

Pneumocystosis in Wild Small Mammals from California

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MICROPARASITE ASSEMBLAGES OF CONSPECIFIC SHREW POPULATIONS IN SOUTHERN CALIFORNIA

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1 RH: *Research Note*

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3 *Eimeria albigulae* (Apicomplexa: Eimeriidae): New Host and Distributional Record from
4 the Bryant's Woodrat, *Neotoma bryanti* (Rodentia: Cricetidae), from California, U.S.A.

5

6 CHRIS T. MCALLISTER,^{1,4} JOHN A. HNIDA,² AND ROBERT N. FISHER³

Three Pathogens in Sympatric Populations of Pumas, Bobcats, and Domestic Cats: Implications for Infectious Disease Transmission

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Pathogen exposure varies widely among sympatric populations of wild and domestic felids across the United States

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ORIGINAL ARTICLE

Evolutionary Applications **WILEY**



Does the virus cross the road? Viral phylogeographic patterns among bobcat populations reflect a history of urban development

Christopher P. Kozakiewicz¹ | Christopher P. Burrridge¹ | W. Chris Funk^{2,3} | Meggan E. Craft⁴ | Kevin R. Crooks⁵ | Robert N. Fisher⁶ | Nicholas M. Fountain-Jones⁴ | Megan K. Jennings⁷ | Simona J. Kraberger⁸ | Justin S. Lee⁸ | Lisa M. Lyren⁹ | Seth P. D. Riley¹⁰ | Laurel E. K. Serieys^{11,12} | Sue VandeWoude⁸ | Scott Carver¹



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Review Paper

Identifying management-relevant research priorities for responding to disease-associated amphibian declines

Evan H. Campbell Grant^{a,*}, Michael J. Adams^{b,1}, Robert N. Fisher^c, Daniel A. Grear^d, Brian J. Halstead^e, Blake R. Hossack^f, Erin Muths^g, Katherine L.D. Richgels^d, Robin E. Russell^d, Kelly L. Smalling^h, J. Hardin Waddleⁱ, Susan C. Wallsⁱ, C. LeAnn White^d

OPEN

Batrachochytrium salamandrivorans (Bsal) not detected in an intensive survey of wild North American amphibians

J. Hardin Waddle^{b,1,✉}, Daniel A. Grear^{b,2}, Brittany A. Mosher^{3,4,5}, Evan H. Campbell Grant^{b,4}, Michael J. Adams^{b,6}, Adam R. Backlin⁷, William J. Barichivich¹, Adrienne B. Brand⁴, Gary M. Bucciarelli^{b,8}, Daniel L. Calhoun^{b,9}, Tara Chestnut¹⁰, Jon M. Davenport¹¹, Andrew E. Dietrich⁴, Robert N. Fisher^{b,7}, Brad M. Glorioso^{b,12}, Brian J. Halstead^{b,13}, Marc P. Hayes^{b,14}, R. Ken Honeycutt¹⁵, Blake R. Hossack¹⁵, Patrick M. Kleeman^{b,16}, Julio A. Lemos-Espinal¹⁷, Jeffrey M. Lorch², Brome McCreary⁶, Erin Muths^{b,18}, Christopher A. Pearl^{b,6}, Katherine L. D. Richgels², Charles W. Robinson², Mark F. Roth¹⁹, Jennifer C. Rowe⁶, Walt Sadinski¹⁹, Brent H. Sigafus²⁰, Iga Stasiak^{b,21}, Samuel Sweet²², Susan C. Walls¹, Gregory J. Watkins-Colwell²³, C. LeAnn White², Lori A. Williams²⁴ & Megan E. Winzeler^{b,2,25}



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Effect of amphibian chytrid fungus (*Batrachochytrium dendrobatidis*) on apparent survival of frogs and toads in the western USA

Robin E. Russell^{a,*}, Brian J. Halstead^b, Brittany A. Mosher^{c,d,1}, Erin Muths^e, Michael J. Adams^f, Evan H.C. Grant^c, Robert N. Fisher^g, Patrick M. Kleeman^h, Adam R. Backlinⁱ, Christopher A. Pearl^f, R. Ken Honeycutt^j, Blake R. Hossack^j



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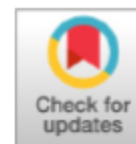
- White nosed syndrome
- RHDV2 - Rabbit Hemorrhagic Disease Virus serotype 2 (in Southern California)
- Turtle shell fungus
- Snake fungal disease



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Virome of Bat Guano from Nine Northern California Roosts

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IMPORTANCE Characterizing the bat virome is important for understanding viral diversity and detecting viral spillover between animal species. Using an unbiased metagenomics method, we characterize the virome in guano collected from multiple roosts of common Northern California bat species. We describe several novel viral genomes and report the detection of viruses with close relatives reported in other bat species, likely reflecting cross-species transmissions. Viral sequences from well-known carnivore and rodent parvoviruses were also detected, whose presence are likely the result of contamination from defecation and urination atop guano and which reflect the close interaction of these mammals in the wild.

