

## EVOLUTIONARY GENETICS

# Comment on “Whole genome sequence analysis shows two endemic species of North American wolf are admixtures of the coyote and gray wolf”

Paul A. Hohenlohe,<sup>1\*</sup> Linda Y. Rutledge,<sup>2†</sup> Lisette P. Waits,<sup>3</sup> Kimberly R. Andrews,<sup>3</sup> Jennifer R. Adams,<sup>3</sup> Joseph W. Hinton,<sup>4</sup> Ronald M. Nowak,<sup>5</sup> Brent R. Patterson,<sup>6</sup> Adrian P. Wydeven,<sup>7</sup> Paul A. Wilson,<sup>2</sup> Brad N. White<sup>2</sup>

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## INTRODUCTION

In a recent article, vonHoldt and colleagues (1) use whole-genome sequence data to address the relationships and evolutionary origins of several North American canid taxa. The authors conclude that two taxa, the red wolf (*Canis rufus*) and the eastern wolf (*Canis lycaon*), are not long-diverged lineages as other researchers have concluded from genetic (2–7) and fossil evidence (8, 9) but are, rather, populations resulting from recent admixture between gray wolves (*Canis lupus*) and coyotes (*Canis latrans*). They use this conclusion to argue that endangered species policy should better account for hybridization and admixture. We agree that hybridization and admixture are widespread in the natural world and that the conservation policy needs to be updated to account for this biological reality. However, we strongly disagree with their conclusion that red and eastern wolves are of recent hybrid origin and we conclude that their analysis does not actually test the hypothesis of a recent hybrid origin. Their data are consistent with multiple hypotheses for the origins of red and eastern wolves, including relatively old origins of these taxa. Furthermore, we argue that their data do not support “a lack of unique ancestry in red and eastern wolves” (1); rather, substantial evidence still supports the conclusion that red and eastern wolves represent genetically distinct taxa among North American canids. Below, we detail this perspective and argue for further analyses that would directly test competing hypotheses for the evolutionary origins of these groups.

## REPRESENTATIVE SAMPLES

Analysis of whole-genome sequence data necessarily relies on a relatively small number of individual samples that are taken to be representative of larger populations or taxa. In this case, the choice of representative samples is problematic in several respects. First, of the three individuals chosen as representative nonadmixed coyotes, two are from outside the historic range of coyotes. These two individuals, from Alabama and Quebec, are actually from within the historic ranges of red and eastern wolves, respectively. In these regions, hybridization between eastward-expanding coyotes and na-

tive canid taxa [considered to be gray wolves by vonHoldt *et al.* (1) and red and eastern wolves by others (9–13)] following wolf extirpation and European settlement has been well-documented. One of these, the Quebec coyote, has at least 15.8% gray wolf ancestry [table S2 in the study of vonHoldt *et al.* (1)]. Introgression from eastern or red wolves into the Quebec and Alabama samples was not directly tested because of the previous assumption that red and eastern wolves are admixed themselves. Any hybrid ancestry in these samples used as representative coyotes would confound estimates of admixture in red and eastern wolves.

Second, some analyses in the study of vonHoldt *et al.* (1) pool two putative eastern wolves from the Algonquin Park region of Ontario, recognized as the best contemporary representation of eastern wolves, with Great Lakes wolves from Minnesota and Isle Royale, despite genetic evidence that supports that Great Lakes wolves are a hybridized population between gray and eastern wolves (14, 15). Analyses where these two very different *Canis* types are grouped together cannot be used to make any conclusions about hybrid ancestry of eastern wolves. Third, Algonquin wolves hybridize with Great Lakes boreal wolves and eastern coyotes to the north and south of Algonquin Park, respectively (15, 16); thus, the uncertain ancestry of the two individuals from Algonquin Park used by vonHoldt *et al.* (1) questions any conclusions regarding the evolutionary history of eastern wolves (17).

