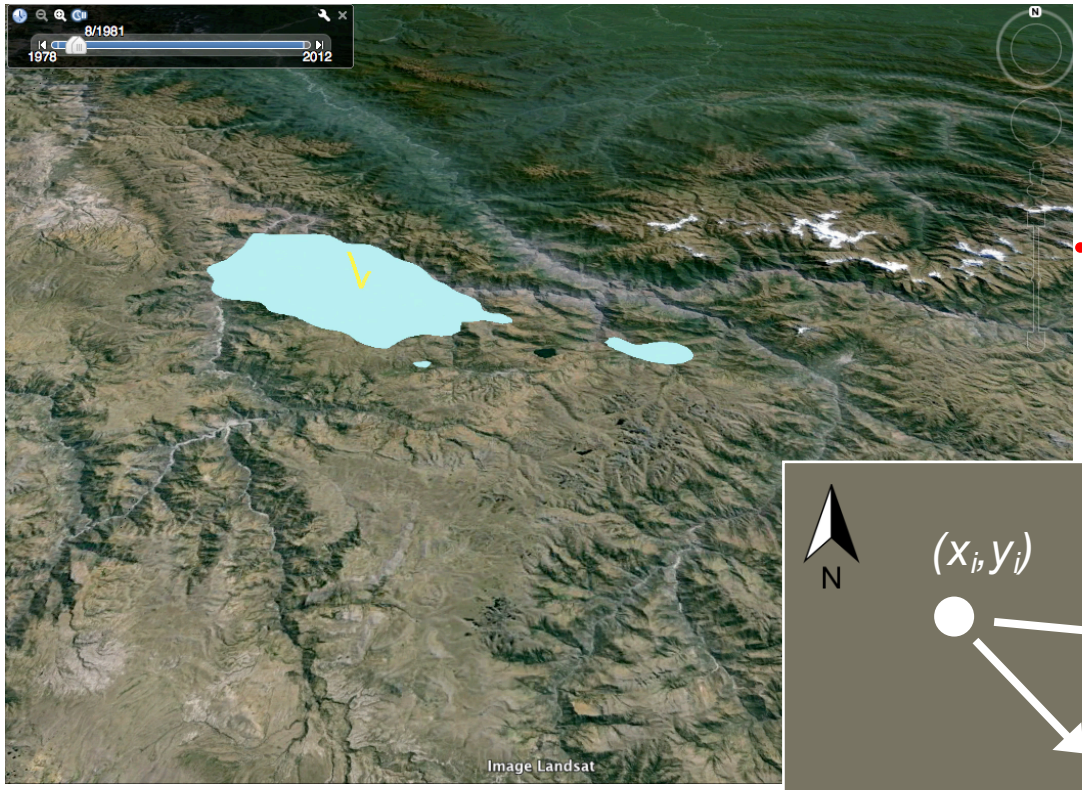


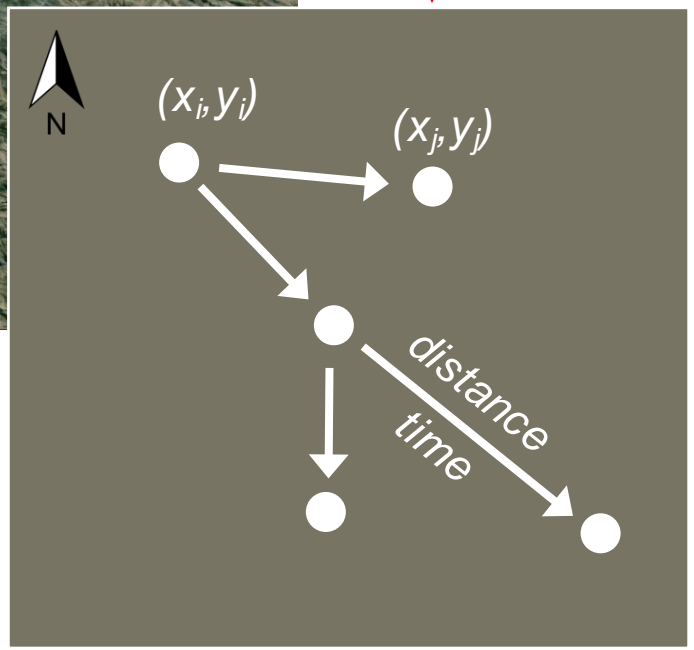
Phylogenetic estimation of viral invasion speeds

