EcoHealth Alliance

Assessing Coronavirus threats

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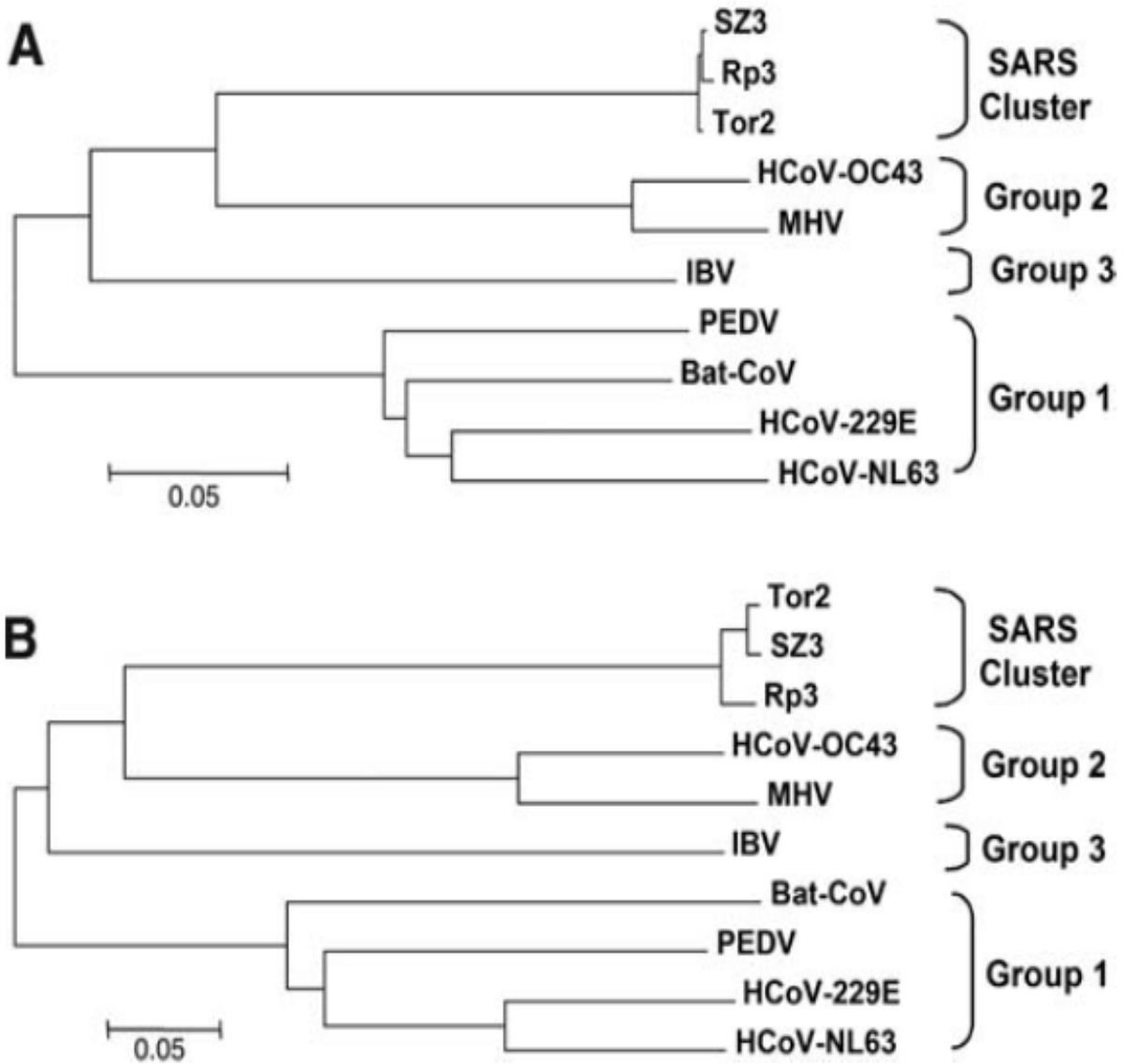
Local conservation.
Global health.