## GENETIC DIFFERENTIATION

vonHoldt *et al.* (1) conduct two analyses of differentiation among taxa that do not assume an evolutionary model a priori. First, they calculate  $F_{ST}$ . Here, red wolves exhibit the greatest differentiation from the other groups, which the authors attribute to recent genetic drift in the captive population; but this degree of differentiation is also consistent with an interpretation of red wolves as a distinct evolutionary lineage. The Mexican wolf, which has a similar history of a small captive founder population, is regarded by the authors as “a distinct North American wolf.” Second, in the principal components analysis (PCA) of individual samples, Eurasian and North American gray wolves are differentiated from coyotes along PC 1, whereas Great Lakes wolves, eastern wolves, red wolves, and eastern coyotes are differentiated from the other two groups along PC 2. This result does not directly test evolutionary hypotheses, although it is consistent with multiple scenarios, including ancient hybridization or a distinct cladogenic origin for red and eastern wolves, and less consistent with a more recent hybrid origin for these taxa (18). With the exception of Great Lakes wolves clustering closer to eastern (Algonquin) wolves, the PCA results are quite similar to those of Rutledge *et al.* (15),

<sup>1</sup>Department of Biological Sciences, University of Idaho, Moscow, ID 83844–3051, USA. <sup>2</sup>Biology Department, Trent University, Peterborough, Ontario K9L 0G2, Canada.

<sup>3</sup>Department of Fish and Wildlife Sciences, University of Idaho, Moscow, ID 83844–1136, USA. <sup>4</sup>Warnell School of Forestry and Natural Resources, University of Georgia, Athens, GA 30602, USA. <sup>5</sup>Falls Church, VA 22043, USA. <sup>6</sup>Ministry of Natural Resources and Forestry, Trent University, Peterborough, Ontario K9L 0G2, Canada. <sup>7</sup>Timber Wolf Alliance, Northland College, Ashland, WI 54806, USA.

\*Corresponding author. Email: hohenlohe@uidaho.edu

†These authors contributed equally to this work.

which were taken as support for eastern wolves as a distinct taxon, possibly with an ancient hybrid origin (18, 19).

### ANALYSIS OF ADMIXTURE

vonHoldt *et al.* (1) conducted two tests for admixture: *D*-statistics (20, 21) and G-PhoCS (22). Both of these tests assume a specific tree structure, in which each group is a distinct lineage. Both of these analyses indicate support for relatively large amounts of shared ancestry and admixture among North American canids. However, a history of admixture implies neither that a taxon's origins trace to a hybridization event nor that a taxon has a "lack of unique ancestry," as the authors conclude. For example, *D*-statistics revealing introgression between Neandertals and Eurasian humans were not interpreted to conclude that Eurasians contained no unique ancestry because they were the product of hybridization between Neandertals and Africans; instead, researchers concluded that introgression occurred between Neandertals and a distinct Eurasian lineage (20). Analogously, the results presented by vonHoldt *et al.* (1) are consistent with a relatively old lineage leading to red and/or eastern wolves, predating recent admixture from coyotes or gray wolves, and this is the model assumed in both the *D*-statistics and G-PhoCS analyses [Fig. 4 in the study of vonHoldt *et al.* (1)].

Nonetheless, it is important to understand when admixture has occurred. G-PhoCS and *D*-statistics provide no information regarding dates of gene flow between lineages [G-PhoCS assumes a constant rate of migration over the time when the lineages co-occur (22)]. Haplotype-based analyses may provide an answer to the time scale of admixture among these taxa [for example, the study of Loh *et al.* (23)]. Dates of introgression are an important consideration for the conservation of red and eastern wolves because current conservation policies regard recent introgression as being less indicative of a distinct evolutionary lineage, compared with more ancient introgression (24).

