





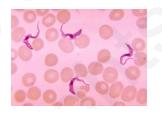
Parasite sharing in wild ungulates and their predators: effects of phylogeny, range of phylogeny overlap, and trophic links

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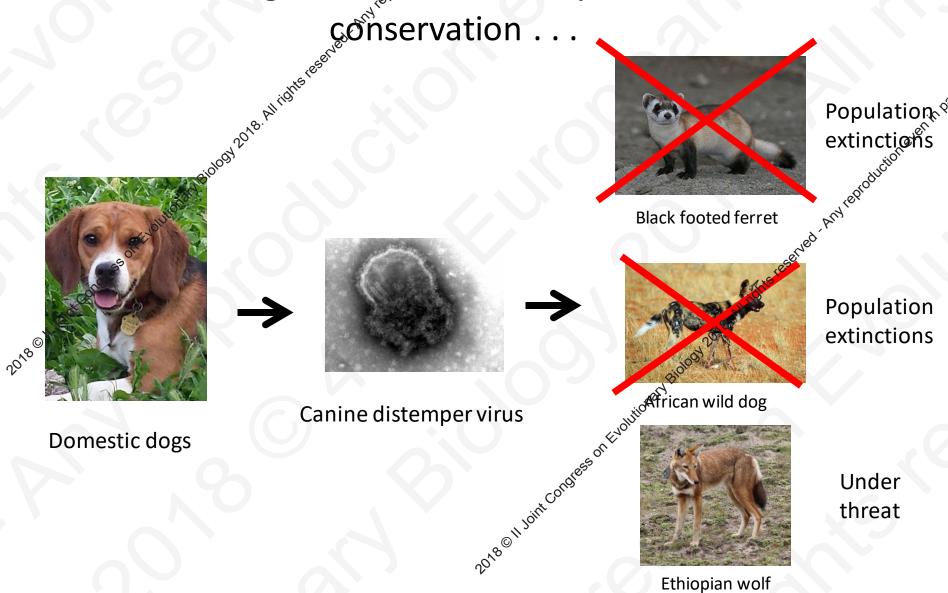
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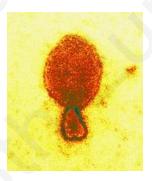
Understanding the factors that allow pathogens to be shared among host species is a key issue for wildlife



Ethiopian wolf

.domestic animal brusbandry/ livestock farming

September 1995 thirteen horses and a trainer killed in Brisbane Australia



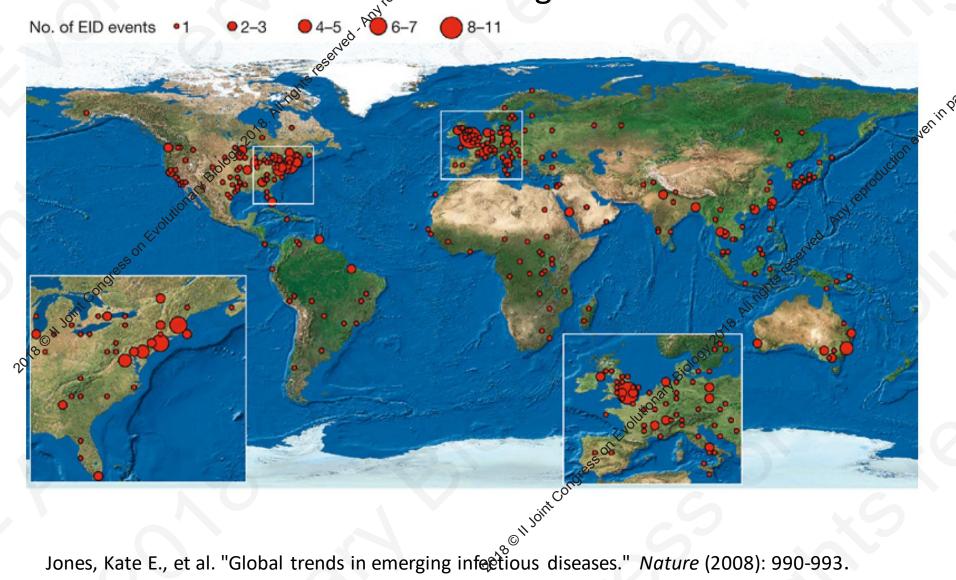
Hendra virus



Flying fox

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... and human health: more than 60% of human EIDs are of zoonotic origin.



## One approach: parasite sharing / community

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## What traits make it likely that a host species pair will share more parasite species?

