

Assessment of coyote-wolf-dog admixture using ancestry-informative diagnostic SNPs

J. Monzón, R. Kays, and D. E. Dykhuizen

Supporting information

Table S1. Populations of 538 wild and domestic canids whose genotypes at 63 ancestry-informative SNPs were analyzed in this study. Populations in bold type served as reference parental populations to assess the ancestry of the other admixed populations. N = sample size.

Population	N	Sampling Region* or Breed	Reference
Western/Midwestern coyote	41	California (12), Manitoba (5), Illinois (5), Washington (4), Utah (3), Ohio† (3), Louisiana (3), Alaska (2), Alabama (2), Mississippi (2)	vonHoldt <i>et al.</i> (2011)
Western wolf	34	Western Canada (15), Wyoming (7), Northern Quebec (6), Alaska (4), Minnesota‡ (1), Ontario‡ (1)	vonHoldt <i>et al.</i> (2011)
Eastern/Great Lakes wolf	17	Minnesota (10), Wisconsin (4), Ontario (3)	vonHoldt <i>et al.</i> (2011)
Dog	10	Rottweiler, Australian Shepherd, Border Collie, Golden Retriever, Labrador Retriever, Giant Schnauzer, German Shepherd, Old English Sheepdog, Doberman Pinscher, Collie	vonHoldt <i>et al.</i> (2011)
Northeastern coyote	9	New York (5), Vermont (2), New Hampshire (1), Southern Quebec (1)	vonHoldt <i>et al.</i> (2011)
Ohio coyote	23	Ohio	Monzón <i>et al.</i> (this study)
Contact zone coyote	167	Pennsylvania (88), New York (79)	Monzón <i>et al.</i> (this study)
Northeast zone coyote	237	New York (110), Pennsylvania (25), Vermont (24), Southern Quebec (21), Maine (20), New Jersey (14), Massachusetts (7), Connecticut (7), New Hampshire (5), Rhode Island (4)	Monzón <i>et al.</i> (this study)

* Sample size per region indicated in parentheses

† One of the Ohio coyotes genotyped by vonHoldt *et al.* was known to have wolf and dog ancestry and was not included as a reference individual

‡ Two wolves from the Great Lakes region had genetic profiles of western gray wolves, as determined from principal component and Bayesian analyses

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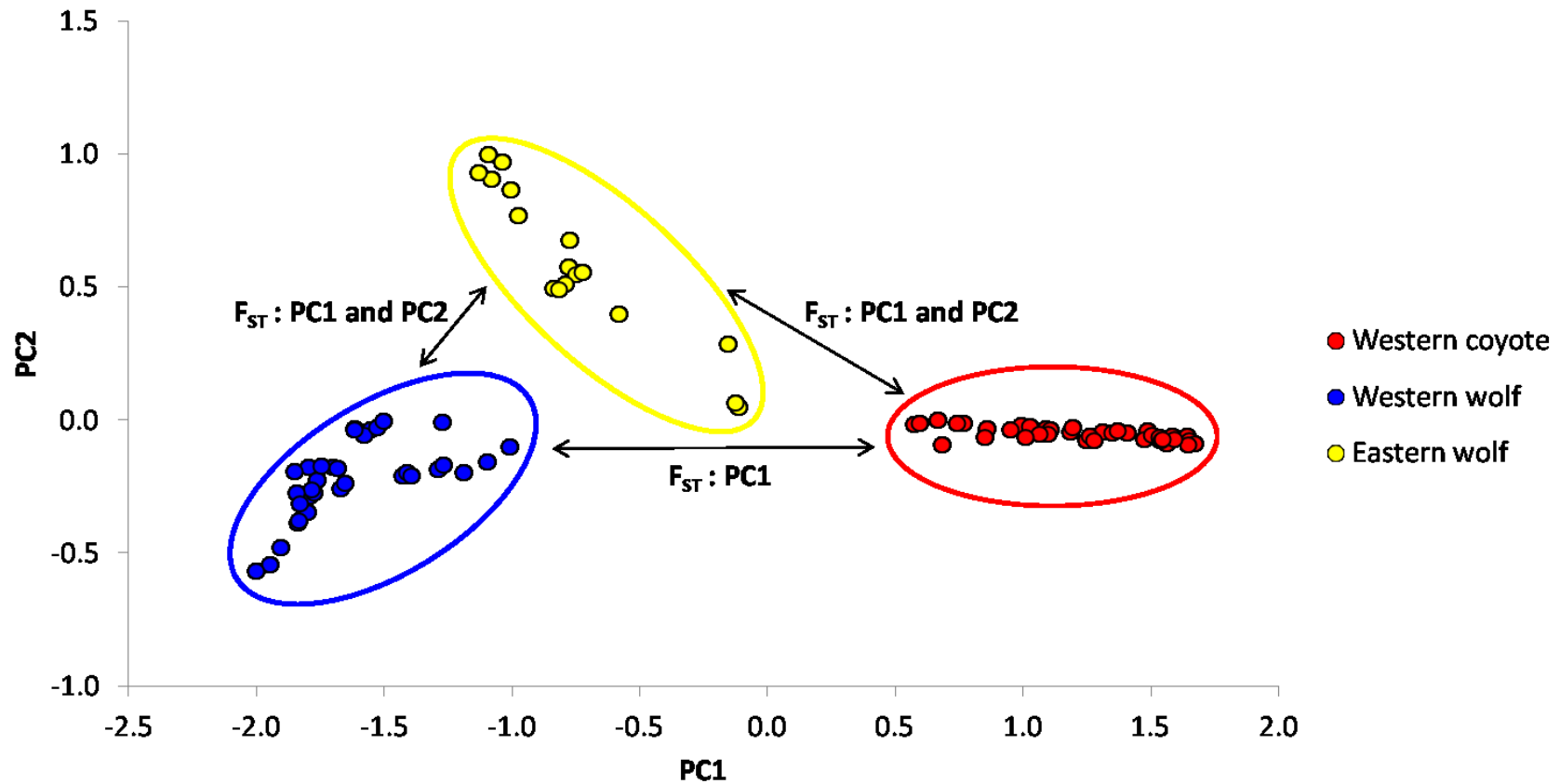


