
Dog Days on the Plains: A Preliminary aDNA Analysis of Canid Bones from Southern Alberta and Saskatchewan

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ABSTRACT. Dogs were an important component of lifeways on the Northern Plains until the reintroduction of the horse following European contact. There has been little investigation into the variability of domestic canids on the Prairies and the potential of that variability as a proxy for identifying relationships between culture-historic entities. Distinguishing between sympatric canids using morphological characteristics can be challenging with degraded specimens that have high intra-specific variability, and where wolf-dog hybridization can result in transitional morphologies. Here, we present preliminary ancient DNA data on archaeological canids recovered from FM Ranch (EfPk-1) and Cluny (EePf-1) in Alberta, as well as from Lake Midden (EfNg-1) in Saskatchewan. Using the mitochondrial control region, we taxonomically reclassify zooarchaeological remains, find potential evidence of European dogs in a protocontact component, and identify preliminary indications of a distinct dog population at the Cluny site that may be of interest for determining the origin of the One Gun phase.

RÉSUMÉ. Le chien portait un rôle significatif au mode de vie dans le Nord des Grandes Plaines jusqu'à la réintroduction du cheval qui suivit le contact européen. Peu de recherches ont été effectuées au sujet de la variabilité des canidés domestiques dans les Prairies ni sur le potentiel de cette variabilité en tant que substitut qui servirait à identifier des relations entre différentes entités culture-historiques. Différencier des

canidés sympatriques en utilisant des caractéristiques morphologiques peut être difficile lorsque les spécimens dégénérés, qui ont une grande variabilité intraspécifique, ou quand des hybrides loup-chien, qui peuvent montrer une morphologie de transition, sont analysés. Ici, nous présentons des données d'ADN fossile préalable, venant de canidés en contexte archéologique, recueillie de FM Ranch (EfPk-1) et Cluny (EePf-1) en Alberta, ainsi que de Lake Midden (EfNg-1) en Saskatchewan. En utilisant la région de contrôle mitochondriale, nous pouvons reclassifier les restes zooarchéologiques de façon taxonomique, prouver la présence de chiens Européens dans composant qui correspondant à la période de protocontact en plus de montrer des indications préalables pour la distinction d'une population de chiens dissemblables sur le site de Cluny, qui pourrait être d'intérêt pour définir l'origine de la phase One Gun.

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OUR UNDERSTANDING OF VARIABILITY in canid populations on the Northern Plains has largely been based on morphological identification, ethnographic accounts, and forensic facial reconstruction (Allen 1920; Crockford and Pye 1997; Wilson 1924). Ancient DNA (aDNA) analyses have addressed many long-debated questions in archaeology and related disciplines, such as the migration of people into the New World (Llamas et al. 2016), and the antiquity and evolution of ancient pathogens (Devault et al. 2014; Wagner et al. 2014). They have also expanded our understandings of the evolutionary history of domesticated canids (*Canis lupus familiaris*) in precontact North America through investigations of early canid migration patterns and the spatial-temporal characteristics of their domestic origins (Brown et al. 2013; Byrd et al. 2013; Leonard et al. 2002; Skoglund et al. 2015; Witt et al. 2015). Biomolecular analysis can provide high resolution data for low taxonomic levels when compared to complementary morphological approaches, allowing for detailed assessments of population variability. Here, our preliminary investigation demonstrates the viability of aDNA for refining taxonomic identification and the potential of using faunal material to delineate archaeological entities, such as cultural phases and European contact, on the Northern Plains.

Eleven canid bones recovered from Late Period components at FM Ranch (EfPk-1) and the Cluny Fortified Village (EePf-1) on the Alberta Plains were targeted for aDNA analysis at the University of Calgary to investigate the population genetic diversity of ancient domestic dogs. Sanger sequence data were compared with those of a previous aDNA study conducted in the

same facility (Verwoerd 2012), which focused on canid elements from the Lake Midden site (EfNg-1) located in Southern Saskatchewan. We hypothesize that genetic variability in domestic North American dogs may be correlated with distinct cultural-historic events (e.g., European contact) and phases (e.g., Mortlach, One Gun, and Old Women's) at archaeological sites across the Northern Plains.