### EVIDENCE FOR DISTINCTIVENESS IN RED AND EASTERN WOLVES

Contrary to the authors' overall conclusions of a recent and admixed history for red and eastern wolves, the G-PhoCS analysis offered support for a relatively old origin of red wolves as a distinct evolutionary lineage (eastern wolves were not included in this analysis). Divergence time from coyotes (using the California sample) was estimated to be 55,000 to 117,000 years ago, and approximately 40,000 years ago if no subsequent gene flow from coyotes is allowed in the model. It is not possible to directly compare the support for these alternative models using G-PhoCS, but these estimates are older than the authors' estimated divergence time between Eurasian and North American gray wolves [ $\sim$ 20,000 years ago; fig. S5 in the study of vonHoldt *et al.* (1)] and between Eurasian gray wolves and coyotes (50,800 to 52,100 years ago). Calibration of these divergence times depends on the mutation rate and generation time and is dependent on estimates of effective population size. For instance, the authors assume a 3-year generation time, compared to empirical estimates of 4.7 years for Minnesota wolves (25), and an effective population size of 45,000 based on the domestic dog literature (26, 27); use of longer generation time or larger effective population size estimates would place the divergence estimates among the different lineages much earlier. All of these estimates indicate that red wolves have experienced significant evolution as a distinct taxon; if they are of

hybrid origin, these data are consistent with a relatively old (Pleistocene) age for that admixture event (7). We suggest that these whole-genome data be used in a model-selection approach to directly test support for alternative evolutionary hypotheses.

The authors also estimate the proportion of unique alleles in North American canids (that is, alleles not found in either reference Eurasian gray wolf or reference coyote samples). Red wolves had an average of 4.41% unique alleles and Algonquin wolves had 3.82%, compared to Great Lakes boreal gray wolves (excluding the Quebec wolf) with fewer unique alleles (3.61%) and North American gray wolves with fewer still (3.30%). The authors state that for red and eastern wolves to be a distinct species, they would expect the proportion of new alleles to be higher than observed, but it is unclear where this expectation originates. Comparison of explicit demographic models is needed to generate quantitative expectations of proportion of unique alleles. Nonetheless, the observed proportions of unique alleles reveal a higher degree of evolutionary distinctiveness in red and eastern wolves relative to other North American canids, a finding that is inconsistent with the hypothesis of recent hybrid origin for these taxa.

### HYBRIDIZATION BETWEEN COYOTES AND GRAY WOLVES

The hypothesis of a recent hybrid origin for red and eastern wolves requires interbreeding between gray wolves and coyotes. Although gray wolves and coyotes have produced fertile offspring, this has only occurred with limited success by artificial insemination in captivity (28), and evidence for interbreeding in the wild is limited. vonHoldt *et al.* (1) suggest that gray wolves would breed naturally with coyotes when wolf population density becomes very low. However, there is no evidence in the Western Great Lakes, where gray wolves and coyotes have coexisted since before European settlement (29, 30), of ongoing or recent hybridization between these two species (31, 32). Other North American canids have undergone severe population bottlenecks, without resulting in hybridization between gray wolves and coyotes, such as the lack of hybridization between coyotes and Mexican wolves (33).

### CONCLUSION

We agree with vonHoldt *et al.* (1) that genetic data support admixture as part of the evolutionary history of North American canids, and we also agree that endangered species conservation policy needs to account for this biological reality in these and other groups (24, 34, 35). However, in contrast to their conclusions, we argue that their data are consistent with multiple evolutionary hypotheses for the origins of red and eastern wolves, including ancient hybridization, but that they do not definitively support a recent origin by hybridization. However, their analyses do not directly test alternative evolutionary models for the origin of red and eastern wolves.

Regardless of the evolutionary details of the origins of red and eastern wolves, the genomic data presented by vonHoldt *et al.* (1) provide support for the genetic and evolutionary distinctiveness of these taxa. Along with the ecological role of top predators and the benefits they provide to ecosystems through natural regulation, we believe that these genomic data argue for continued recognition of red and eastern wolves as distinct taxa for the purpose of conservation policy.

