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Source: Journal of Wildlife Diseases, 60(2) : 554-555

Published By: Wildlife Disease Association

URL: https://doi.org/10.7589/JWD-D-23-00178a

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LETTERS TO THE EDITOR

DOI: 10.7589/JWD-D-23-00178a

Journal of Wildlife Diseases, 60(2), 2024, pp. 554–555

Host Taxonomy is Critical in Zoonotic Disease Surveillance and Reporting

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In their recent review, Hareza et al. (2023) reported that two of 109 Alaska marmots (*Marmota broweri*) tested for rabies between 2011 and 2020 were positive. Of North America's six marmot species, the Alaska marmot's range is the most remote, extending across the Brooks Range in northern Alaska and smaller mountain ranges in the state's interior (Gunderson et al. 2009). As a result, *M. broweri* remains the continent's least-studied marmot, making the purported acquisition of 109 individuals for rabies testing—and the claim that two tested positive—notable, to say the very least. However, we were unable to find any mention of *M. broweri* in the sources cited by Hareza et al. (2023). Other than woodchucks (*M. monax*), the only marmots in any of the 10 reports are two identified as "*Marmota* sp." from Virginia that tested positive in 2013 (Dyer et al. 2014); these appear to correspond to the two purported rabies-positive Alaska marmots in Hareza et al. (2023).

A review of the publications used to generate the tables in Hareza et al. (2023), whose summary data were used for the statistical tests performed therein, revealed several additional instances wherein species identifications appear to have been inexplicably assigned to records originally identified only to genus, broadly inclusive colloquial name (e.g., "squirrel"), or a different species altogether; we detail these and other discrepancies (see Supplementary Material) and take this opportunity to reiterate some of the many reasons host taxonomy is important in and, indeed, critical to zoonotic disease research.

Accurate and specific host identification is prerequisite for understanding and predicting pathogen distribution, transmission, and spillover. For example, species identification is necessary for mapping the host's geographic range, often used to model the ecological niche and transmission risk of rabies (Escobar et al. 2015). It would be impossible to study species-specific establishment and cross-species transmission rates (Streicker et al. 2010) with a dataset lacking high taxonomic resolution. Similarly, host prediction hinges on a consistent taxonomic backbone (Worsley-Tonks et al. 2020).

At best, a taxonomically unspecific dataset hinders the feasibility of these studies; at worst, feeding inaccurate data into models leads to the misprediction of host species, pathogen ranges, and the spatial and temporal windows of spillover. The stakes are especially high when considering downstream impacts of this research, such as species management and spillover mitigation policies (e.g., culling, vaccination), all of which rely, to some degree, on accurate identification of wild hosts. Host taxonomy is the foundation of disease ecology research, and misreported surveillance ensures the failure of future studies reliant on these data.

That taxonomy matters in zoonotic disease reporting should, by now, be a universal truism. We therefore echo and amplify De Benedictis et al. (2022) and emphatically urge researchers, coauthors, editors, reviewers, program officers, public health agencies, and everyone else in the scientific funding, research, and publishing arenas to prioritize taxonomic rigor as they would any other foundational tenet. That which is not identified correctly cannot be studied meaningfully, and the consequences are nontrivial.

Supplementary material for this article is online at https://dx.doi.org/10.7589/JWD-D-23-00178a.

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