

## Contents

### Week 2

Dog Domestication . . . . .	2
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### Week 3

## Week 2

### 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)?
  - The most recent common ancestor would indicate origin and genetic data would help confirm time frame.

#### ▷ 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?
  - Wolves: Switzerland 214,500.
  - Dogs: Argentina, USA (8,500, 1,000)
- In Figure 1, which clade of modern dog sequences has the oldest origin? Approximately how old is this clade?
  - Dog clade A, Russia, 18,000 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**