Archaeological Sites

FM Ranch (EfPk-1)

FM Ranch (EfPk-1) is an Old Women's phase (1100–250 B.P.) (Fromhold 2012:67; Peck 2011:375) campsite in Southern Alberta (Figure 1). The site is located northeast of the Two Trees (EfPk-2) buffalo jump situated on a terrace of the Bow River, and is likely directly associated with the jump. Richard Forbis began excavations in the summer of 1959, unearthing a large assemblage of faunal material. The remains were principally bison (*Bison bison*), with a smaller component of birds and other small mammals (Forbis 1960; Vickers 1982). Canid remains were identified at the time as domestic dog (*C.l. familiaris*), kit fox (*Vulpes macrotis*), coyote (*C. latrans*), wolf (*C. lupus*), long-faced Indian dog, and either dog or small wolf (Forbis 1960; Fromhold 1993). The site is believed to have been occupied from ca. 1000–1650 A.D. (Peck 2001; Vickers 1982), based on the identification of Old Women's type materials and 21 obsidian hydration dates.

Cluny Fortified Village (EePf-1)

The Cluny Fortified Village (EePf-1) is a terminal Late Period One Gun phase (250–200 B.P.) (Peck 2011:435) campsite in Southern Alberta (Byrne

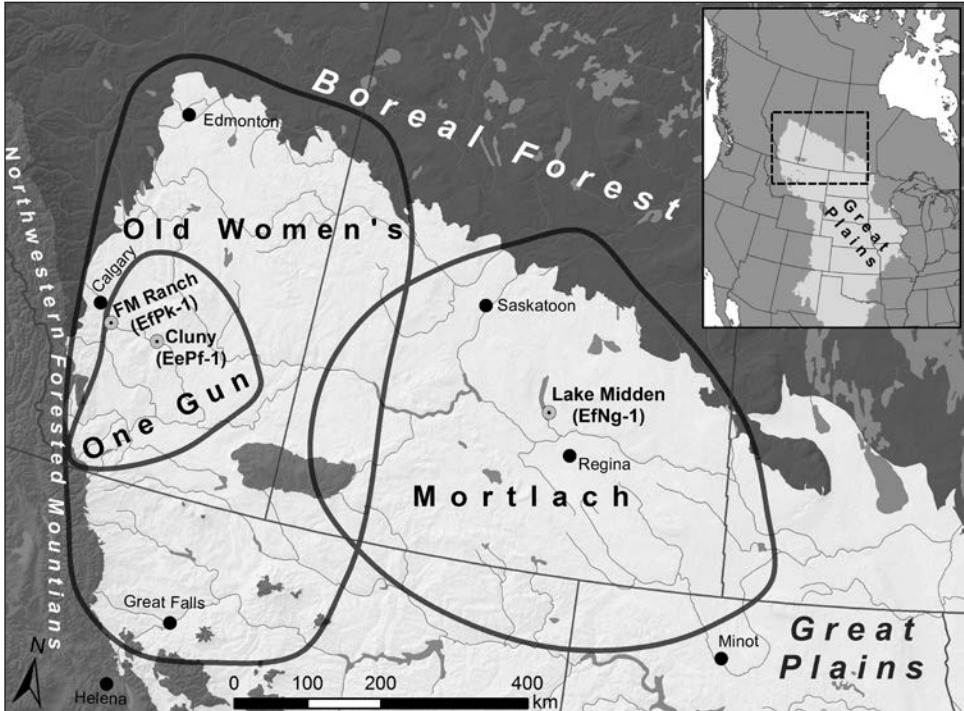


FIGURE 1. Late Period phases on the Northern Plains. Northern Plains phase delineations after Murchie (2013:251). Ecozone data from the Commission for Environmental Cooperation (2014).

1973:478; Forbis 1977; Peck 2011:440). The site is unique on the Canadian Plains for its distinct fortifications and material remains. The One Gun phase is considered by many archaeologists to represent an intrusive Siouan-speaking group on the Northern Plains, possibly related to horticultural groups of the Middle Missouri area (Byrne 1973; Edwards et al. 2016; Forbis 1977; Walde 2008:53). Cluny has been argued by some to have been established in the late eighteenth century and abandoned shortly thereafter (Forbis 1977; Peck 2011:435), but recent surveys and excavations at the site have found new evidence of multiple palisade construction events and extended or frequent use of at least two hearth features, which

suggest a longer term or repeated habitation (Walde et al. 2011:61, 86).

Canid bones represent a large portion of the non-bison faunal assemblage at Cluny originally recovered by Forbis (1977:70–71). This material includes the remains of at least eight adult dogs identified by Jon Driver and divided into medium and large categories (Forbis 1977:70). Canid material was also unearthed in recent excavations at Cluny (NISP = 382 [2009–2015 excavations]) (Dale Walde, personal communication 2016) conducted by Brian Kooyman and Dale Walde (Walde 2008; Walde and Evans 2014; Walde et al. 2011, 2013). The majority of recently excavated canid material is believed to be domestic dog (Walde et al. 2011:80).