Reconstruction of virus spread on landscape



Viral phylogeny

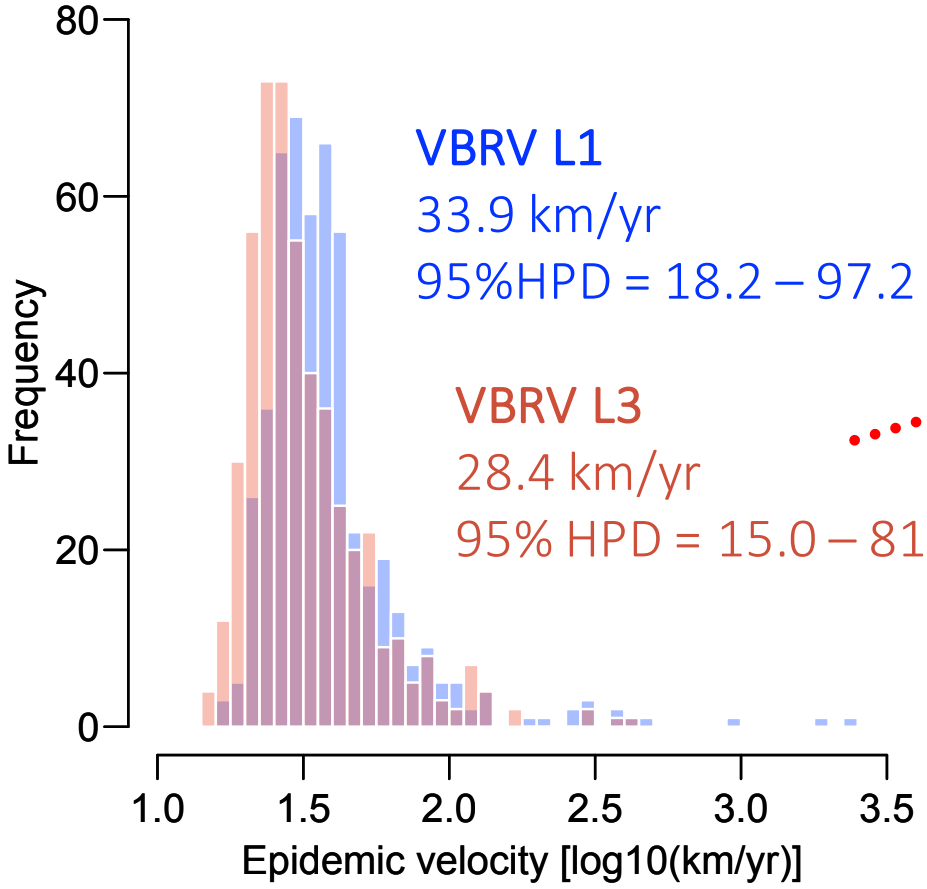




Speed of viral invasion

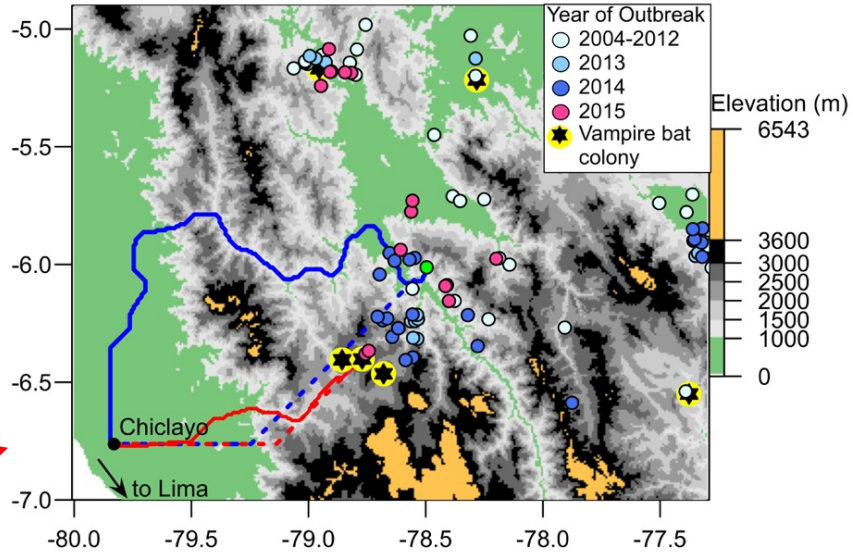
(*Seraphim* package in R)