Human and Civet SARS-CoV nestle phylogenetically within Bat SL-CoV cluster



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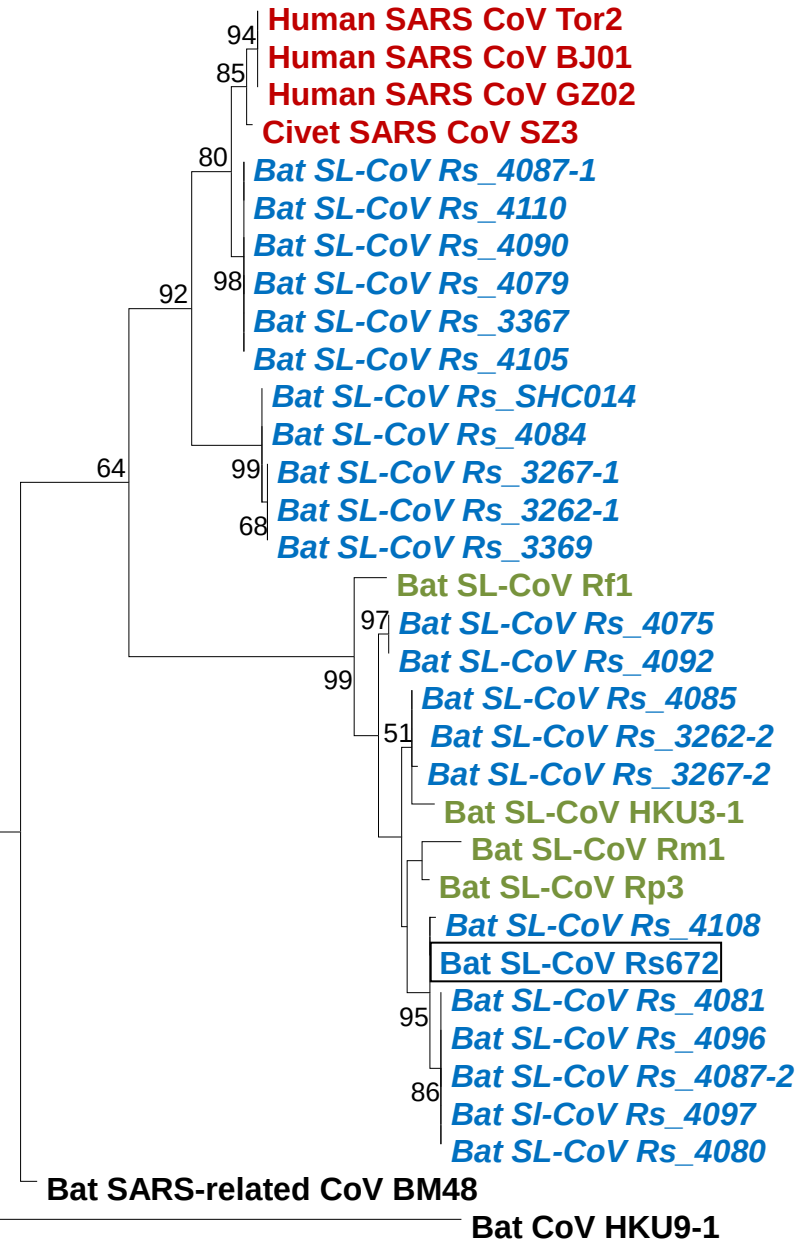
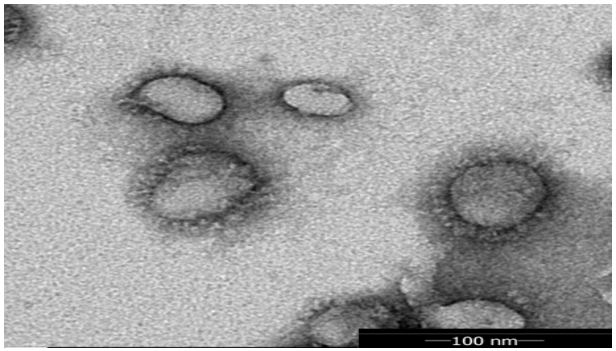
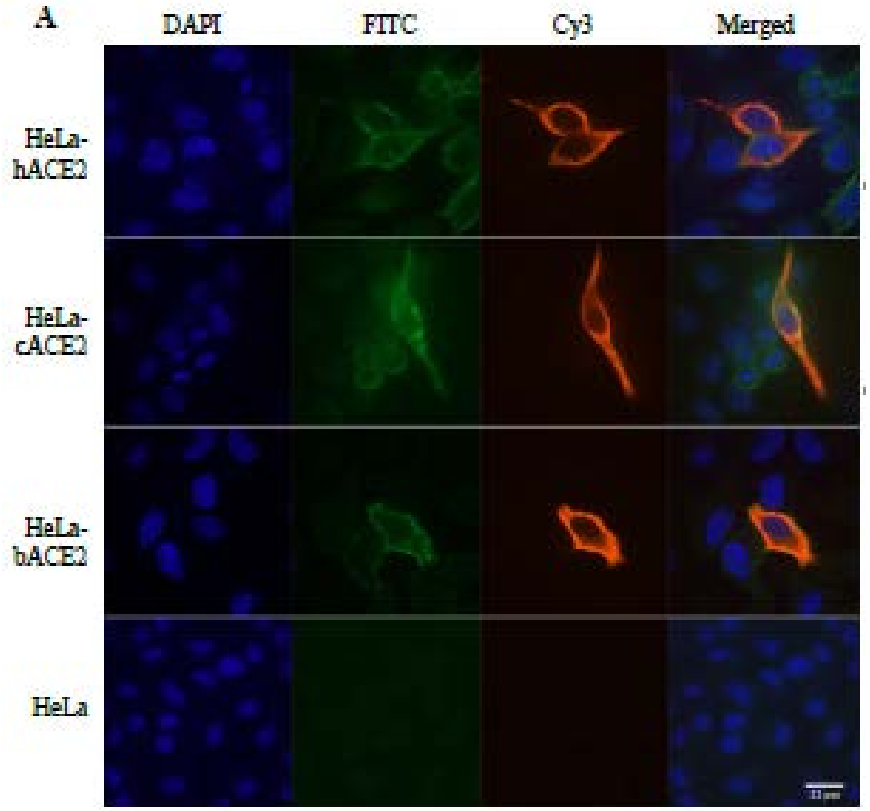
Li *et al.* Science 2005