Figure S1. Principal component analysis of initial reference populations of western coyote, western wolf, and eastern wolf genotyped at 60,584 SNPs (vonHoldt *et al.* 2011). Arrow labels indicate how pairwise per-locus F_{ST} estimates were compared to per-locus contributions to the first or second principal component. An initial set of 138 candidate ancestry-informative SNPs was selected because they were present both in the top 1% of loci loading the principal component that separates each pair of source populations and in the top 1% of an analogous F_{ST} comparison. From this set, 63 ancestry-informative SNPs were selected: 21 SNPs diagnostic between western coyote and western wolf, 21 diagnostic between western coyote and eastern wolf, and 21 diagnostic between western wolf and eastern wolf (Table 1).

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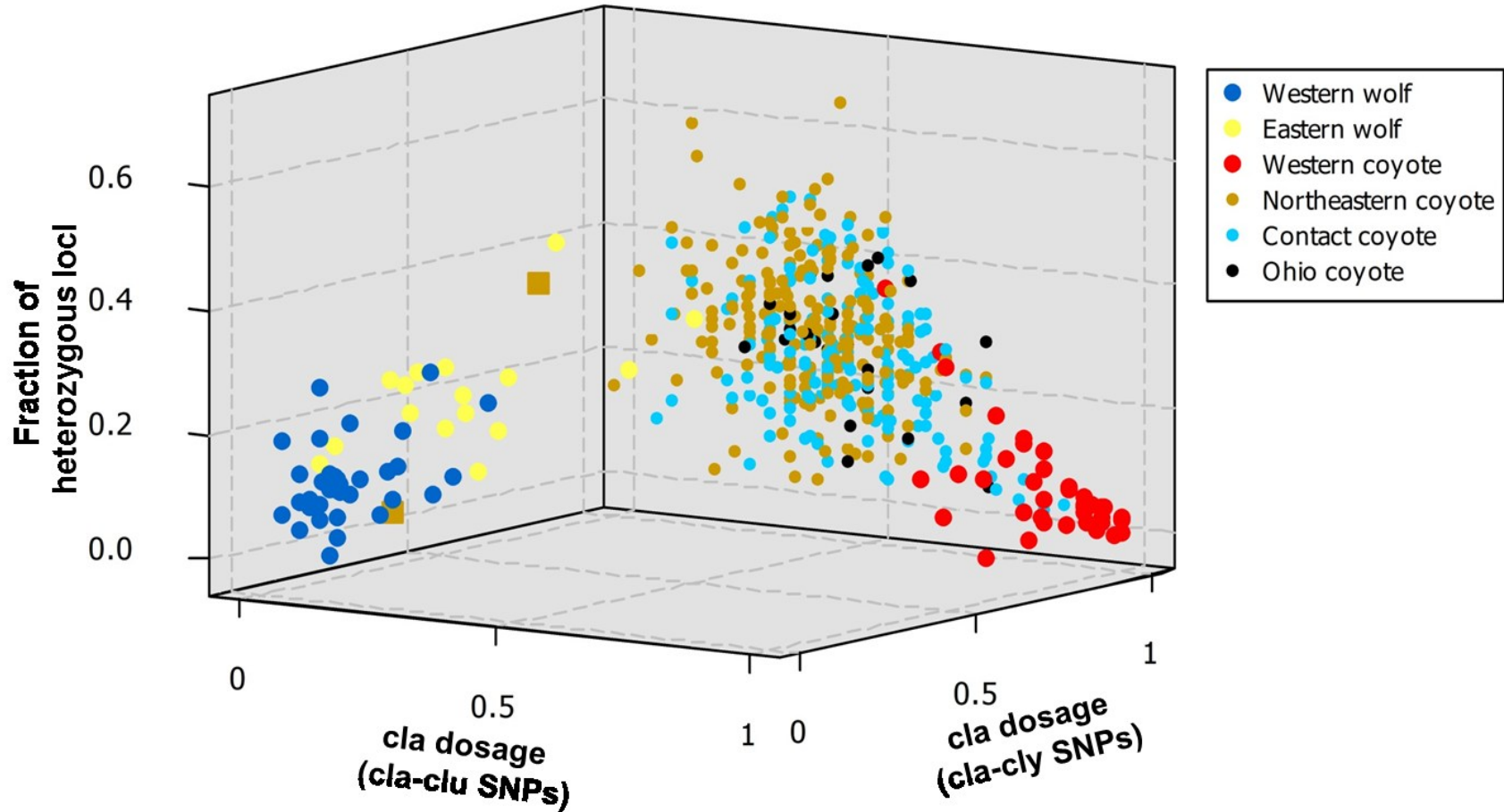


Figure S2. Plot of dosage of coyote alleles and observed heterozygosity. Dosage was calculated in PLINK for the set of 21 SNPs diagnostic between western coyote and western wolf (cla-clu) and separately for the set of 21 SNPs diagnostic between western coyote and eastern wolf (cla-cly). The vertical axis is the fraction of 42 SNPs that are in the heterozygous state.