## REFERENCES AND NOTES

1. B. M. vonHoldt, J. A. Cahill, Z. Fan, I. Gronau, J. Robinson, J. P. Pollinger, B. Shapiro, J. Wall, R. K. Wayne, Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. *Sci. Adv.* **2**, e1501714 (2016).
2. P. J. Wilson, S. Grewal, I. D. Lawford, J. N. M. Heal, A. G. Granacki, D. Pennock, J. B. Theberge, M. T. Theberge, D. R. Voigt, W. Waddell, R. E. Chambers, P. C. Paquet, G. Goulet, D. Cluff, B. N. White, DNA profiles of the eastern Canadian wolf and the red wolf provide evidence for a common evolutionary history independent of the gray wolf. *Can. J. Zool.* **78**, 2156–2166 (2000).
3. P. J. Wilson, S. Grewal, T. McFadden, R. C. Chambers, B. N. White, Mitochondrial DNA extracted from eastern North American wolves killed in the 1800s is not of gray wolf origin. *Can. J. Zool.* **81**, 936–940 (2003).
4. P. J. Wilson, L. Y. Rutledge, T. J. Wheelton, B. R. Patterson, B. N. White, Y-chromosome evidence supports widespread signatures of three-species *Canis* hybridization in eastern North America. *Ecol. Evol.* **2**, 2325–2332 (2012).
5. L. Y. Rutledge, B. R. Patterson, B. N. White, Analysis of *Canis* mitochondrial DNA demonstrates high concordance between the control region and ATPase genes. *BMC Evol. Biol.* **10**, 215 (2010).
6. L. Y. Rutledge, K. I. Bos, R. J. Pearce, B. N. White, Genetic and morphometric analysis of sixteenth century *Canis* skull fragments: Implications for historic eastern and gray wolf distribution in North America. *Conserv. Genet.* **11**, 1273–1281 (2010).
7. K. B. Brzeski, M. B. DeBiasse, D. R. Rabon Jr., M. J. Chamberlain, S. S. Taylor, Mitochondrial DNA variation in southeastern pre-Columbian canids. *J. Hered.* **107**, 287–293 (2016).
8. R. M. Nowak, The red wolf is not a hybrid. *Conserv. Genet.* **6**, 593–595 (1992).
9. R. M. Nowak, The original status of wolves in eastern North America. *Southeast. Nat.* **1**, 95–130 (2002).
10. J. L. Paradiso, Canids recently collected in east Texas, with comments on the taxonomy of the red wolf. *Am. Midl. Nat.* **80**, 529–534 (1968).
11. P. J. Wilson, S. K. Grewal, F. F. Mallory, B. N. White, Genetic characterization of hybrid wolves across Ontario. *J. Hered.* **100**, S80–S89 (2009).
12. R. Kays, A. Curtis, J. J. Kirchman, Rapid adaptive evolution of northeastern coyotes via hybridization with wolves. *Biol. Lett.* **6**, 89–93 (2010).
13. J. G. Way, L. Rutledge, T. Wheelton, B. N. White, Genetic characterization of eastern “coyotes” in eastern Massachusetts. *Northeast. Nat.* **17**, 189–204 (2010).
14. T. Wheelton, B. N. White, Genetic analysis of historic western Great Lakes region wolf samples reveals early *Canis lupus/lycaon* hybridization. *Biol. Lett.* **5**, 101–104 (2009).
15. L. Y. Rutledge, S. Devillard, J. Q. Boone, P. A. Hohenlohe, B. N. White, RAD sequencing and genomics simulations resolve hybrid origins within North American *Canis*. *Biol. Lett.* **11**, 20150303 (2015).
16. L. Y. Rutledge, C. J. Garroway, K. M. Loveless, B. R. Patterson, Genetic differentiation of eastern wolves in Algonquin Park despite bridging gene flow between coyotes and grey wolves. *Heredity* **105**, 520–531 (2010).
