

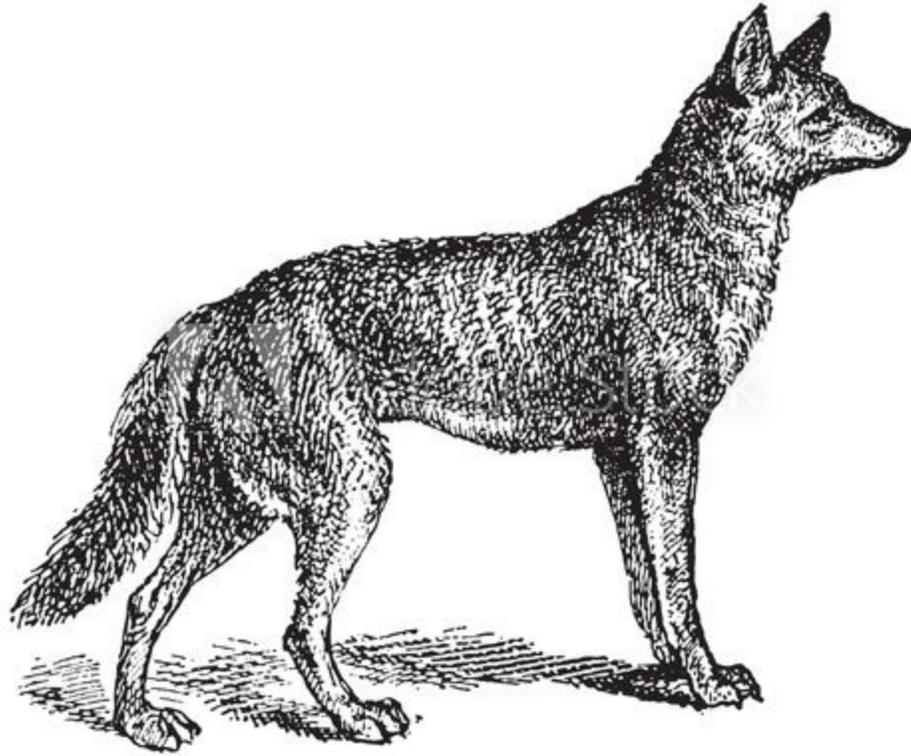
SPECIATION & PHYLOGENY IN N. AMERICAN CANIDS

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Discussion: Speciation And Phylogeny In North American Canids

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Gray wolf (*Canis lupus*). Image courtesy of Adobe Stock.

A number of wolves (*Canis lupus*) currently living throughout North America are not a true genetic representation of the population that historically roamed significantly larger regions of the continent, but instead are the byproduct of hybridization, which, in a taxonomic sense, remains a topic of significant debate among evolutionary biologists, wolf conservationists, ecologists, and policymakers.

The regional extirpation of wolves from North America's forests, coupled with deforestation resulting from the historical increase in anthropocentric agricultural production, inadvertently favored the growth of the smaller canid, the coyote (*Canis latrans*), expanding beyond its plains and desert-dwelling habitats into swathes of previous gray wolf territory.

Researchers posit that this inevitably led to the meeting of small populations of gray wolves and coyotes in geographical areas of the United States known as hybrid zones, where two different species will cross paths and subsequently hybridize (Stearns & Hoekstra, 2005). Consequently,

the union of these genera (*Canis*) of the family Canidae produced an inter-species wolf hybrid (Stearns & Hoekstra, 2005).

Leonard and Wayne suggest that the current wolf population is derived from this *C. lupus/C. latrans*, admixture (Leonard & Wayne, 2008), with possible contributions from what is known as the Great Lakes wolf, also known as the Eastern wolf (*Canis lycaon*). But upon comparing extant samples with historic samples, Wheeldon and White (2009) argued that, “the pre-recovery [wolf] population was [already] admixed over a century ago by [an] eastern wolf (*C. lycaon*)/gray wolf (*C. lupus*) hybridization.” This hybridization may have coincided with occasional coyote introgressions, resulting in the transmission of coyote genes into the Great Lakes wolf population, thus introducing coyote and eastern wolf genetics into other gray wolf populations (Rutledge, 2010; Wilson et al., 2000).

In 2003, Wilson et al., “analyzed the mitochondrial DNA (mtDNA) from two historical samples of eastern [New York] wolves,” which existed well before the expansion of coyotes into the area; both wolves were killed in the 1890s. They also analyzed samples from a Maine wolf that was killed in the 1880s. Results showed no gray wolf mtDNA, thus suggesting that the eastern wolf is conspecific with the red wolf (*Canis rufus*) and the eastern timber wolf (Wilson et al., 2003; Wilson et al., 2000). Further studies, however, have painted a much tighter picture, as Morell (2016) succinctly observes:

Now, a study of the complete genomes of 28 canids reveals that despite differences in body size and behavior, North American gray wolves and coyotes are far more closely related than previously believed, and only recently split into two lineages. Furthermore, the endangered red and eastern wolves are not unique lineages with distinct evolutionary histories, but relatively recent hybrids of gray wolves and coyotes...

Such a study falls under the overarching theme of hybrid speciation, given that two different species crossing paths in the same geographic area - this area being a hybrid zone - interbred with one another. As Stearns and Hoekstra rightfully point out, this is problematic when taking the biological species concept (BSC) and taxonomy into account. With so much blurring of, “gene flow between gene pools,” how can the BSC successfully be applied here (Stearns & Hoekstra, 2005)?

Hybridization and introgression in this particular case (mammalogy) does not appear to fit the BSC; even with gene introgression, a species can maintain morphological and ecological distinctness (Boggs, 2001). This, therefore, fits more with the genetic species concept, which, according to Baker and Bradley, emphasizes the, "recognition of species that are genetically

isolated (but not reproductively isolated)," resulting in the genetic species concept bringing more of, "an enhanced understanding of biodiversity and the nature of speciation as well as speciation-based issues and [the] evolution of mammals" (Baker & Bradley, 2006).

Moreover, this phenomenon can be tricky when applied to the fields of ecology and systematics, though it remains an integral part of studying speciation and adaptation; hybridization accelerates speciation in lieu of the slower effects of genetic and evolutionary processes promulgated by recombination and natural selection (Schwenk et al., 2008).

Insofar as the fate of the gray wolf is concerned, hybridization could yield one of two possible outcomes. First, it may drive this rare taxa to extinction through a process known as genetic swamping (genetic pollution), where, according to Todesco et al., "population growth rates are reduced due to the wasteful production of maladaptive hybrids." Alternatively, hybridization could preserve the genetic viability of isolated, inbred populations (Todesco et al., 2016) of gray wolves.

All told, a better understanding of how hybridization can contribute to a destructive or constructive outcome for a species is critical for the present and future conservation of *Canis lupus*, the only true wolf species left in North America (Zimmer, 2016).

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