Ancient DNA evidence suggests dogs as commodities of exchange at Jamestown Colony

Ariane Thomas[1], Alida de Flamingh[2], Kelsey E. Witt[3], Matthew E. Hill, Jr.[1], Ripan S. Malhi[2], Andrew Kitchen[1]

[1]Department of Anthropology, University of Iowa, [2]Department of Anthropology, University of Illinois Urbana-Champaign, [3] Center for Computational and Molecular Biology, Brown University

Introduction

The European arrival to the Americas had cumulative and long-lasting ecological consequences on indigenous dogs that significantly altered the human-dog relationship. Human migrants traveled with their dogs, introducing dog mitochondrial lineages to the Americas from Asia 17-13 kya (Ní Leathlobhair *et al.* 2018). However, recent genomic studies show that few of these indigenous dog lineages survived to the present day due to European colonization (van Asch *et al.* 2013, Castroviejo-Fisher *et al.* 2011, Leonard 2002). Yet, the rate and timing of the replacement of indigenous dog lineages by European ones remains an underexplored issue of colonial impacts. To further explore the complicated genetic history of European and North American dogs, we extracted mitochondrial DNA from cranial elements recovered from the earliest permanent English colony in the Americas, Jamestown.

Archaeological Context

JR2361C Layer from Structure 183

Structure 183 is the cellar of a 1607-1617 metalworking/bakery shop located at the north end of a fort. The cellar is filled with eleven stratigraphic layers. The number of layers and the unique artifacts found within each layer suggests that this structure was reused many times before its abandonment. Two fragments of a left *Canis* maxilla, known as JR68100, were recovered stratum JR2361C, which is the upper most layer of fill in the cellar which likely was deposited between 1617-1624.

JR2718W Layer from Structure 185

Structure 185 is the colony's first well that was dug to a depth of 14 ft. After the abandonment of the well, four refuse layers were deposited in the base of the well ca. 1607 to 1610. The bottom layers contained numerous Native American artifacts including pipes, bone needles, nutting stones, and a burned reed mat which had been fused with European fabric. The basal layer (JR2718W) contained a right *Canis* maxillary fragment with a fourth premolar and first molar (JR118236) along with thousands of oyster shell, sturgeon, dolphin, crab, shark, and fish bones, and more than 2000 finished and unfinished shell beads.

Fig. 1: Provenience of Structures 183 and 185. A. Stratigraphic layers of Structure 183. Red star indicates that layer from which sample JR68100 was recovered. B. Map of Jamestown archaeological site. The features containing dog remains sequenced in this study, Structures 183 and 185, have been outlined in black rectangles (modified from Kelso and Straube (2012) field report).

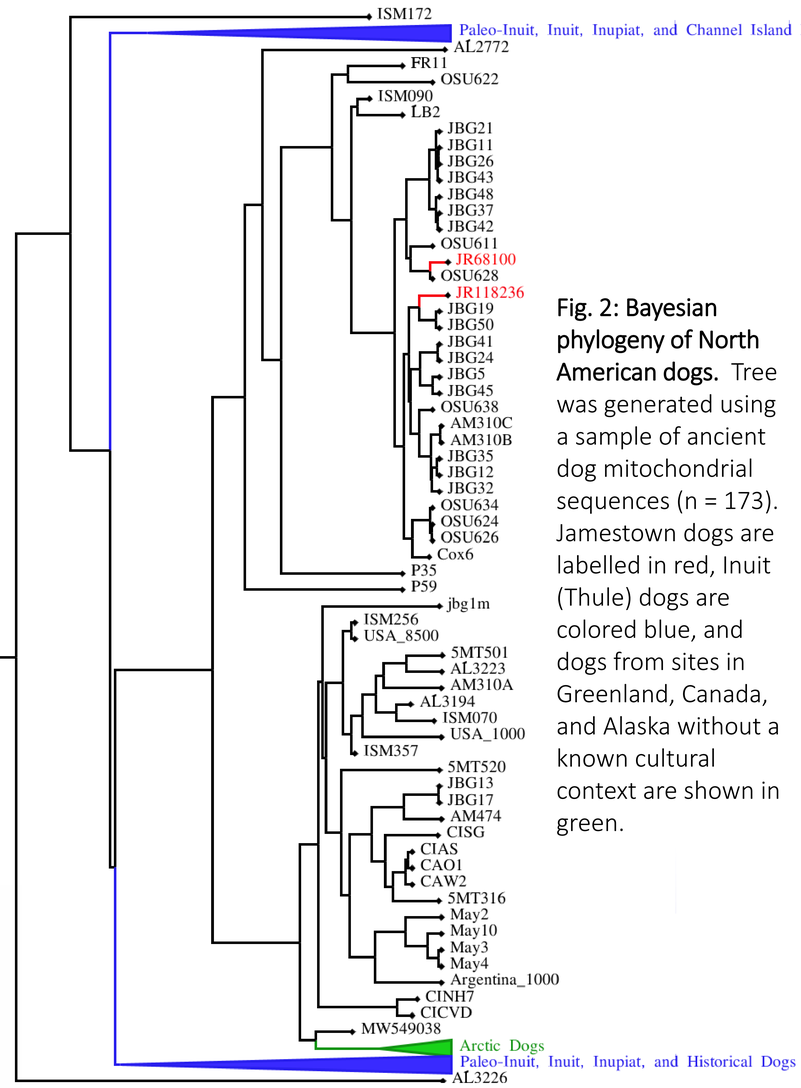

Fig. 2: Bayesian phylogeny of North American dogs. Tree was generated using a sample of ancient dog mitochondrial sequences (n = 173). Jamestown dogs are labelled in red, Inuit (Thule) dogs are colored blue, and dogs from sites in Greenland, Canada, and Alaska without a known cultural context are shown in green.