17. L. Y. Rutledge, P. J. Wilson, C. F. C. Klütsch, B. R. Patterson, B. N. White, Conservation genomics in perspective: A holistic approach to understanding *Canis* evolution in North America. *Biol. Conserv.* **155**, 186–192 (2012).
18. K. M. Sefc, S. Koblmüller, Ancient hybrid origin of the eastern wolf not yet off the table: A comment on Rutledge *et al.* (2015). *Biol. Lett.* **11**, 20150834 (2016).
19. L. Y. Rutledge, S. Devillard, P. A. Hohenlohe, B. N. White, Considering all the evidence: A reply to Sefc and Koblmüller (2016). *Biol. Lett.* **11**, 20151009 (2016).
20. R. E. Green, J. Krause, A. W. Briggs, T. Maricic, U. Stenzel, M. Kircher, N. Patterson, H. Li, W. Zhai, M. H.-Y. Fritz, N. F. Hansen, E. Y. Durand, A.-S. Malaspina, J. D. Jensen, T. Marques-Bonet, C. Alkan, K. Prüfer, M. Meyer, H. A. Burbano, J. M. Good, R. Schultz, A. Aximu-Petri, A. Butthof, B. Höber, B. Höffner, M. Siegemund, A. Weihmann, C. Nusbaum, E. S. Lander, C. Rüss, N. Novod, J. Affourtit, M. Egholm, C. Verna, P. Rudan, D. Brajkovic, Ž. Kucan, I. Gušić, V. B. Doronichev, L. V. Golovanova, C. Lalueza-Fox, M. de la Rasilla, J. Fortea, A. Rosas, R. W. Schmitz, P. L. F. Johnson, E. E. Eichler, D. Falush, E. Birney, J. C. Mullikin, M. Slatkin, R. Nielsen, J. Kelso, M. Lachmann, D. Reich, S. Pääbo, A draft sequence of the Neandertal genome. *Science* **328**, 710–722 (2010).
21. E. Y. Durand, N. Patterson, D. Reich, M. Slatkin, Testing for ancient admixture between closely related populations. *Mol. Biol. Evol.* **28**, 2239–2252 (2011).
22. I. Gronau, M. J. Hubisz, B. Gulko, C. G. Danko, A. Siepel, Bayesian inference of ancient human demography from individual genome sequences. *Nat. Genet.* **43**, 1031–1034 (2011).
23. P.-R. Loh, M. Lipson, N. Patterson, P. Moorjani, J. K. Pickrell, D. Reich, B. Berger, Inferring admixture histories of human populations using linkage disequilibrium. *Genetics* **193**, 1233–1254 (2013).
24. R. K. Wayne, H. B. Shaffer, Hybridization and endangered species protection in the molecular era. *Mol. Ecol.* **25**, 2680–2689 (2016).
25. L. D. Mech, S. M. Barber-Meyer, J. Erb, Wolf (*Canis lupus*) generation time and proportion of current breeding females by age. *PLOS ONE* **11**, e0156682 (2016).
26. K. Lindblad-Toh, C. M. Wade, T. S. Mikkelsen, E. K. Karlsson, D. B. Jaffe, M. Kamal, M. Clamp, J. L. Chang, E. J. Kulkarni, M. C. Zody, E. Mauceli, X. Xie, M. Breen, R. K. Wayne, E. A. Ostrander, C. P. Ponting, F. Galibert, D. R. Smith, P. J. deJong, E. Kirkness, P. Alvarez, T. Biagi, W. Brockman, J. Butler, C.-W. Chin, A. Cook, J. Cuff, M. J. Daly, D. DeCaprio, S. Gnerre, M. Grabherr, M. Kellis, M. Kleber, C. Bardeleben, L. Goodstadt, A. Heger, C. Hitte, L. Kim, K.-P. Koepfli, H. G. Parker, J. P. Pollinger, S. M. J. Searle, N. B. Sutter, R. Thomas, C. Webber, J. Baldwin, A. Abebe, A. Abouelleil, L. Aftuck, M. Ait-zahra, T. Aldredge, N. Allen, P. An, S. Anderson, C. Antoine, H. Arachchi, A. Aslam, L. Ayotte, P. Bachantsang, A. Barry, T. Bayul, M. Benamara, A. Berlin, D. Bessette, B. Blitshteyn, T. Bloom, J. Blye, L. Boguslavskiy, C. Bonnet, B. Boukhgalter, A. Brown, P. Cahill, N. Calixte, J. Camarata, Y. Cheshatsang, J. Chu, M. Citronen, A. Collymore, P. Cooke, T. Dawoe, R. Daza, K. Decktor, S. DeGray, N. Dhargay, K. Dooley, K. Dooley, P. Dorje, K. Dorjee, L. Dorris, N