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# Factors correlated with parasite sharing / community similarity in past studies of wild mammals

• Geographic range overlap

Phylogenetic affinity

Morphological/ ecological similarity

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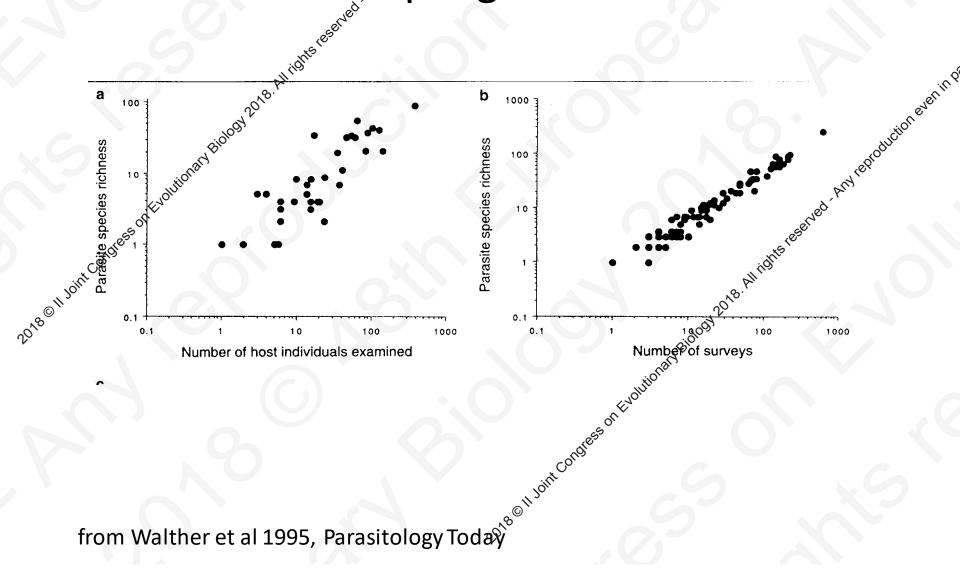
# Previous broad comparative studies confined to two groups

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Primates (several studies)



# Studies have not considered differences in sampling effort



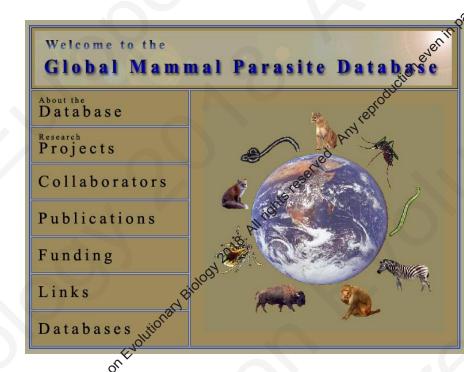
## Studies have not considered trophic links or other direct ecological interactions

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## Parasite sharing in wild ungulates\*

- Host-parasite associations from the latest iteration of the Global Mammal Parasite Database\*\*
- Ungulate data includes 11930 lines of data from 1083 literatures sources
- Latest update includes all published studies through early 2010



<sup>\*</sup>Stephens, P. R., S. Altizer, V. Ezenwa, J. L. Gittleman, E. Moan, B. Han, S. Hwang and P. Pappalardo. 2018. Parasite sharing in wild ungulates and their predators: effect of phylogeny, range overlap, and trophic links. *Journal of Animal Ecology* (in revision, invited resubmission)

<sup>\*\*</sup>Stephens, P. R., Pappalardo, P., Huang, S., et al. 2017. Global mammal parasite database version 2.0. Ecology, 98: 1476-1476.

• 116 host species including both artical actyls and rerissod actyls • Wild species from all over

Domestic species and zoo records excluded

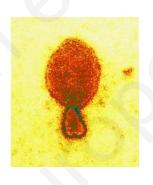


All disease causing rganisms from viri minths anisms from helminths

• 1298 species total

2018 • Both

Both combined and separate analysis of each parasite group performed





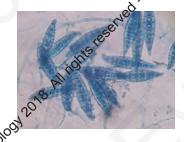
protozoa



helminths



bacteria



fungi



arthropods

<sub>zo, Per</sub>ignous Questions

 Are phylogenetic affinity, range overlap, and ecological similarity correlated with parasite overlap among ungulate hosts?

• Are well studied species more likely to have known shared parasites?

• Are carnivores that feed on ungulates infected by more ungulate parasites than those that don't?

