

The Dogs of Tsenacomoco: Jamestown Phylogeny Reconstruction

The goal of this project is to reconstruct Figure 2 from the unpublished manuscript of the relationship between ancient DNA and indigenous dogs at the Jamestown Colony. This phylogenetic tree illustrates the situation of Jamestown dogs in the 17th century among the indigenous dog population; a phylogenetic tree of the dogs indigenous to the Americas and those found in the Jamestown Colony.

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Introduction

Due to the colonization of the Americas during and after Columbus' infiltration, like many things, there followed a drastic change in the preexisting environment. Specifically, this research interrogates the replacement of indigenous North American dogs with European dogs genetically between this initial contact and modern day. Because of a messy history with the specific utility of dogs in relation to human civilization, it is difficult to determine where the lineages overlap from just archeological evidence or historical record. Specifically, it is in question whether the dogs owned by the colonists at Jamestown were wholly European, Indigenous, or mixed. In order to gather data, Thomas and others collected and sequenced ancient mitochondrial DNA from 3 different archaeological dogs from between 1609 and 1617 AD, and found that the dogs from the Jamestown Colony had maternal ties to North American dogs. This creates a complexity of inquiry into social history and usages of dogs in colonialist environments.

I chose this project as I don't have copious experience with coding or data to reproduce something wholly original without help or error. The three results show the mitochondrial genomes were indigenous to North America, stemming from the earliest movement of dogs in the Americas. In 2019 and 2021, DNA was extracted and sequenced from 7 dogs and compared to ancient North American wolves, coyotes, dogs, ancient dogs, and others. The North American lineages had high levels of diversity, and proved the dogs dated from 1609 and 1620 were in fact those attained in the Americas, as opposed to England/UK heritage.

The below phylogenetic tree shows the Jamestown Dogs nested within the mitochondrial lineages of pre-European contact North American Dogs. If they were indeed European dogs, they would show up in a monophyletic series; they would not cluster within the North American clade as shown in red.

Original

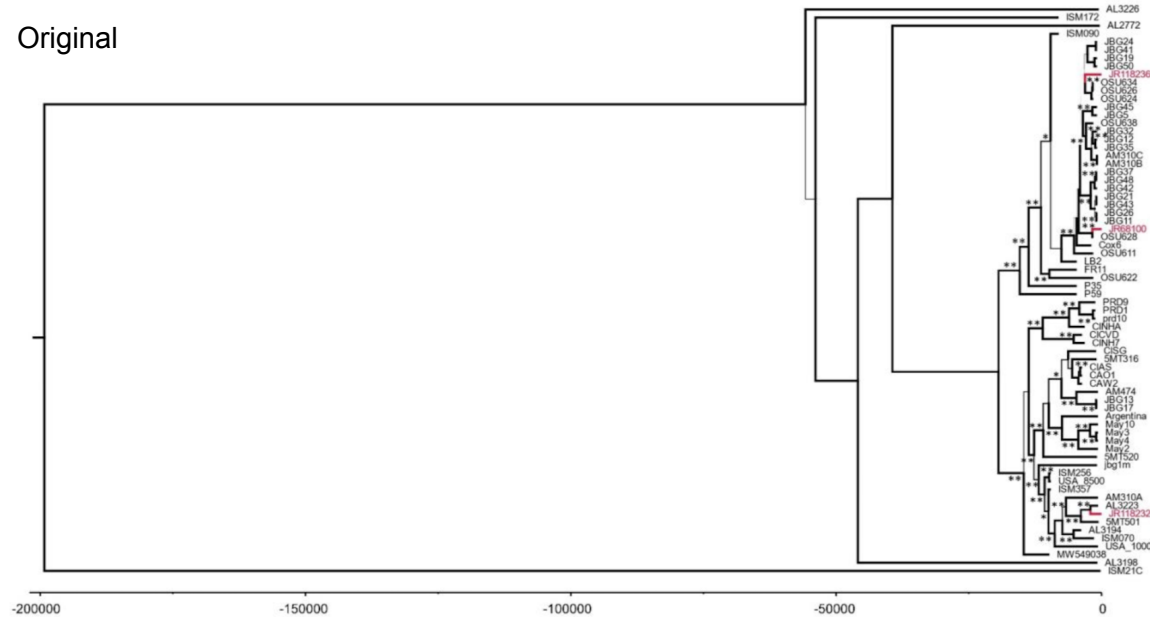


Figure 2. Bayesian phylogeny ancient North American canids. Posterior probabilities greater than 0.60 are marked, with values between 0.6 and 0.79 represented by one asterisk and posterior values between 0.80 and 1 represented by two asterisks. Jamestown dogs are indicated in red.

Methods (Original Figure)

- Raw reads run through PALEOMIX (ancient DNA pipeline)
- Multiple Sequence Alignment using MUSCLE
- Maximum Likelihood Tree RaxML
- Bayesian Phylogenetic Tree using BEAST v1. 10:
 - Using a fixed mutation rate 1.0×10^{-7} substitutions/site/year
 - Using a constant demographic model
 - Using an HKY substitution model with gamma distribution test

Recreation

Figure 2(.2) ggplot/ggtree North American canids. This Figure shows the nested configuration of the Jamestown Colony dogs within Indigenous Dog clades via mitochondrial DNA. The outgroup species (coyote) are highlighted in green.

Methods (Recreated Figure)

- Fasta file aligned in Sequotron
- ggtree created via Newick file in RStudio