Speeds of rabies invasion from 2 main virus lineages



VBRV L1
33.9 km/yr
95%HPD = 18.2 – 97.2

VBRV L3
28.4 km/yr
95% HPD = 15.0 – 81.9



Predicted Arrival to Pacific Coast

July 2019
95% HPD: Oct 2016 – Mar 2023

June 2020
95% HPD: Feb 2017 – Nov 2024

Streicker *et al.* (2016) **PNAS**

New risks for humans, livestock and wildlife in historically rabies-free areas

Risks for livestock

Vol. 360: 285–289, 2008
doi: 10.3354/meps07393

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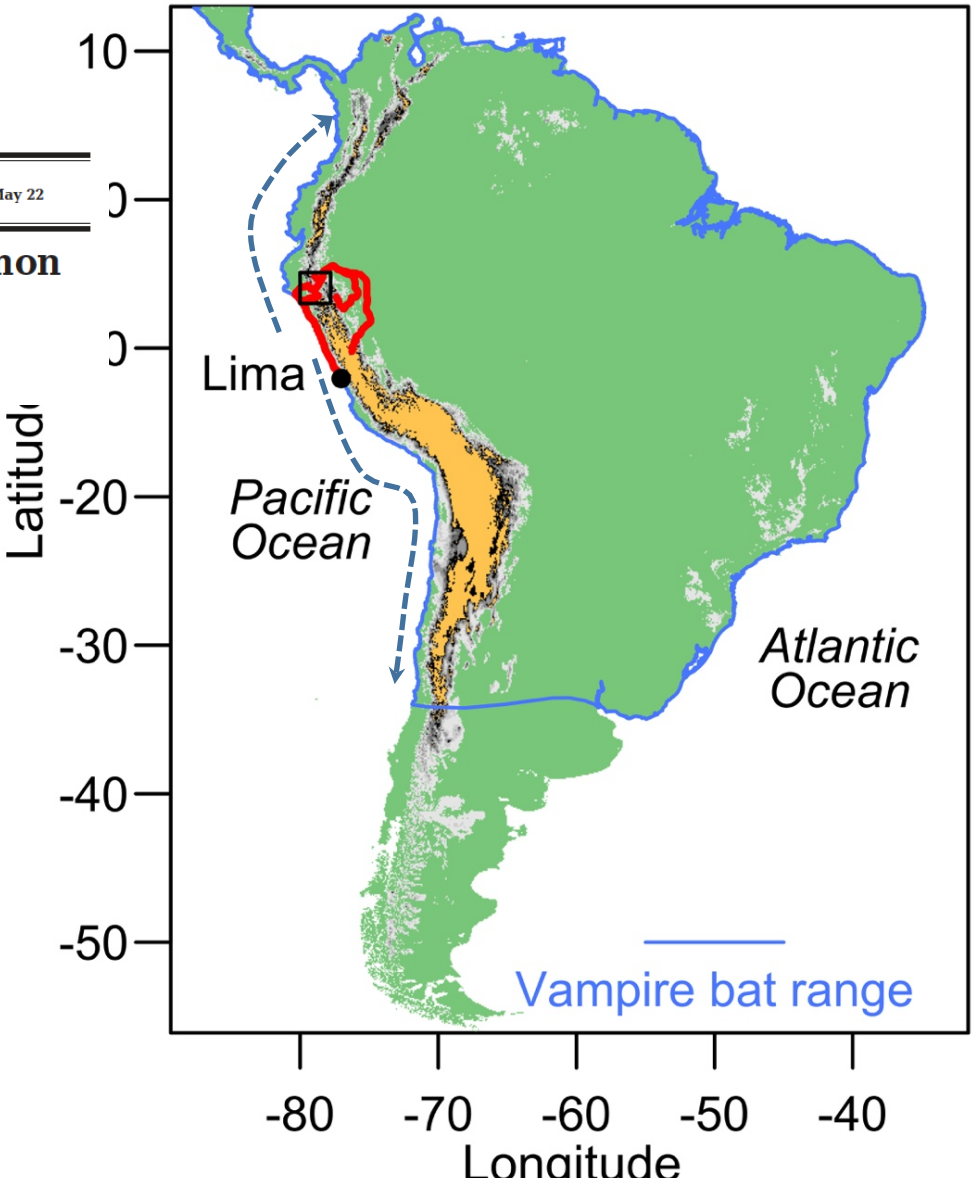
Mar Ecol Prog Ser