. Duffey, A. Dupes, O. Egbiremolun, R. Elong, J. Falk, A. Farina, S. Faro, D. Ferguson, P. Ferreira, S. Fisher, M. FitzGerald, K. Foley, C. Foley, A. Franke, D. Friedrich, D. Gage, M. Garber, G. Gearin, G. Giannoukos, T. Goode, A. Goyette, J. Graham, E. Grandbois, K. Gyaltsen, N. Hafez, D. Hagopian, B. Hagos, J. Hall, C. Healy, R. Hegarty, T. Honan, A. Horn, N. Houde, L. Hughes, L. Hunnicutt, M. Husby, B. Jester, C. Jones, A. Kamat, B. Kanga, C. Kells, D. Khazanovich, A. C. Kieu, P. LeVine, J. Liu, X. Liu, Y. Lokyitsang, T. Lokyitsang, A. Lui, J. Macdonald, J. Major, R. Marabella, K. Maru, C. Matthews, S. McDonough, T. Mehta, J. Meldrim, A. Melnikov, L. Meneus, A. Mihalev, T. Mihova, K. Miller, R. Mittelman, V. Mlenga, L. Mulrain, G. Munson, A. Navidi, J. Naylor, T. Nguyen, N. Nguyen, C. Nguyen, T. Nguyen, R. Nicol, N. Norbu, C. Norbu, N. Novod, T. Nyima, P. Olandt, B. O'Neill, K. O'Neill, S. Osman, L. Oyono, C. Patti, D. Perrin, P. Phunkhang, F. Pierre, M. Priest, A. Rachupka, S. Raghuraman, R. Rameau, V. Ray, C. Raymond, F. Rege, C. Rise, J. Rogers, P. Rogov, J. Sahalie, S. Settipalli, T. Sharpe, T. Shea, M. Sheehan, N. Sherpa, J. Shi, D. Shih, J. Sloan, C. Smith, T. Sparrow, J. Stalker, N. Stange-Thomann, S. Stavropoulos, C. Stone, S. Stone, S. Sykes, P. Tchuinga, P. Tenzing, S. Tesfaye, D. Thoulutsang, Y. Thoulutsang, K. Topham, I. Topping, T. Tsamla, H. Vassiliev, V. Venkataraman, A. Vo, T. Wangchuk, T. Wangdi, M. Weiand, J. Wilkinson, A. Wilson, S. Yadav, S. Yang, X. Yang, G. Young, Q. Yu, J. Zainoun, L. Zembek, A. Zimmer; Broad Sequencing Platform members, E. S. Lander, Genome sequence, comparative analysis and haplotype structure of the domestic dog. *Nature* **438**, 803–819 (2005).
27. M. M. Gray, J. M. Granka, C. D. Bustamante, N. B. Sutter, A. R. Boyko, L. Zhu, E. A. Ostrander, R. K. Wayne, Linkage disequilibrium and demographic history of wild and domestic canids. *Genetics* **181**, 1493–1505 (2009).
28. L. D. Mech, B. W. Christensen, C. S. Asa, M. Callahan, J. K. Young, Production of hybrids between western gray wolves and western coyotes. *PLOS ONE* **9**, e88861 (2014).
29. H. H. T. Jackson, *Mammals of Wisconsin* (Univ. Wisconsin Press, 1961).
30. A. P. Wydeven, C. M. Pils, in *The Vanishing Present: Wisconsin's Changing Lands, Waters, and Wildlife*, D. M. Waller, T. P. Rooney, Eds. (Univ. Chicago, 2008), pp. 257–272.
31. T. J. Wheelton, B. R. Patterson, B. N. White, Sympatric wolf and coyote populations of the western Great Lakes region are reproductively isolated. *Mol. Ecol.* **19**, 4428–4440 (2010).
32. L. D. Mech, Non-genetic data supporting genetic evidence for the eastern wolf. *Northeast Nat* **18**, 521–526 (2011).
33. F. Hailer, J. A. Leonard, Hybridization among three native North American *Canis* species in a region of natural sympatry. *PLOS ONE* **3**, e3333 (2008).
34. R. N. Jackiw, G. Mandil, H. A. Hager, A framework to guide the conservation of species hybrids based on ethical and ecological considerations. *Conserv. Biol.* **29**, 1040–1051 (2015).
35. S. Pietti, H. A. Hager, C. Gerrard, Characteristics for evaluating the conservation value of species hybrids. *Biodivers. Conserv.* **24**, 1931 (2015).

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