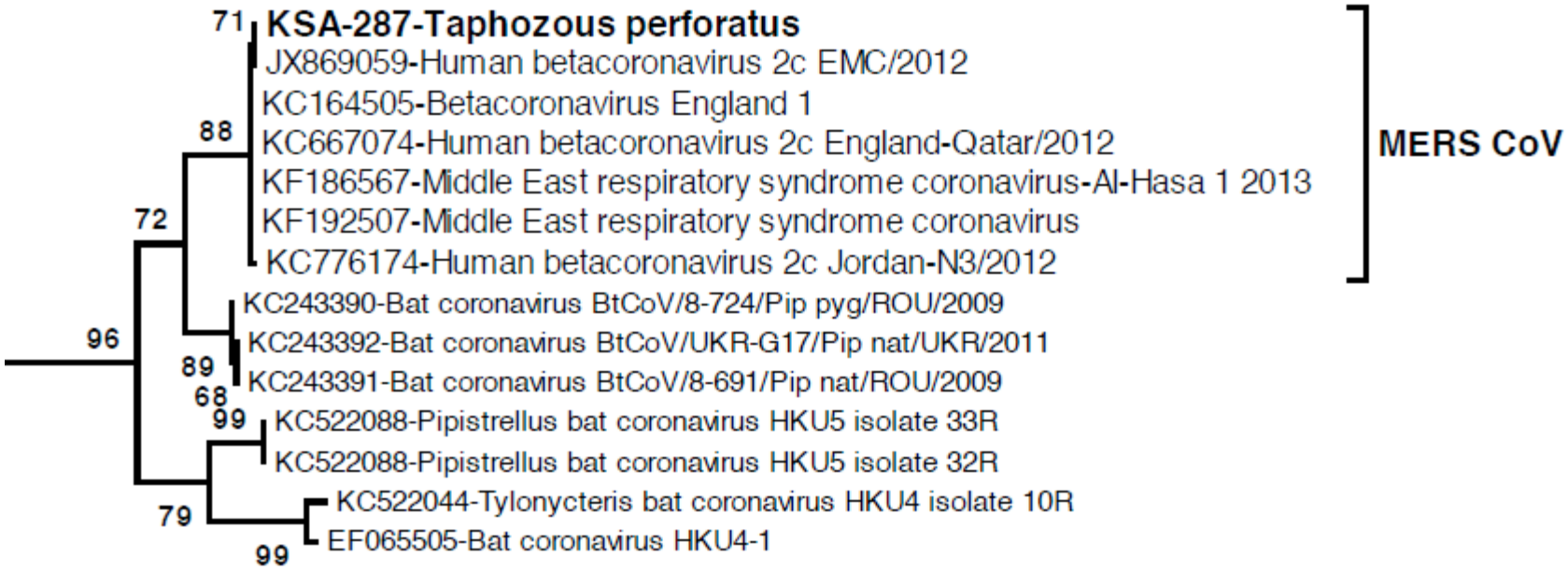


Ge *et al.* (2013) *Nature*

New isolate from bats (2015), even closer to SARS-CoV

	Bat SL-CoV WIV16	Human SARS CoV Tor2	Human SARS CoV BJ01	Human SARS CoV GZ02	Civet SARS CoV SZ3	Bat SL-CoV WIV1
Bat SL-CoV WIV16	**----**	**96**	**97**	**97**	**97**	**93**
Human SARS CoV Tor2	**96**	----	99	99	98	92
Civet SARS CoV SZ3	**97**	98	98	99	----	92
Bat SL-CoV WIV1	**93**	92	92	92	92	----