Methods

Extractions and ancient DNA pipeline

Six premolars underwent ancient DNA extraction and library preparation protocols as outlined in Cui *et al.* (2013) at a dedicated ancient DNA facility at the Carl R. Woese Institute for Genomic Biology at the University of Illinois Urbana-Champaign. Five of six samples were sequenced using the NovaSeq(TM) 6000 platform. Read files were run through Schubert *et al.*'s (2014) PALEOMIX pipeline and mapped to the dog mitochondrial genome (NC_002008.4) using BWA-MEM. Consensus sequences were generated using a Perl script (Bergey 2018).

Phylogenies

Jamestown sequences were complied with publicly available modern and ancient canid sequences including coyotes and wolves. Sequences (n = 1380) were aligned using MUSCLE (Edgar 2004) and manually curated. Neighbor-joining trees were created using PAUP* (Swofford 2003) with red fox (*Vulpes vulpes*) as the outgroup. A Bayesian phylogeny was constructed using BEAST 1.10.4 (Suchard *et al.* 2018) with a strict clock informed by tip dates, a Bayesian skyline plot demographic model, and a GTR substitution model. Multiple MCMC chains were run for 250 million generations and inspected for convergence in Tracer v1.7 (Rambaut *et al.* 2018).

Results

Of the five samples submitted for sequencing, only two, JR68100 and JR118236, had enough quality reads to reconstruct the mitochondrial genome. The Jamestown sequences clustered with other ancient North American dog sequences from previously published works (Ameen *et al.* 2019 and Ni Leathlobhair *et al.* 2018) in both the neighbor-joining tree and the Bayesian phylogeny. In these analyses, they form a clade with dogs from the Janey B. Goode, Angel Mounds, and Scioto Cavern sites in the Midwest.

Zooarchaeological analysis identified cutmarks on the cranial elements of all dogs except one. Most of the cutmarks were located on the lateral surface of the maxilla, posterior to the infraorbital foramen, and superior to fourth premolar. Cutmarks were also found along the medial surface of the mandible inferior to the first molar. Cutmarks were relatively shallow and narrow.

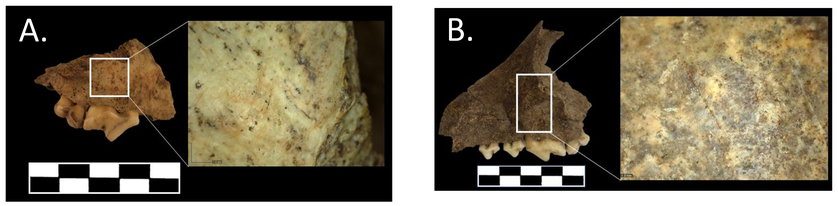

Fig. 3: Cutmark analysis. Location and magnification (30x) of cutmarks identified on A. JR118236 and B. JR68100.

Conclusions

Our results indicate that dogs of indigenous ancestry were used by the Jamestown colonists during the first few decades of the fort's occupation. This finding corroborates with historical accounts (Haile 1998) and archaeological data that suggests indigenous Americans and Europeans were living and working within the Jamestown fort. The Cellar/Well feature (Structure 185) produced tens of thousands of artifacts and bones indicating on-site production by indigenous peoples as well heavy reliance on imported European items (Kelso and Straube 2012). Combined, the DNA, historical, and archaeological evidence suggest that indigenous peoples were co-habituating at Jamestown or provided a great deal of resources, including dogs, to European settlers.

The relationship between these dogs and indigenous and European people is unknown. Cutmarks on the bones and their context in rubbish heaps suggests that these dogs were consumed by the residents of Jamestown. Layer JR2718W is contemporaneous with the "Starving Time", a period during the winter of 1609-1610 when resources were diminishing, and supply ships were delayed. Jamestown individuals during this period resorted to consuming dogs, horses, cats, and rats during this period of extreme stress. Dog remains from layer JR2361C, however, likely represent continued reliance on indigenous dogs perhaps a decade or more after the Starving Time. The colony suffered many periods of potential collapse because of failure to generate reliable food sources. Though our analysis cannot determine if these dogs were a common food source for either indigenous or European individuals at Jamestown, it was not unusual for indigenous North Americans (Tito *et al.* 2011) or European colonists (Schwartz 1997) to use dog meat as a protein source during periods of stress. Further research into the complete ancestry of Jamestown dogs will provide greater resolution into the human-dog relationship.

Acknowledgements: Brian Kemp &

References:

Funding Sources:

Graduate and Professional Student Government