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Dear Editor,

We appreciate the feedback from Olson and Juman (2024) on our manuscript (Hareza et al. 2023). After conducting a thorough review of the original surveillance data, we acknowledge that both rabid marmots in question were indeed identified in states along the East Coast, and we have supplied a corrected table to address this.

While we concur with the significance of precise taxonomic nomenclature, it is imperative to note certain nuances regarding the functioning of the United States National Rabies Surveillance System (NRSS), which may not have been fully appreciated in the Letter by Olson and Juman. The NRSS compiles data from over 130 rabies laboratories across the United States, representing 54 reporting jurisdictions (Ma et al. 2022). These data are received in unstandardized formats and are collated by the Centers for Disease Control and Prevention (CDC). CDC is often unable to impute missing data elements (like species) or verify the taxonomic naming that reporting jurisdictions have provided.

It is pertinent to highlight that the Council for State and Territorial Epidemiologists (CSTE) requests states to submit species-level information for any animal tested for rabies. However, the availability of such information, particularly for bats, is not consistently ensured. This issue is described in various citations included in our original article, namely, "Rabies Surveillance in the United States" and the CSTE Position Statement (CSTE 2011; Ma et al. 2022).

Addressing the concerns raised regarding De Benedictis et al (De Benedictis et al. 2022), we find it necessary to emphasize the challenges associated with implementing costly technologies within large surveillance systems or publicly funded initiatives. Factoring in all associated expenses of DNA barcoding assays, inclusion of this as a routine test in a rabies diagnostic lab would likely cost $75 USD per sample. The NRSS laboratory network tests nearly 100,000 animals annually (CDC 2011) which would add $7.5 million in public funding if the suggested cytochrome B testing were to be adopted. It is crucial to contextualize this against the backdrop of the current cost for rabies diagnostic services across the 130 US rabies laboratories participating in the NRSS, which is estimated at $6 million USD (ADHS 2017). Selective DNA barcoding technology may have a role, but we must remember that the NRSS operates to prevent rabies infections

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TABLE 1. Rabies in rodents and lagomorphs in the USA and Puerto Rico, 2011–2020.

Rodent or Lagomorph	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	Total positive	Total tested	Percent positive
Groundhog (*Marmota monax*)	45	42	37	43	25	44	33	23	38	38	368	9,084	4.1%
Beaver (*Castor canadensis*)	3	4	0	2	2	5	0	4	1	0	21	283	7.4%
Rabbit (Family Leporidae)	0	0	1	0	7	0	0	0	0	0	8	1,364	0.6%
Marmota spp.[a]	0	0	2	0	0	0	0	0	0	0	2	109	1.8%
Squirrel (Family Sciuridae)	0	0	0	0	1	0	0	0	1	0	2	6,195	0.0%
Rat (*Rattus* spp.)	0	0	0	0	0	0	0	0	0	0	0	1,052	0.0%
House mouse (*Mus musculus*)	0	0	0	0	0	0	0	0	0	0	0	840	0.0%
Muskrat (*Ondatra zibethicus*)	0	0	0	0	0	0	0	0	0	0	0	835	0.0%
Chipmunk (*Tamias striatus*)	0	0	0	0	0	0	0	0	0	0	0	658	0.0%
All others[b]	0	0	0	0	0	0	0	0	0	0	0	1,505	0.0%
Grand total	**48**	**46**	**40**	**45**	**35**	**49**	**33**	**27**	**40**	**38**	**401**	**21,925**	**1.8%**
All tested	2,516	2,504	2,243	2,309	2,273	2,168	2,090	2,090	1,904	1,828	21,925		
Percent positive	1.9%	1.8%	1.8%	1.9%	1.5%	2.3%	1.6%	1.3%	2.1%	2.1%	1.8%		

[a] Includes animals recorded only as '*Marmota*' or '*Marmota* sp.', which may have included *Marmota monax* individuals.
[b] All others (small mammals not rodents or lagomorphs): Moles (e.g., Subfamily Scalopinae) and shrews (Family Soricidae); note that surveillance records are usually applied with common names only.

TABLE 2. Rabies percent positivity in rodents, lagomorphs and raccoons in the USA and Puerto Rico from 1985 to 2020.

	Raccoon (*Procyon lotor*)			Groundhog (*Marmota monax*)			Beaver (*Castor canadensis*)			Rabbit (Family Leporidae)			Other rodents and lagomorphs[a]			All rodents and lagomorphs[b]		
Timespan	Tested	Positive	% Pos	Tested	Positive	% Pos	Tested	Positive	% Pos	Tested	Positive	% Pos	Tested	Positive	% Pos	Tested	Positive	% Pos
1985–1994	122,394	27,284	22.29%	5,985	327	5.46%	206	12	5.82%	3,380	17	0.50%	52,266	19	0.04%	61,837	375	0.61%
1995–2010	202,426	46,637	23.04%	14,051	663	4.72%	551	31	5.63%	5,502	25	0.45%	53,571	16	0.03%	73,675	735	1.00%
2011–2020	123,704	16,172	13.07%	9,084	368	4.05%	283	21	7.42%	1,364	8	0.59%	11,194	4	0.04%	21,925	401	1.83%
Total	448,524	90,093	20.09%	29,120	1,358	4.66%	1,040	64	6.15%	10,246	50	0.49%	117,031	39	0.03%	157,437	1,511	0.96%

[a] Other rodents and lagomorphs: Marmot (*Marmota* spp.), squirrel (*Family Sciuridae*), rat (*Rattus sp.*), house mouse (*Mus musculus*), muskrat (*Ondatra zibethicus*), chipmunk (*Tamias striatus*), all other.
[b] All rodents and lagomorphs: Groundhog, beaver, rabbit, marmot, squirrel, rat, mouse, muskrat, chipmunk, all other.

in people and animals, epidemiologic studies such as this are conducted opportunistically, taking advantage of the data generated by this large and routine public health system. Until truly low cost and accurate means of taxonomic identification are available, large-scale, publicly funded surveillance systems will struggle to implement the suggestions provided by Olson and Juman.

In light of the aforementioned challenges and constraints, we propose a pragmatic solution by correcting the table to reflect "*Marmota* sp." to prevent any future misinterpretations. Additionally, we recommend replacing the specific taxonomies for rabbit and squirrel with more general taxonomic names, as indicated in the corrected table. Furthermore, we would like to clarify that discrepancies raised by Olson and Juman are due to differences in data included in our analysis (we did not include guinea pigs or chinchilla in our study, for example, so we did not include these animals from previous publications in our analyses).

While we acknowledge the significance of addressing errors and ensuring accuracy, we assert that the issues raised by Olson and Juman primarily pertain to a straightforward erratum in Table 1 (please see Table 2 for corrections). The challenges associated with working with a vast surveillance database and the limited accessibility of accurate taxonomic identification tools in public health laboratories contributed to the issue raised by Olson and Juman.

Dariusz A. Hareza, Ricky Langley, Xiaoyue Ma, Ryan Wallace, and Charles E. Rupprecht

Disclaimer: The findings and conclusions in this letter are those of the authors and do not necessarily represent the views of the Centers for Disease Control and Prevention.

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