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VETERINARY MEDICINE
Veterinary Genetics Laboratory

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To whom this may concern:

I write this review to summarize my evaluation of the Ph. D. Dissertation of **Francelly Martínez Sosa**, entitled "**The Effect of Environmental Factors on Adaptive Genetic Variation in Grey Wolves and Free-Ranging Dogs**." I am an Adjunct Professor of wildlife genomics in the Veterinary Genetics Laboratory at the University of California, Davis in the USA, where my students and I conduct research on the evolution and ecology of canids and other mammals.

Specific comments

Overall, the structure of the dissertation was clear and logical. The Abstract adequately encapsulates the content of the dissertation, while the General Introduction lays out clearly the rationale, aims, and methodological approach, along with a summary of results. The General Discussion and Conclusions section provides a more detailed discussion of findings. Each of the four chapters, the meat of this dissertation, reflects a distinct topic corresponding to a manuscript for a journal article.

Chapter 1 was published as an article in the peer-reviewed journal, *Genes*. It represents a comprehensive review of molecular mechanisms underlying adaptive evolution in vertebrates and, as such, provides a platform on which to build subsequent chapters, having laid out a long list of genes to target in investigations of adaptation to particular mechanisms and modes, such as diet and reproduction.

Chapter 2 presents a study of population genetic structure and evidence for genes under diversifying selection in both grey wolves and free-ranging dogs. This was an especially novel study, leveraging the common evolutionary origins but distinct recent ecological circumstances to explore similarities and differences in both connectivity and natural selection across the genome. The study used an impressive number (hundreds) of wolves and dogs, genotyping >700,000 SNPs throughout the genome. Population structure was investigated using multiple tools, such that the emerging inferences were robust. Several patterns were clearly exposed in both wolves and dogs, which responded differently to the same human-dominated landscapes; this pattern was interpreted, I believe correctly, to reflect differences in the relationships between wolves and dogs to humans, including their demographic histories. Lastly, a comparison of signatures of selection on several targeted genes showed similarities between dogs and wolves highlighting similar responses to diversifying selection in these two canids. Overall, I found this to be a well-conceived study.

Although I have no substantive criticisms, some suggestions that could help clarify

530-752-2211 tel • 530-752-3556 fax
One Shields Avenue, Davis, CA 95616-8744
vgl.ucdavis.edu

findings when published follow: First, on page 54, I was unclear why the number corresponding to wolf samples that passed filtering was 232 in one place and 230 in another. In figure 1A, it would help to add a key indicating which colored symbol represents which species of canid. In Fig 1B, it would be helpful to enlarge the font and symbols. For example, it was difficult for me to differentiate Northern Asia from Southeastern Europe based on the colors used and small size of symbols. In the Discussion where genetic differentiation within wolves is discussed in terms of the Arabian Peninsula, it would be helpful to integrate the findings of Hennelly et al. (2021, 2024, 2025).

Hennelly et al. 2021. Ancient divergence of Indian and Tibetan wolves revealed by recombination-aware phylogenomics. Molecular Ecology 30:6687–6700.

Hennelly et al. 2024. Genomic analysis of wolves from Pakistan clarifies boundaries among three divergent wolf lineages. Journal of Heredity 115:339–348

Hennelly et al. 2026. Continent-wide view of genomic diversity and divergence in the wolves of Asia. Communications Biology 9:330. https://doi.org/10.1038/s42003-025-09379-9

Chapter 3 continues the comparative approach, this time investigating genomic evidence of local selection associated with climatic and environmental variation among 10 biomes between free-ranging dogs and wolves. Interestingly, similar numbers of genes coding for similar functions (e.g., metabolism, immune response, morphology, and sensory perception) in wolves and dogs stood out as having environmentally specific associations, yet the particular genes differed between them, underscoring the redundancy in the genome for phenotypic evolution.

Chapter 4 was an especially clever and interesting approach to investigating the geographic origins of the domestic dog. Ms. Sosa used a species distribution modeling and genetic offset approach to infer environmental conditions best suited to dogs, and then projected those conditions back into the past when dogs originated to identify locations most suitable for dogs. The inference was that regions where dogs were best suited closer to their time of origin were also the most likely regions for them to have originated. What I especially appreciated was the use of a genetic offset approach to inferring the past. More often, this is used as a means of assessing a population's prognosis for the future depending on climatic changes. In this case, although that was also addressed, the main purpose of the analysis was to use locations where the genetic offset was lowest to infer that those are the locations where they were best adapted in the past.

While this study does not in and of itself prove anything about where dogs originated, it does provide an orthogonal piece of evidence in a growing body of evidence for a southern origin of dogs. For studies arguing that dogs originated in Eastern Siberia, for example, this study raises important questions those proponents must contend with. That is exactly the type of science that moves the field forward. My only concern about this study is whether the dog data utilized in the modeling might not

have been affected by modern aspects of the human-dog relationship that were not relevant at the time of their origins. While I appreciated the treatment of other potential biases in the dataset, I am not sure this one was addressed. In any case, this is not at all a disagreement with the conclusions of the study; rather, it is a caveat that should be weighed.

Conclusion

One thread that ran through all of the chapters was an impressive deep dive into the functional genomics of dogs and wolves. Although many studies employ statistical procedures to identify gene-phenotype or gene-environment associations, few go the next step of assessing physiological pathways for those effects, and even fewer go as far as Ms. Sosa to list particular genes and understand through comparative analysis of the literature their possible functions. I was very impressed by their command of the field. I also appreciated the progression from a solid review of particular genes likely to be related to both diversifying selection and local environmental selection, to two papers tacking each of these, along with population structure, and finally utilizing the findings with respect to genes associated with climatic variables to study the genetic offset as a means of addressing an age-old question in the center of dog evolution: center of origins.

In sum, I hereby state that the doctoral dissertation submitted for evaluation by Ms. Sosa constitutes an original solution to a research problem. The candidate demonstrates general theoretical knowledge in the relevant scientific discipline and proves the ability to conduct independent scientific research, thereby fulfilling the conditions set out in Article 187 of the Act of 20 July 2018 – Law on Higher Education and Science (Journal of Laws 2018, item 1668, as amended). In view of the above, I submit a motion to the Scientific Council of the Museum and Institute of Zoology of the Polish Academy of Sciences to admit Ms Sosa to the further stages of the proceedings for the award of the doctoral degree in the field of exact and natural sciences, in the discipline of biological sciences.

Sincerely,

BENJAMIN N SACKS

Digitally signed by BENJAMIN N SACKS
Date: 2026.03.23 05:22:54 -07'00'

Dr. Benjamin N. Sacks
Adjunct Professor
Veterinary Genetics Laboratory,
Department of Population Health and Reproduction
School of Veterinary Medicine
University of California, Davis