Lake Midden (EfNg-1)

The Lake Midden site (EfNg-1) is located within a coulee east of Last Mountain Lake in southern Saskatchewan (Verwoerd 2012). The site has been assigned to the Mortlach phase, and the inhabitants may have been ancestors of modern Assiniboine groups (Walde 1983, 2004, 2010). Watrall (1979) argued for an occupation between ca. 1000 and 1500 A.D., although a subsequent radiocarbon date (re-calibrated with the IntCal13 calibration curve [Reimer et al. 2013]) has pushed the occupation to ca. 1600 A.D. (380 ± 100 ^{14}C cal B.P., S-2246 [A.D. 1442–1634, 1σ]) (Walde 1983:13). This later date is supported by the identification of European influences found at the site, including glass beads and a copper-bladed knife (Walde 1994:359, 374). Verwoerd's (2012) aDNA analysis identified a range of canids, including domestic dog, wolf, coyote, and swift fox (*Vulpes velox*). Additionally, Walde (1983) found evidence of butchering and potential marrow extraction among the remains of eight large canids, including a domestic dog.

Dogs on the Canadian Plains

The “Dog Days” refers to a time before the introduction of the horse, ca. 250 B.P. (Barsh and Marlor 2003), when dogs served a crucial role in the highly mobile lifeways of people living on the Plains (Ewers 1955, 1958). Two morphologically distinct variants of domestic dog were identified by Allen (1920:449, 455): the Plains-Indian dog, with its erect ears and medium build, and the Sioux dog, which was identified as large, gray, and wolf-like. Both were utilized for the transportation of goods via travois, a specially designed sled for dogs.

A third type, the Hidatsa dog, was identified by Wilson (1924:197), which

he notes as being similar to the Sioux variety. It had a number of different roles, including providing security from strangers, and preventing theft by rival tribes (Wilson 1924:204–205). They were also used for the transportation of goods—such as wood, tent poles, water, and meat—during hunting trips and seasonal rounds. Many of these tasks were performed using a travois (Wilson 1924:225–228).

Dogs may also have been a food source on the Northern Plains, particularly in times of scarcity (Callahan 1997:7–8). Thurman (1988) believed eating dogs was more common and widespread than depicted by the ethnographic accounts, with some dogs being raised specifically for consumption. The Hidatsa reportedly adopted the practice of ceremonial consumption of dogs from the Santee Sioux around the late 1800s (Wilson 1924:230).

One downside of raising dogs is the additional resource drain. An overabundant dog population can lead to difficulties with camp maintenance, such as food stealing (Callahan 1997:5; Wilson 1924:229), aggression, and camp disorder (Wilson 1924:204, 229). Dogs were selectively bred to maintain desirable traits such as large size and robustness, as well as to manage less desirable traits, such as aggression (Callahan 1997; Henderson 1994; Wilson 1924). Callahan (1997:7) considered dogs to be advantageous overall, as they could be maintained on scraps and other undesirable cuts of meat (Wilson 1924:201).

Archaeological investigation into the use of dogs on the Northern Plains has been limited by challenges to taxonomic identification and resolution of canid material for population assessments. Here, we use aDNA to evaluate previous morphological identifications and

to better understand the role of dogs in the region.

Methodology

Three specimens originally identified as *C.l. familiaris* from FM Ranch (minimum number of individuals [MNI]=3), and eight from the Cluny Fortified Village (MNI=5), were sampled in this analysis (Figure 2), targeting a portion of the mitochondrial (mtDNA) control region with one primer set (Table 1). The prim-

ers and methodology were based on Verwoerd (2012) to facilitate data comparison with the Lake Midden material. Following Cooper and Poinar’s (2000) criteria of authenticity, sample preparation, extraction, and polymerase chain reaction (PCR) setup were conducted in the physically isolated and dedicated aDNA facility at the University of Calgary, with multiple controls in place. One-way post-PCR analysis was restricted to a physically separate laboratory.

