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Dog Domestication

▷ Background and Goals

- What hypotheses about dog domestication are examined in this paper?
 - The origin of domestic dogs was the main focus; genetic data suggests East Asia, but other data suggests Europe and Siberia.
- What predictions do these hypotheses make? What would the expected phylogenetic trees look like under each of these hypotheses (i.e. what are the expected topologies)?
 - Dogs and wolves would fall under a monophyletic group from a particular area indicating origin.

▷ Methods

- What taxa were sampled for this study?
 - Hypothesis was tested using DNA extracted to trace mitochondrial genomes from 18 prehistoric canids and 20 modern wolves from Eurasian and American origin.
- What gene sequences were used for this study?
 - Wolves, dogs, including divergent breeds, recently published Chinese indigenous dogs, and coyotes. (148 mitochondrial genomes)
- What phylogenetic methods were used to reconstruct the phylogenetic tree in Figure 1?
 - Maximum likelihood, coalescence, and Bayesian.

▷ Results and Discussion

- In Figure 1, which wolf sequence is most closely related to the extant dog clade A, and what geographic region is it from?
 - Argentina (pre-Columbian within clade A)
- In Figure 1, which clade of modern dog sequences has the oldest origin? Approximately how old is this clade?
 - Dog clade C, Germany, 14,700 years ago.
- Based upon Figure 1, how many times does it appear that modern extant dogs could possibly have been domesticated?
 - Figure 1 suggests 4, but the authors state, "the inferred recent divergence of clade B from wolves now found in Sweden and

Ukraine implies that it might represent a mitochondrial genome introgressed from wolves rather than one established by domestication."

- What was the topology of the phylogenetic tree that was recovered, and therefore, which hypothesis was supported?
 - The findings support the conclusion that legacy of dogs derives from wolves of European origin.
 - Analysis of coalescence times support divergence time of >15,000 years ago.
 - Past mitochondrial and Y chromosome analysis suggested non-European, but had less supported data than these findings.

▷ Conclusions

- What are the major conclusions of the paper?
 - Three of four modern dog clades are more closely related to sequences from ancient European rather than extant wolves with divergence times >15,000 years ago.
- Was the taxonomic sampling sufficient to rule out alternative hypotheses?
 - Ancient panel did not contain specimens from Middle East or China. No, no ancient dog remains older than 13,000 years are known from those regions.
 - The mtDNA sequence tree is well supported, but represents a single genetic locus. Independent loci could offer more power to resolve phylogenetic relations.

Week 3