Published May 22

Sea lion *Otaria flavescens* as host of the common vampire bat *Desmodus rotundus*

Alessandro Catenazzi[1,2,*], Maureen A. Donnelly[1]



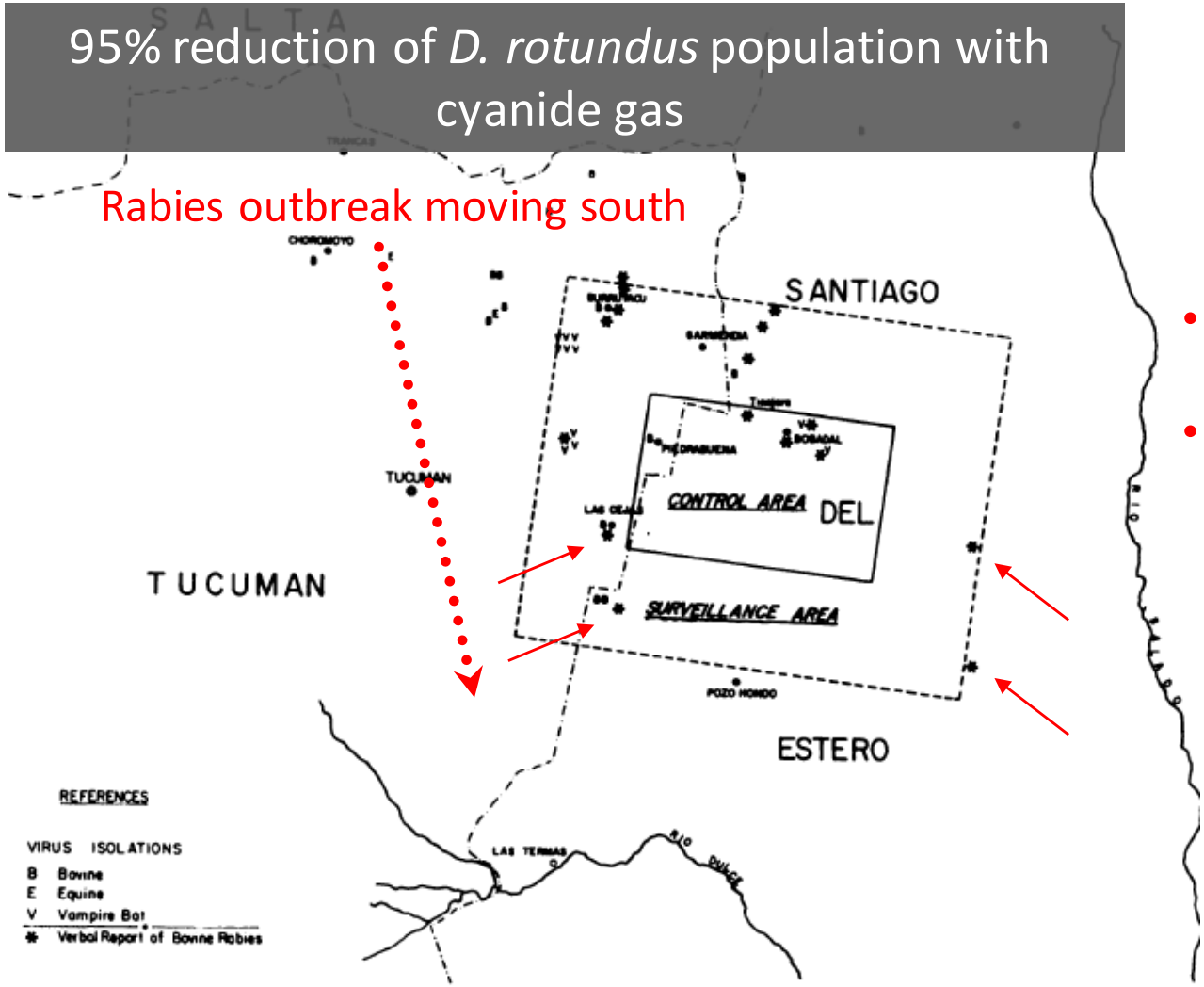
New opportunities for prevention and control ahead of advancing wavefronts

Vaccination and education in high risk areas

Interventions within bat population ahead of outbreaks

Culling experiment in Argentina

95% reduction of *D. rotundus* population with cyanide gas



Lessons

- High levels of population reduction needed
- Need for geographic barriers

Culling alone probably insufficient to prevent viral invasion in large, inaccessible areas with many unknown roosts

Fornes *et al.* (1974) JWD

Oral vaccination of bats ahead of wavefronts?