TABLE 1 Summary of guano samples used in this study

California county	Collection date	Name ^a	Primary bat species ^b	No. of samples ^c	Estimated no. of animals ^d
Bat roosts					
Marin	February 2020	CR1	<i>Corynorhinus townsendii</i>	1*	~300
	February 2020	CR2	<i>Corynorhinus townsendii</i>	1*	~500
	February 2020	MR1-A	<i>Myotis yumanensis</i>	1*	>100
	June 2020	MR1-B	<i>Tadarida brasiliensis</i>	10	>100
	June 2020	UR	<i>Myotis yumanensis</i>	10	>100
Yolo	June 2020	TR1	<i>Tadarida brasiliensis</i>	10	>1,000
Sacramento	June 2020	TR2	<i>Tadarida brasiliensis</i>	10	>100,000
	June 2020	TR3	<i>Tadarida brasiliensis</i>	10	>1,000
	June 2020	TR4	<i>Tadarida brasiliensis</i>	10	>1,000
Individual bats ^e					
Marin	February 2020	MB	<i>Myotis californicus</i> and <i>Myotis yumanensis</i>		5

^aRoost name.^bSpecies found in each roost.^cNo. of samples refers to the number of individual vials filled (an asterisk [*] indicates that many guano samples from the same roost were collected and mixed into one larger jar) from guano piles. For other roosts, 10 smaller guano samples were pooled prior to processing.^dEstimated total size of the colony.^eFor individual bat samples, guano samples were collected from free-flying individual bats captured during a field study.

