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The Bridge River Dogs: Interpreting aDNA and Stable Isotope Analysis Collected From Dog Remains

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INTRODUCTION

Excavations at the Bridge River site in the Middle Fraser Canyon, near Lillooet British Columbia, have been on-going since 2003. Semi-subterranean, circular housepits housed a shared living space divided for social purposes, such as cooking or tool production. Village organization shifted from the Bridge River (BR 2) period, 1,600 to 1,500 cal. B.P., to the Bridge River 3 period (BR 3), 1,300 to 1,000 cal. B.P. During BR 2, the village saw peak occupancy and was arranged in a circular pattern, with a noticeable separation between northern and southern areas (Prentiss et al. 2012, Prentiss et al. 2004). Analysis based on material culture in excavated housepits suggests the village’s neighborhood of housed wealthier homes than those in the south (Prentiss and Keatley 2012). Recent zooarchaeological evidence also suggests the village shifted through two periods of occupation, with substantive related areas associated with population growth, the first just prior to the end of the BR 2 period, and the second near the end of the BR 3 period (Walsh 2015). Excavations at the northern housepits have uncovered significant evidence of domesticated dogs, Canis lupus familiaris. Dogs played an important role in the everyday functions of the village including transportation labor, hunting aids, protection from other animals, companionship, and hair for weaving (Toit, 1906).

This study was focused on the comprehensive interpretation of dog aDNA and stable isotope analysis. Three research questions were posed, the first in consideration of DNA and the latter two in consideration of dog stable isotopes as a rough proxy for their human owners. Samples were chosen to best address these questions:

1. Where do the mitochondrial DNA (mtDNA) haplotypes of Bridge River dogs fit into the phylogeny created from other prehistoric dogs in British Columbia?
2. Can social inequality be seen through distinctive changes in the diets of dogs between different households during the same occupation period?
3. How does dog diet change through various occupations of a single household and how is it correlated to changes in the faunal assemblage?

RESULTS

Stable carbon and nitrogen isotope values were collected from 15 Canis samples and 45 comparative faunal samples (Figure 2). The fifteen samples identified as belonging to the genus Canis through morphological comparison were separated into two distinct groups with unique stable isotope values. Nine representing C. lupus familiaris (dog), three of the nine samples were also identified as C. lupus familiaris in aDNA analysis, the six remaining Canis samples clustered near herbivore samples, and were assumed to represent C. lupus lupus (Figure 3). Only five samples were applicable for the comparison of housepits in the northern versus the southern portions of the village. Of these five samples, four represented the northern village from HP 24 and 54, and one from the southern village from HP 20. Stable isotopic values of meat were studied and showed no discernible difference. Change in diet in a single household was hypothesized by comparing HP 54 dog samples to two groups, BR 2 and BR 3. Test for the difference between the HP 54 and HP 52 sample showed C. lupus familiaris samples clustered near herbivore samples, and were assumed to represent C. lupus lupus (Figure 3). Only five samples were applicable for the comparison of housepits in the northern versus the southern portions of the village. Of these five samples, four represented the northern village from HP 24 and 54, and one from the southern village from HP 20. Stable isotopic values of meat were studied and showed no discernible difference. Change in diet in a single household was hypothesized by comparing HP 54 dog samples to two groups, BR 2 and BR 3. Test for the difference between the HP 54 and HP 52 sample showed C. lupus familiaris samples clustered near herbivore samples, and were assumed to represent C. lupus lupus (Figure 3).

DISCUSSION

Bridge River dog aDNA haplogroup, DHap2, is genetically most closely related to those in Cline A dogs descended from East Asian wolf stock and derived from one of the founding haplotypes of dogs in the New World (Leonard et al. 2002, Swadling et al. 2002). Results mirrored previous results, linking the dogs to other Northwest coast sites like Namu and Dixon Point (Barra et al. 2006, Call 2011). The current results were collected from samples in the earlier BR 2 occupation, suggesting D HaP was present in the village longer than previously thought. The prevalence of this martlaine at the site could reflect a lack of female dogs being traded or otherwise introduced to the village; however, this interpretation assumes stable haplotype variation in the region. Given the identification of two other haplotypic, F HaP and B HaP, at Kunes Creek, only miles from Bridge River, some haplotype variation, though potential limited, is suggested for the region. The small sample size included here may explain the lack of other haplogroups being identified.

The lack of differentiation between the stable isotopic values of the southern and northern regions of the village may simply reflect similar diets, or the lack of recognition of prestigious food consumption. It has been suggested that mammal meat represented the most sought after food, and would be linked to signs of wealth (Prentiss et al. 2012). Dog stable isotopes results suggest similar diet composition of meat. This suggests that certain terrestrial meats may have been considered prestigious, and they may not be easily distinguishable in stable isotope values.

The difference in average dog δ13C‰ values between BR 2 and BR 3 was 0.43C‰, and while this change is statistically significant (P-value < 0.0010) it is still slight and likely a result of minor climatic changes taking place between the BR 2 and BR 3 periods, or an artifact of the limited sample size. Subsistence changes were also assessed through a floor-by-floor analysis of deer stable isotope samples (Figure 4). Deer samples showed complementary trends to those seen in Walsh’s faunal analysis, with noticeable fluctuations just prior to the end of BR 2 and at the end of BR 3. This suggests the cerer at these times were harnessed from different ecological zones, possibly as a result of depleted local resources due to increased population.

CONCLUSION

Results provided mere evidence for lack of variation of dog martlaine haplotypes in the Bridge River village and the Middle Fraser River Canyon. Stable isotopic values added further support to archaeological evidence showing subsistence strategies in northern are consistent with changing village demographics. This study and others like it are to help to gain a better understanding of the complex relationship between the people at Bridge River, and the community’s interactions with the changing environment around them.

DATA

All faunal remains were identified through morphological comparison. Twenty Canis skeletal elements were selected with another 128 faunal samples representing sockeye salmon (O. nerka), rainbow trout (O. mykiss), mule deer (O. hemionus), sheep (O. aries), and bear (U. americanus) for stable isotope comparison (Figure 1). Five of the six housepits excavated were sampled in this study. HP 24 and 54 are located in the northern area, where HP 11, 16, and 20 are positioned in the southern area.

METHODS

The samples were sent to the Ancient DNA Laboratory at the Simon Fraser University in Vancouver, British Columbia. aDNA analysis was performed by experienced Ph.D. student Antonia Rodrigues under the supervision of Professor Dongya Yang (Rodrigues 2015). After aDNA sampling, samples were transported to the Archaeology Isotope Laboratory at the University of British Columbia Vancouver campus for stable isotopic analysis, focused on carbon and nitrogen levels, by experienced Ph.D. student Alessia Diaz under the supervision of Professor Michael Richards (Diaz 2015).

RESULTS

Successful amplification of Canis aDNA and haplotype identification was possible in five samples, matching identically to the Genbank reference sequence of Canis lupus familiaris, mtDNA haplotype DHap2 (Rodrigues 2015).

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