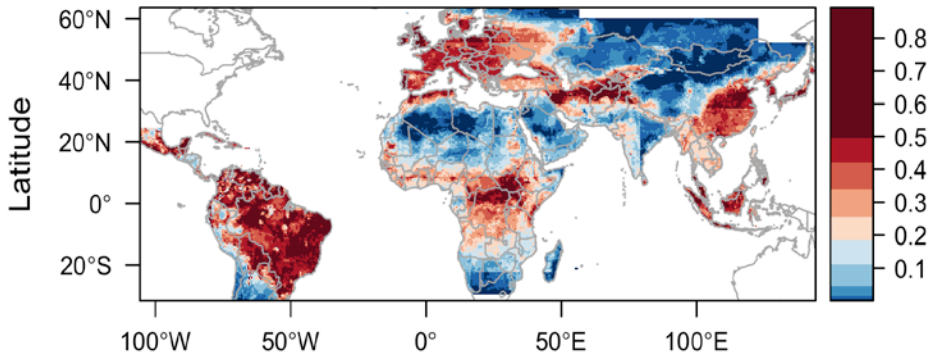
Spike protein gene homology, Bat SARS-Like CoVs vs. Human, Civet SARS-CoV



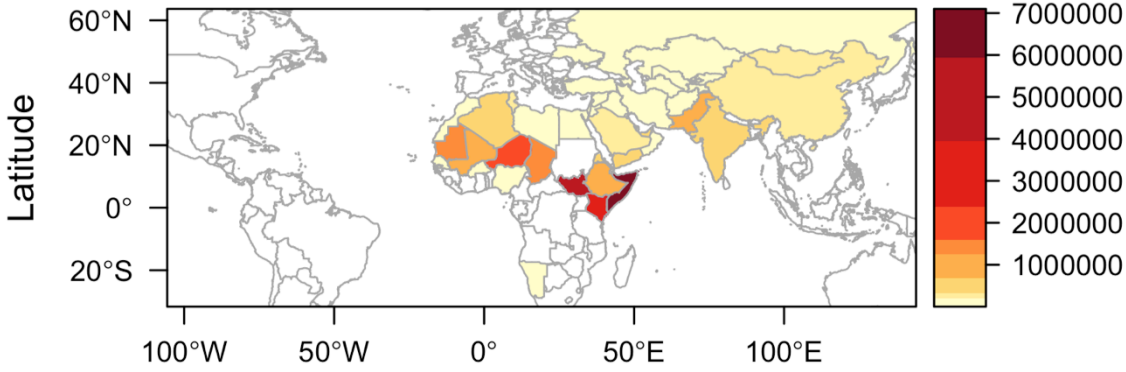
Memish *et al.* 2013 *EID*

Ecological Niche Models to identify MERS “EpiZone”

