

# Considering Pleistocene North American wolves and coyotes in the eastern *Canis* origin story

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## Abstract

The evolutionary origins and hybridization patterns of *Canis* species in North America has been hotly debated for the past 30 years. Disentangling ancestry and timing of hybridization in Great Lakes wolves, eastern Canadian wolves, red wolves, and eastern coyotes is most often partitioned into a 2-species model that assigns all ancestry to grey wolves and/or coyotes, and a 3-species model that includes a third, North American evolved eastern wolf genome. The proposed models address recent or sometimes late Holocene hybridization events but have largely ignored Pleistocene era opportunities for hybridization that may have impacted the current mixed genomes in eastern Canada and the United States. Here, we re-analyze contemporary and ancient mitochondrial DNA genomes with Bayesian phylogenetic analyses to more accurately estimate divergence dates among lineages. We combine that with a review of the literature on Late Pleistocene *Canis* distributions to illuminate opportunities for ancient hybridization events between extinct Beringian grey wolves (*C. lupus*) and extinct large wolf-like coyotes (*C. latrans orcutti*) that we propose as a potentially unrecognized source of introgressed genomic variation within contemporary *Canis* genomes. These events speak to the potential origins of contemporary genomes and provide a new perspective on *Canis* ancestry, but do not influence/negate current conservation priorities of dwindling wolf populations with unique genomic signatures and key ecologically critical roles.

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