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### Geographic range overlap

- Based on IUCN range data, three measures of host range overlap
  - Any overlap at all (0 or 1)

ூ<sup>்தீ</sup> Area of overlap (km 2)

- Percentage range overlap (smaller range/area of overlap)
- Nearly identical positive correlations with community similarity

### Phylogenetic affinity

- Based on supertree of all mammals\*, two measures of host phylogeneticadistance
  - Divergence time in millions of years that separates hosts
  - Number of divergence (speciation) events that separate hosts
- Similar negative correlations with community similarity, number of divergence events slightly stronger

<sup>\*</sup>Bininda-Emonds, Olaf RP, et al. (2007)"The delayed rise of present-day mammals." *Nature* 446: 507-512. Fritz, S. A., Bininda-Emonds, O. R. P. & Purvis, A. (2009) Geographical variation in predictors of mammalian extinction risk: big is bad, but only in the tropics. *Ecol. Lett.* 12: 538–549

### Ecological similarity

 Two measures of host ecological similarity using data from PanTHERIA\* supplemented with data from <a href="http://www.ultimateungulate.com/">http://www.ultimateungulate.com/</a>

- Difference in host median body size (grams)

 Euclidean distance matrix constructed from mine host morphological and ecological traits

Similar weak correlations, direction sometimes varied

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Study effort

Study effort measured as the summed Web of Science Citations for each pair of host species binomials (searches included recent synonyms)

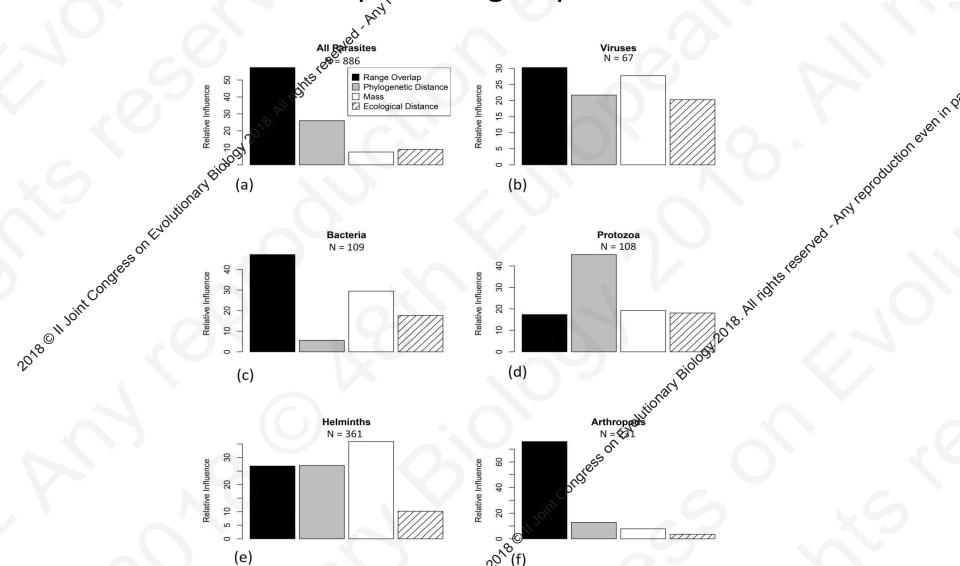
**Overall:** better studied pairs of host species more likely to show overlap in known parasite community composition

# GAM analyses and boosted regression trees used to assess relative influence of predictors

	$^{\prime 0}$		
	Predictor (GAM analysis)	F	p-value
3°	Percent Range Overlap	79.38	<0.0001
	log(Divergence Time, mybp)	43.77	<0.0001
	log(Total WOS Citations)	6.86	<0.0001 <sub>0</sub> 0 <sup>10</sup> .All
	log(Mass Difference, g)	1.73	g:0092
	log(Ecological Dissimilarity)	0.51	<0.0001 <0.0001 2018 A  <0.0001 2018  0.283
		^~	

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## Relative influence of predictors varied widely among parasite groups



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by more ungulate parasites than those that don't?

### Trophic Links

 Carnivore species in GMPD grouped by whether or not they are known to prey on ungulates

• Number of known ungulate parasites (i.e. parasites found in the ungulate GMPD) found in each host species calculated

• Analyses both of raw data and residuals of model of ungulate parasites vs host sampling effort