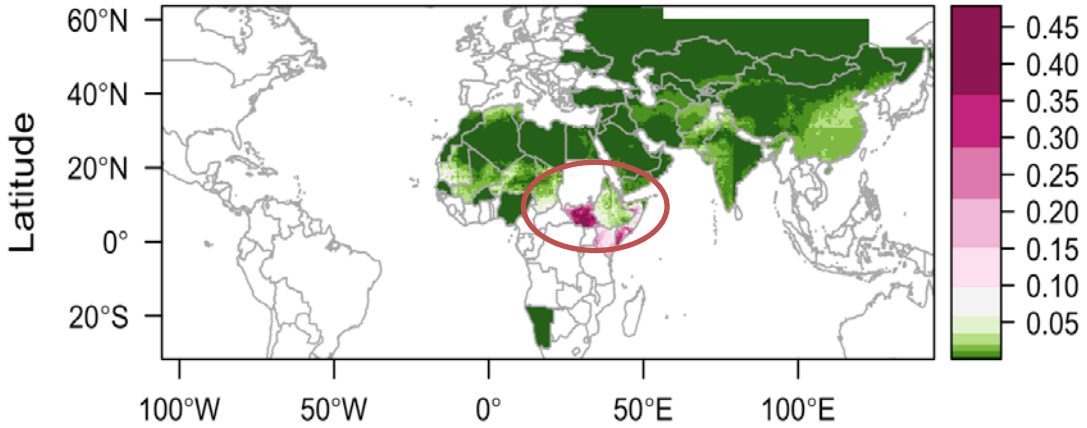
- Modeled distribution of MERS-CoV bats



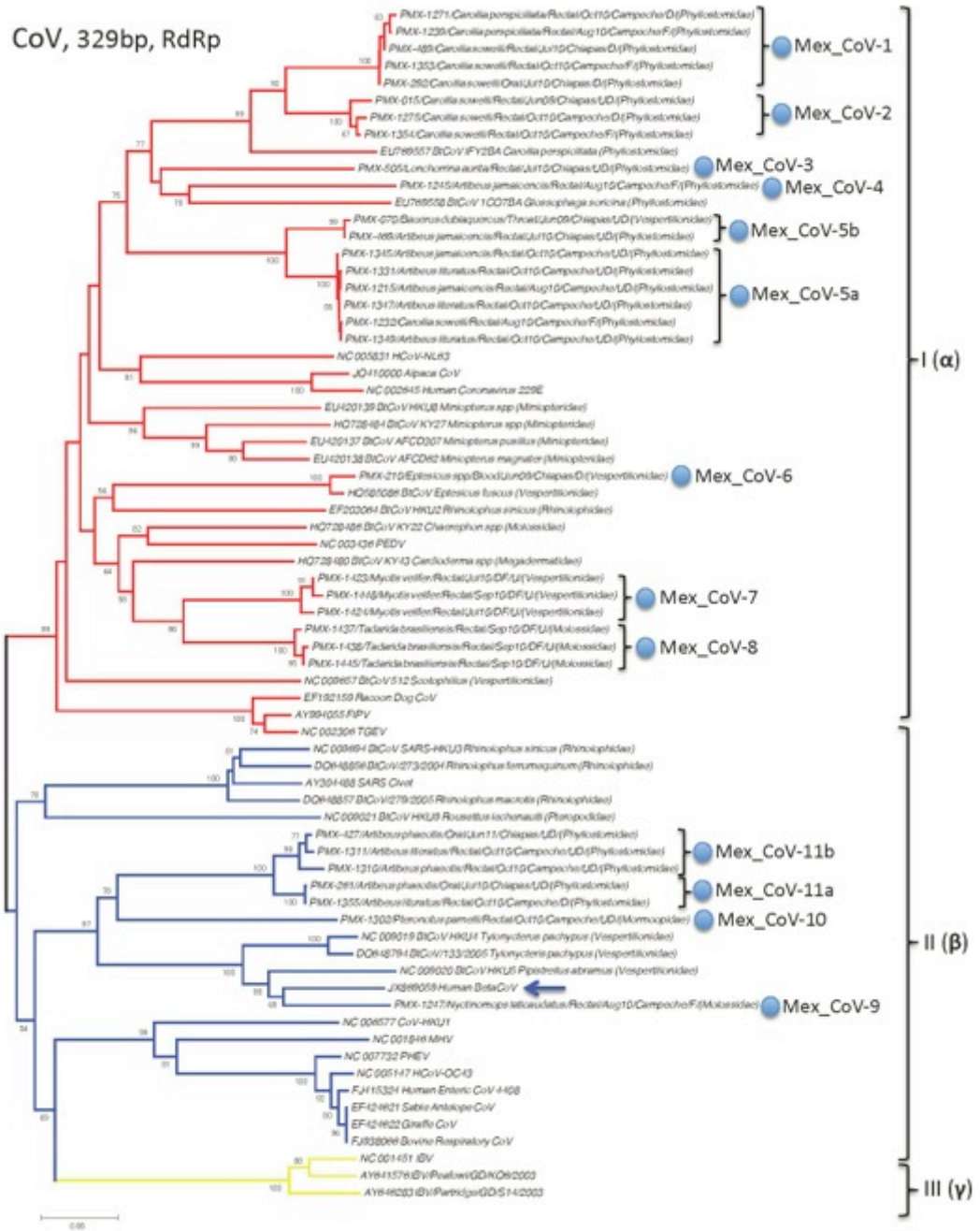
- Camel production (FAO)



- Modeled risk of MERS spillover (horn of Africa)