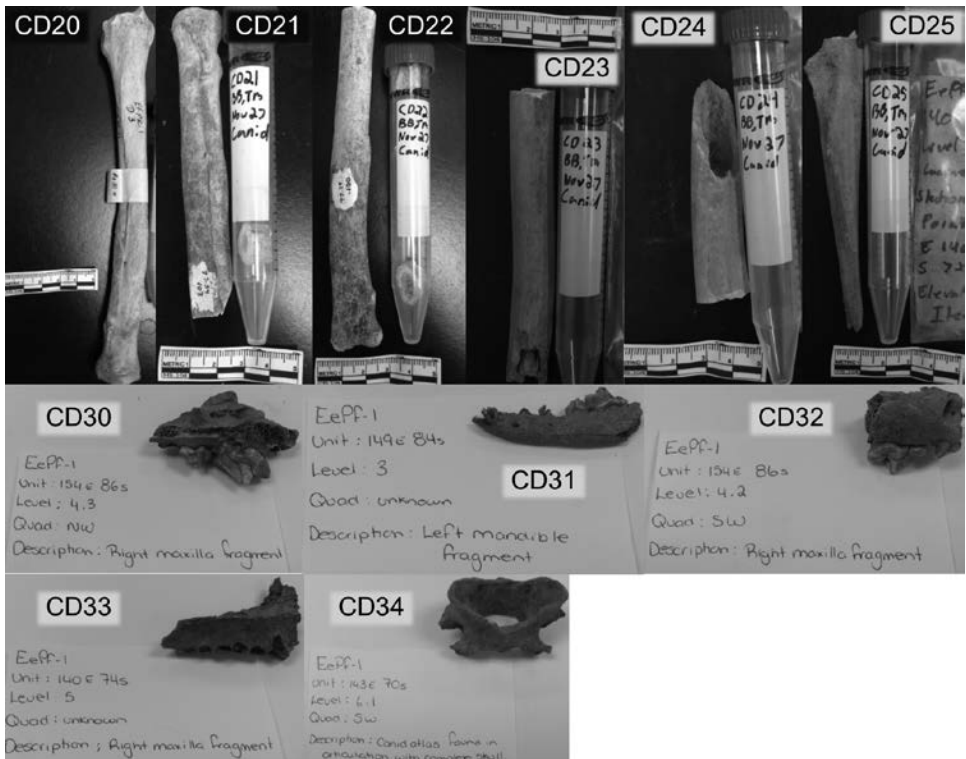


FIGURE 2. Canid samples from FM Ranch (white text) and Cluny (black text).

TABLE 1. Primers targeting mtDNA control region (partial) of Canidae.

Primer	Sequence (5’-3’)	Genome Coordinates	Amplicon
MitH52	TCGAGGCATGGTGATTAG	15680–15698	198 bp
MitL63	ACCCCTACATTCATATATTGAAT	15460–15482	

Note: Primers from Ishiguro et al. (2000). Genomic coordinates in reference to *C.l. familiaris* reference sequence NC_002008 (Kim et al. 1998).

Subsamples of canid bone were superficially decontaminated in a 6% sodium hypochlorite solution for 10 minutes, followed by 60 minutes of UV irradiation (120 mJ/cm²) to remove external contaminants (Speller 2009:48). Following pulverization, ≈1 g of bone powder was incubated for 18–24 hours with constant agitation in a lysis buffer of 0.5 M EDTA, 0.25% sodium dodecyl sulphate, and 0.5 mg/ml proteinase K. Extraction followed a modified silica-spin column protocol (Speller et al. 2010; Yang et al. 1998), using the QIAquick PCR Purification Kit (QIAGEN, Toronto, ON); 100 µl was eluted twice, with the second elution consistently producing brighter UV bands when run on an agarose gel. A ratio of one extraction blank (n=4) per three samples (n=11) was utilized in addition to a negative PCR for each amplification. No contamination was observed in any of the controls or extracts. We used direct Sanger sequencing without cloning. Electropherograms received from Eurofins MWG Operon were visually edited using Chromas Pro 1.7.5 (Technelysium Pty Ltd. 2013), aligned using ClustalW (Thompson et al. 1994) in BioEdit (Hall 1999), with comparable sequences from GenBank (Benson et al. 2013), and phylogenetically analyzed in MEGA 6.0 (Tamura et al. 2013).