- poison

+ oral rabies vaccine

VACCINATION OF VAMPIRE BATS USING RECOMBINANT VACCINIA-RABIES VIRUS

Alvaro Aguilar-Setién,[1,4] Yolanda Leon Campos,[1] Emiliano Tesoro Cruz,[1] Roberto Kretschmer,[1] Bernard Brochier,[2] and Paul-Pierre Pastoret[3]

1998

Experimental rabies infection and oral vaccination in vampire bats (*Desmodus rotundus*)

Alvaro Aguilar Sétien*, Bernard Brochier†[1], Noël Tordo‡, Octavio De Paz§, Philippe Desmettre¶, Daniel Péharpré‖ and Paul-Pierre Pastoret†

2002

Indirect oral immunization of captive vampires, *Desmodus rotundus*

Marilene F. Almeida[a,c,*], Luzia F.A. Martorelli[c], Caroline C. Aires[d], P.C. Sallum[c], Eduardo Massad[a,b]

2005

Short communication

Vaccinating the vampire bat *Desmodus rotundus* against rabies

M.F. Almeida[a,c,*], L.F.A. Martorelli[c], C.C. Aires[d], R.F. Barros[c], E. Massad[a,b]

2008

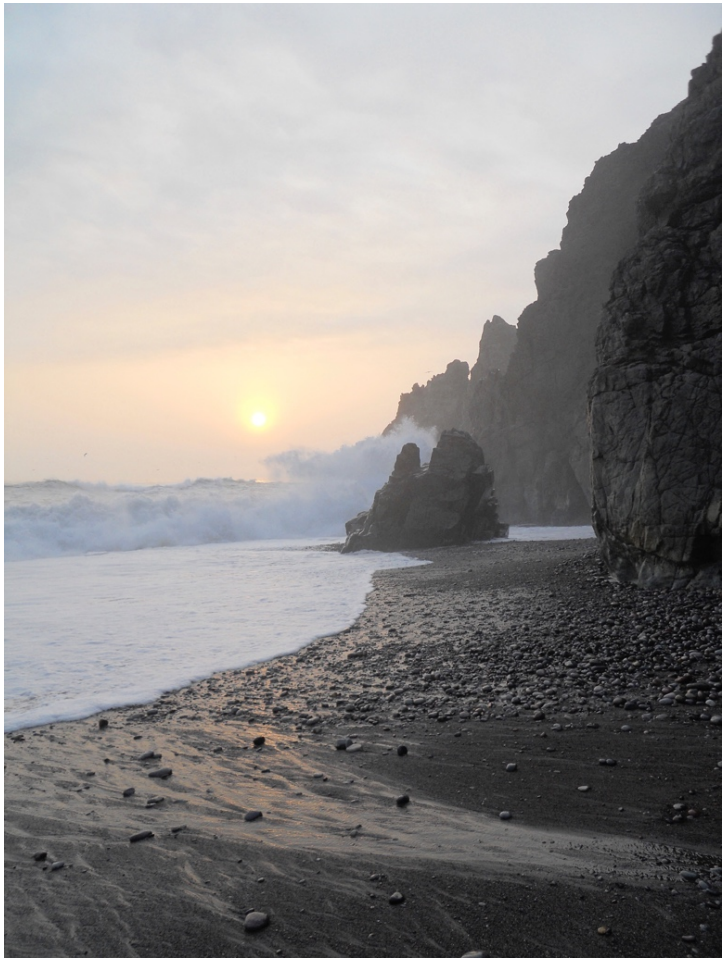
Infectivity of attenuated poxvirus vaccine vectors and immunogenicity of a raccoonpox vectored rabies vaccine in the Brazilian Free-tailed bat (*Tadarida brasiliensis*)

Ben R. Stading[a,b], Jorge E. Osorio[a], Andres Velasco-Villa[c], Michael Smotherman[d], Brock Kingstad-Bakke[a], Tonie E. Rocke[b,*]

2016

Summary and Implications

- Host genetics & viral phylogeography can provide insights into the mechanisms, routes and speed of viral invasions
  - Male dispersal allows viral spread across landscape
  - Forecast viral invasion to rabies free areas
- New risks to livestock, humans and wildlife that are bitten by *Desmodus*
- Need to support epidemiological surveillance & explore new strategies for rabies prevention and control



Acknowledgements

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RD 054-2016-SERFOR

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