New Coronaviruses from bats in Mexico

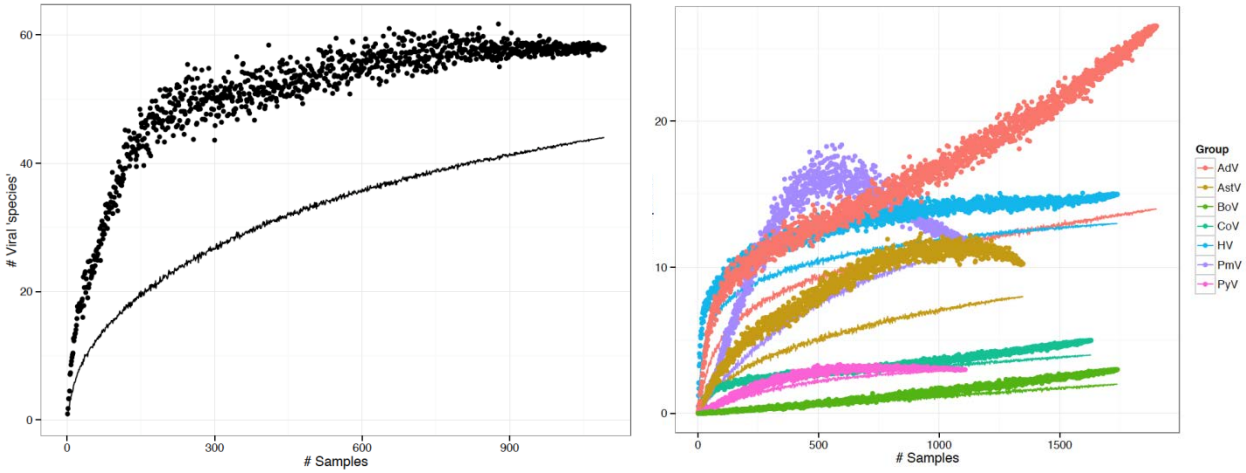


Anthony et. al. 2013 *J. Gen Virol.*

A Strategy To Estimate Unknown Viral Diversity in Mammals

Simon J. Anthony,[a,b] Jonathan H. Epstein,[b] Kris A. Murray,[b] Isamara Navarrete-Macias,[a] Carlos M. Zambrana-Torrelio,[b] Alexander Solovyov,[a] Rafael Ojeda-Flores,[c] Nicole C. Arrigo,[a] Ariful Islam,[b] Shahneaz Ali Khan,[d] Parviez Hosseini,[b] Tiffany L. Bogich,[e,f] Kevin J. Olival,[b] Maria D. Sanchez-Leon,[a,b] William B. Karesh,[b] Tracey Goldstein,[g] Stephen P. Luby,[h] Stephen S. Morse,[g,i] Jonna A. K. Mazet,[g] Peter Daszak,[b] W. Ian Lipkin[a]

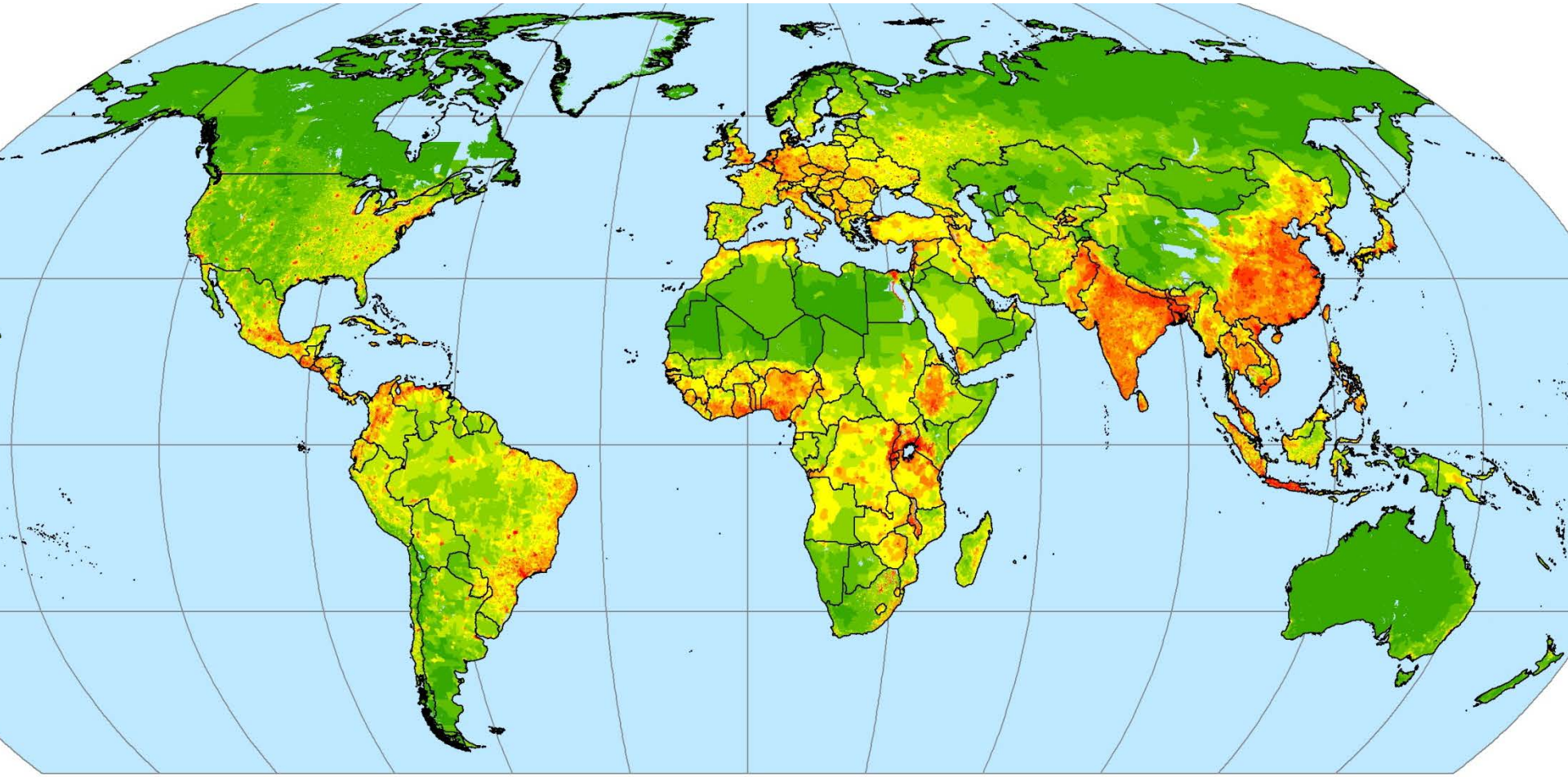
Center for Infection and Immunity, Mailman School of Public Health, Columbia University, New York, New York, USA[a]; EcoHealth Alliance, New York, New York, USA[b]; Facultad de Medicina Veterinaria and Zootecnia, Universidad Nacional Autónoma de México, Ciudad Universitaria, Mexico City, Distrito Federal, Mexico[c]; Chittagong