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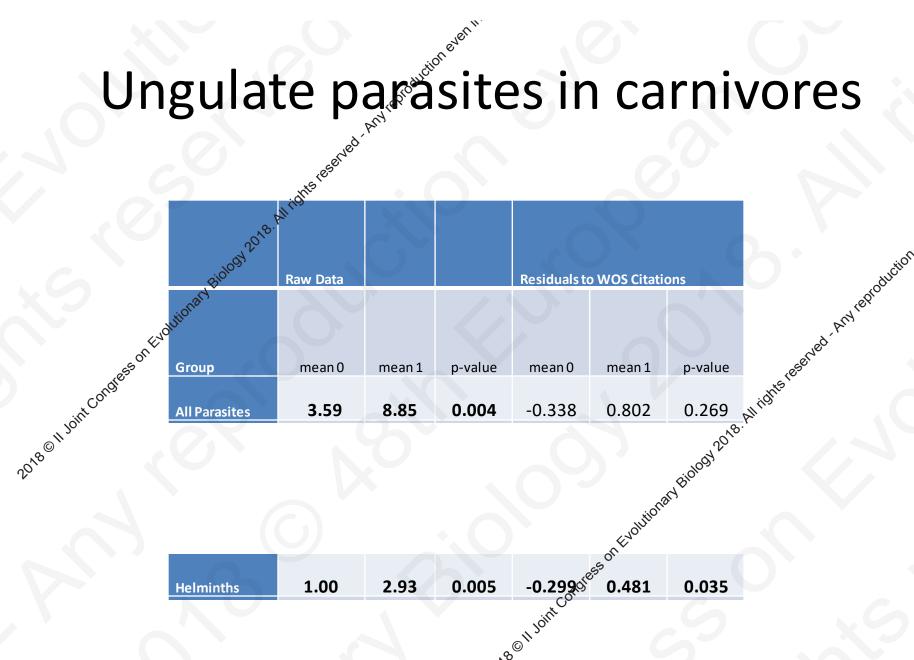
Le parasites in carnivore.

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# Ungulate parasites in carnivores

		nts les						
	intional Biology 2018.	Raw Data			Residuals to WOS Citations			
o L	intionary.						9	
	Group	mean 0	mean 1	p-value	mean 0	mean 1	p-value	
	All Parasites	3.59	8.85	0.004	-0.338	0.802	0.269 0.647 0.390 0.382 0.035	
	Viruses	1.39	1.81	0.152	-0.052	0.082	0.647	
	Bacteria	2.96	3.19	0.803	0.246	-0.269 r	ry 0.390	
	Protozoa	1.34	1.46	0.630	0.070	-06101	0.382	
	Helminths	1.00	2.93	0.005	-0.29 <b>9</b> %	9.481	0.035	
	Arthropods	1.45	3.24	0.047	70.161	0.361	0.425	

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# Results robust to how carnivores scored rey on ungularity to Drange of the control of the contro

Never prey on ungulates

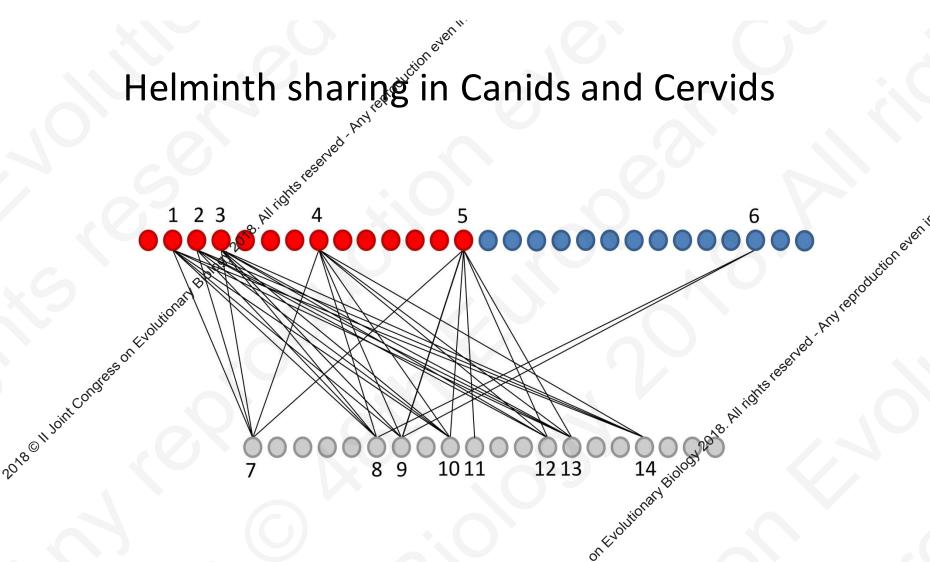
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rare occasions



Ungulates primary/ consistent prey item





**Canidae:** 1. Canis aureus, 2. Canis latrans, 3. Canis lupus, 4. Picalopex culpaeus, 5. Vulpes vulpes, 6. Vulpes lagopuso

Cervidae: 7. Alces alces, 8. Capreolus capreolus, 9. Cervus elpahus, 10. Cervus nippon, 11. Dama dama, 12. Odocoileus virginianus, 13. Odocoileus hemionus, 14. Rangifer tarandus.

Questions

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# MACknowledgments

NSF/NIH/ USDA funded Research Coordination Network: Macroecology of Infectious Disease (DEB 1316223)

**Odum School of Ecology** 

Altizer and Ezenwa lab groups

## Research Coordination Network: the Macroecology of Infectious Disease



Search for "Disease Macroecology" for our website, or go to:

http://diseasemacroecology.ecology.uga.edu/