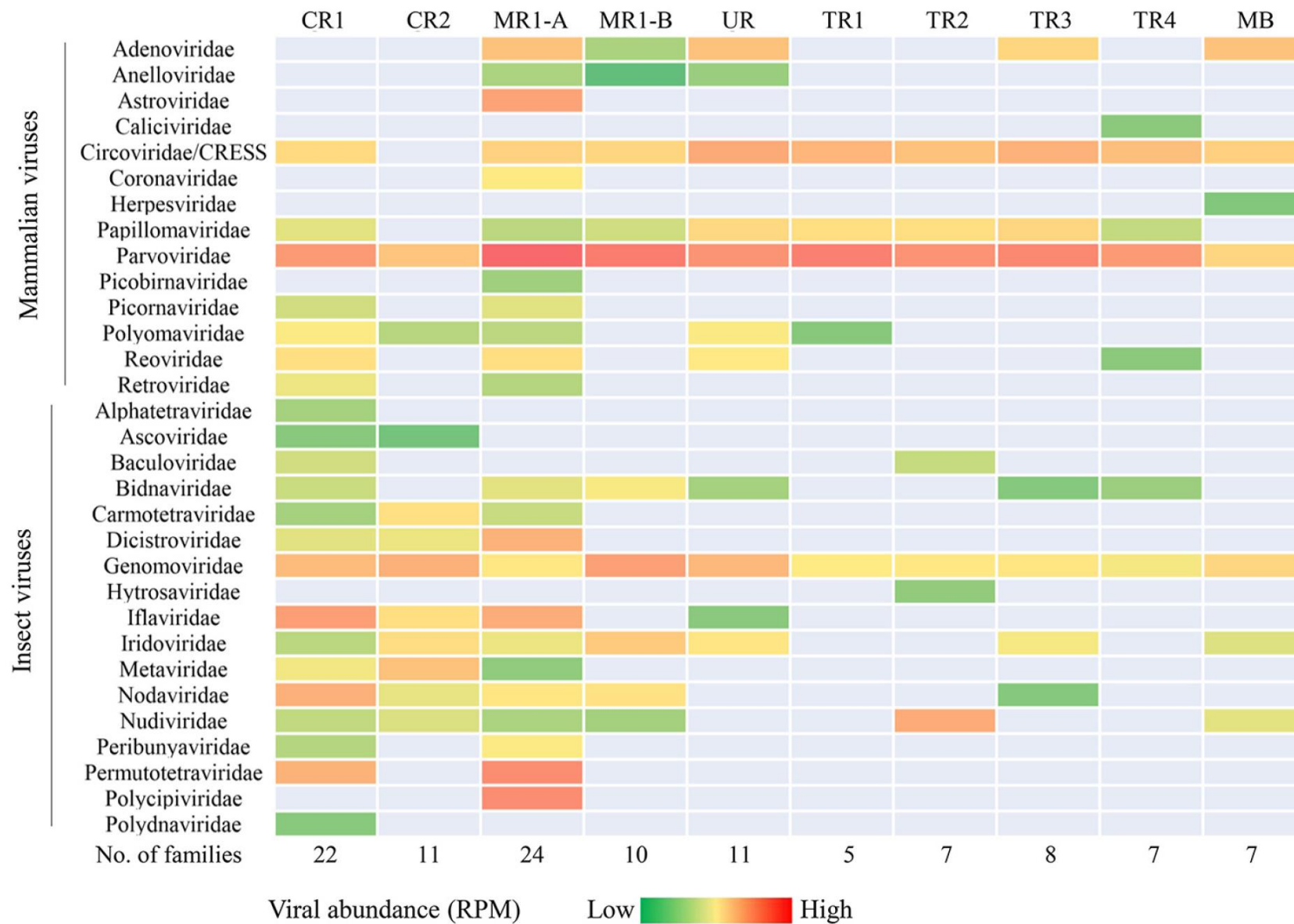


FIG 2 Summary of the bat-associated viruses. All viral families identified from the 10 bat guano samples with E scores of $<10^{-10}$. Only those eukaryotic viruses that could potentially infect mammals or insects are shown. Heat map was used to indicate the viral abundance (calculated as reads per million [RPM]), and RPM was displayed in \log_{10} of each family. The numbers of viral families detected from each guano sample are listed at the bottom.

TABLE 2 Viral sequences that share high similarity with those of known viruses

Virus hit ^a	GenPept or GenBank accession no. ^b	Sample origin	Country ^c	E value	Identity (%)	No. of contigs/reads	Total length (bp)	Roost
Bat calicivirus A10	AWK23451	<i>P. subflavus</i>	USA	8E–58	100%	1	284	TR4
Bat circovirus POA/V	AIX11629	<i>M. molossus/T. brasiliensis</i>	Brazil	2E–78	93.4%	1	369	TR1
Bat hepatovirus	YP_009505614	<i>Coelura afra</i>	Ghana	1E–23	93.9%	1	150	CR1
Bat mastadenovirus	AWT57880	<i>Myotis emarginatus</i>	Spain	8E–61	96.8%	1	289	MR1-A
Bat mastadenovirus G	YP_009325345	<i>Corynorhinus rafinesquii</i>	USA	~1E–39 to 2E–68	~93 to 97.2	2	757	MR1-A
Bat bocaparvovirus	AIF74240	<i>Myotis pequinius</i>	China	~1E–41 to 4E–51	~92.8 to 97.6	2	462	MR1-A
Bocaparvovirus sp.	AYG97822	Rodents	China	~7E–47 to 9E–68	~93.7 to 98.7	3	812	MR1-B
Canine parvovirus 2	–	Carnivores	*	0	100	2	549	TR4
Bocaparvovirus 1	AUD40074	Himalayan marmot	China	~6E–57 to 3E–97	~93.9 to 96.8	2	743	MR1-B
Mouse kidney parvovirus	NC_040843	<i>Mus musculus</i>	Australia/USA	~1E–177 to 0	~97.5 to 98.6	4	2,063	MR1-A
<i>Myotis myotis</i> bocavirus 1	YP_009508788	<i>Myotis myotis</i>	China	~8E–24 to 1E–53	~91.4 to 93.7	2	452	MR1-A
Porcine bocavirus 1	AEM43610	Pig	*	1E–30	91.20	1	251	MR1-B
Bat polyomavirus	AIF74282	<i>Rhinolophus ferrumequinum</i>	China	4E–42	94.50	1	221	UR
Gammapapillomavirus 11	ATQ38341	Human	USA	1E–46	100	1	225	CR1
Peromyscus papillomavirus 1	YP_009508760	<i>Peromyscus</i> (deer mouse)	USA	~6E–10 to 2E–101	91.6 to 100	3	834	UR
Human rotavirus A	AIE45278	Human	*	1E–45	95.0	1	245	MR1-A
Rotavirus H	–	Pig	*	~1E–18 to 4E–76	~93.7 to 100	9	2,000	UR

^aVirus hits from NCBI database that shared high identity to the viral contigs/reads in this study.

^bA dash (–) indicates that the sequence shared the same identity (%) with multiple reference genomes.

^cAn asterisk (*) indicates that the reference sequence could be found in multiple locations.