- ~58 unknown viruses in *Pteropus giganteus*
- ~320,000 unknown viruses in all mammals; ~72,152 in the 1,244 known bat species
- One-off cost to identify 100% = $6.8 Billion
- One-off cost to identify 85% = $1.4 Billion
- Cost of SARS = $10-50 Billion
- ~250 bat viruses in last 5 years, 530 total = 7% of the estimated #

Anthony et al. *mBio* 2013

Global emerging disease ‘hotspots’



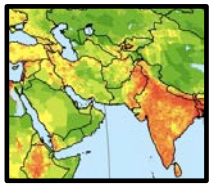
Jones *et al. Nature* 2008

Follow up Genetic and Experimental studies (post-PREDICT) to Further Assess Spillover Potential

- Virus isolation
- Sequence whole genome
- With temporally sampled viruses, measure mutation rates and phylodynamics
- Sequence receptor binding domain, if known
- Structural comparison with human receptors (e.g. 3D models, *In silica*)
- Cell line infection experiments *(in vitro)*
- Humanized mice and other animal experiments

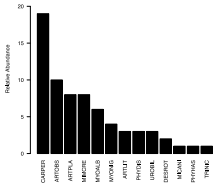
Ranking risk for zoonotic potential of novel viruses

VIRUS-INDEPENDENT TRAITS + **VIRUS-SPECIFIC TRAITS** = **RISK OF SPILLOVER**



GEOGRAPHIC HOTSPOTS FOR EMERGENCE

HOST SPECIES TRAITS, GEOGRAPHIC RANGE, RELATEDNESS

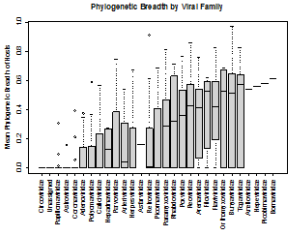


HOST ABUNDANCE

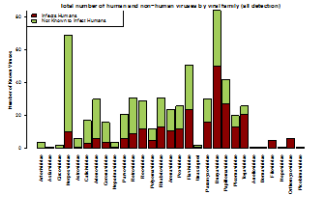
% pos

VIRAL PREVALENCE IN HOST

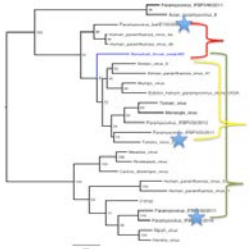
EPIDEMIOLOGICAL/ CONTACT INTERFACE



HOST BREADTH/PLASTICITY



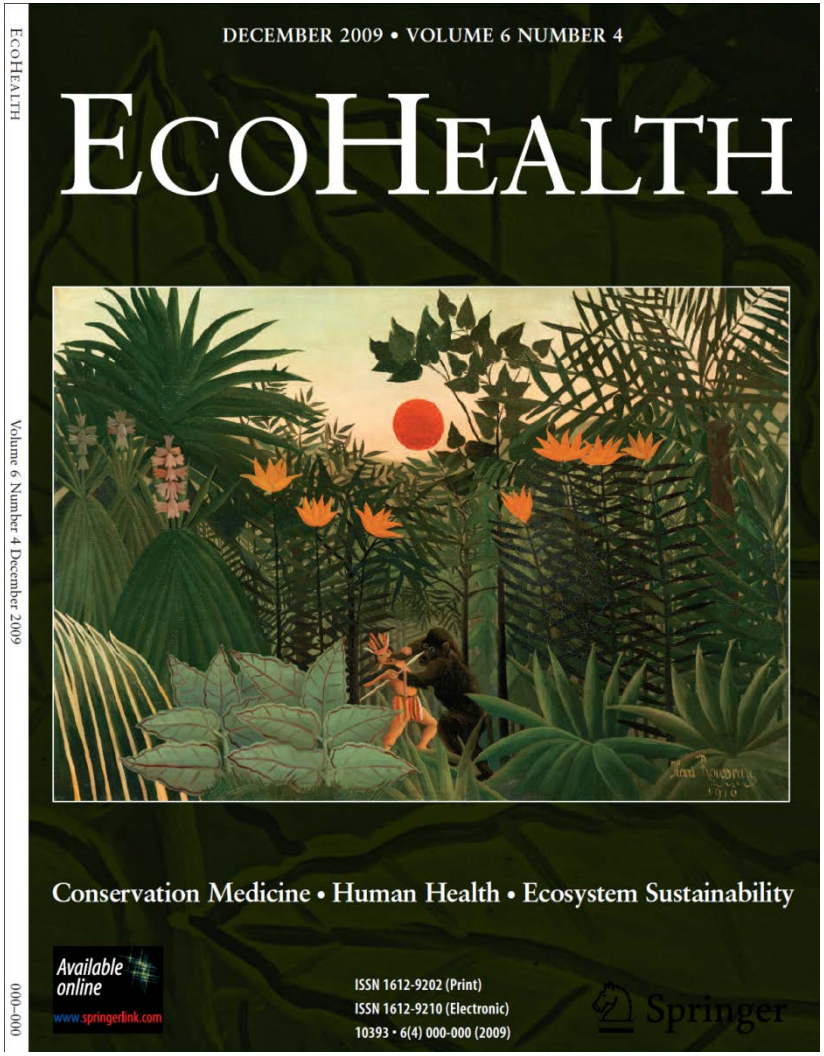
PROPORTION KNOWN ZOONOSES IN VIRUS FAMILY



PHYLOGENETIC RELATEDNESS TO KNOWN ZOONOSES

OTHER VIRUS-SPECIFIC TRAITS

MODEL/FACTOR	Increased Risk	Decreased Risk	Data Used/Needed
1. Hotspots v2	Hotspot	Coldspot	**EHA**- Human pop density, mammal diversity, environmental drivers, landuse
2. Geographic viral range	More sites (=large viral spatial range)	Few sites	**GAINS** – lat/long **HP3** -sum of host ranges
3. Interfaces	High risk interface	Low risk activity	**GAINS** data and (**CKJ's** lit review model)
4. Viral prev. in host	High	Low	**GAINS** test data, need denominator
5. Host abundance	High	Low	**GAINS** surveillance data; need effort
6a. Host Taxa	Rodents, bats, primates	Other mammals	**HP3** and **CKJ** - Use if only have Order or Family level info.
6b. Host Species Traits and Phylog	High predicted number shared	Low predicted viruses shared	**HP3**- Use if host Species or Genus info. Categorize continuous model output
7. Viral Family –Host Phylog Breadth	Large breadth and decent dataset	Small breadth	**HP3** -Mean/median host phylogenetic range per viral family or genus. **GAINS** data on hosts if new virus.
8. Viral Family – % zoonotic	>50% of viruses known to be human	<50%	**HP3**- Based on known zoonoses/viral diversity for each viral family. Factor in # viruses too, not just %.
9. Nearest Neighbor	Validity? See Kitchen et al. 2011, PNAS	Cutoff values?	**GAINS** - viral seq data; and other published seqs from **Genbank.** Robust phylogeny needed
10. Cophylogeny	Disrupted cophy	Concordant cophy	**GAINS** and **Genbank**- need host and viral seq data. Categorize # events/virus.



Collaborators

- UC Davis, Metabiota, WCS, Smithsonian
- Univ. Wyoming (David Finnoff)
- Columbia Univ. (Ian Lipkin, Simon Anthony)
- 100+ partners in 24 countries
- Wuhan Institute of Virology, Yunnan CDC
- Universiti Malaysia Sabah, Sabah Wildlife Dept.

Funders

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