Results

Of the 11 samples processed, 10 amplified successfully at least once (Table 2); only CD22 from FM Ranch failed to amplify with our primer set. Sanger sequence data confirmed that all eight of the Cluny samples were *C.l. familiaris* (Figure 3), while the two sequenced samples from FM Ranch were genetically identified as grey wolf (*C. lupus*), likely the northwestern wolf subspecies

(*C.l. occidentalis* [Chambers et al. 2012]). All dog samples fall within clade A, as identified by Thalmann et al. (2013)—the most diverse group, but which also shows a Eurasian origin for New World domestic dogs ca. 20,000 B.P. (Thalmann et al. 2013:872). A small set of single nucleotide polymorphisms (SNP) divide the Cluny dogs into two subclades. One is consistent with ancient North American lineages derived from an Asian origin (e.g., Leonard et al. 2002; Witt et al. 2015), and the other with SNPs associated with some small European dog breeds, namely terriers. Three of Verwoerd's (2012) domestic dog sequences from the Lake Midden site also fit within this European-like clade. The small set of SNPs in this short, single amplicon resulted, not unexpectedly, in poor bootstrap support overall. Further genetic data, preferably the whole mitogenome, would be needed to improve confidence in these clades and the phylogenetic resolution.

All but two (CD22 and CD31) of the sequences were reproduced, and the data make phylogenetic sense. We did not evaluate molecular behavior or biochemical preservation, nor were amplified products tested by bacterial cloning, and the results were not replicated in another aDNA facility (Cooper and Poinar 2000).

Discussion

Ancient DNA is well-suited to address questions of evolutionary history in archaeological populations. The fragility of DNA molecules is an important consideration, since factors such as annual temperature fluctuations, UV radiation, water, oxygen, and other variables can significantly degrade DNA fragments (Brown and Brown 2011; Mitchell et al. 2005). The Late Period on the Northern

TABLE 2. Sample site and faunal aDNA results.

Sample	Site	Side, Element, Portion	GenBank Accession #	Taxon
CD1	LM	L. Tibia, P.		dog
CD2	LM	R. Tibia, C.	AF531678 ^c	dog
CD3	LM	R. Tibia, C.		wolf-dog
CD4	LM	L. Tibia, C.	FM201773 ^c	wolf
CD5	LM	L. Tibia, C.	AF531678 ^c	dog
CD6	LM	L. Tibia, C.	FJ213926 ^c	coyote
CD7	LM	R. Tibia, C.	FM201773 ^c	wolf
CD8	LM	L. Tibia, P.		
CD9	LM	L. Tibia, P.		coyote
CD10	LM	L. Tibia, P.	AF036479 ^c	swift fox
CD11	LM	L. Tibia, D.	GQ376505 ^c	wolf
CD12	LM	L. Tibia, S.	AF531678 ^c	dog
CD13	LM	L. Tibia, C.		fox
CD20	FMR	L. Radius, C.	KX373693	wolf
CD21	FMR	L. Radius, P.	KX373694	wolf
CD22	FMR	L. Radius, P.		
CD23	CFV	Tibia, S.	KX373695	dog
CD24	CFV	Ulna, S.	KX373696	dog
CD25	CFV	Ulna, P.	KX373697	dog
CD30	CFV	R. Maxilla	KX373698	dog
CD31	CFV	L. Mandible ^a	KX373699	dog
CD32	CFV	R. Maxilla	KX373700	dog
CD33	CFV	R. Maxilla	KX373701	dog
CD34	CFV	Atlas ^b	KX373702	dog

Note: LM=Lake Midden; FMR=FM Ranch; CFV=Cluny Fortified Village. L=Left; R=Right; C=Complete; P=Proximal; D=Distal; S=Shaft.

^aVery small, but fully developed adult.

^bArticulated with r. maxilla and full skull.

^c100 percent match to previous GenBank entry.

FIGURE 3. (*Opposite*) Phylogenetic neighbor-joining tree (Saitou and Nei 1987) of Canidae using the mtDNA control region (partial). GenBank accession number listed after taxon acronym. The percentage of replicate trees in which the associate taxa clustered together in the bootstrap test (2,000 replicates) are shown next to the branches (Flensenstein 1985); only bootstrap values greater than 50 percent are shown. Computed using Kimura 2-parameter method (Kimura 1980), displayed in units of the number of base substitutions per site (branch length=1.10127121). All positions with less than 90 percent site coverage were eliminated, leaving 138 positions in the dataset with 145 nucleotide sequences. The low amplicon length and limited number of informative SNPs within the control region for *C.l. familiaris* explains the low bootstrap values, which could be improved with a mitogenomic analysis. Dog clades A–D in reference to Thalmann et al. (2013).



Plains is amenable for aDNA survival in bone due to the shallow time depth for taphonomic decay (Allentoft et al. 2012), dry and cold conditions leading to reduced hydrolysis, oxidation, microbial activity, a neutral-to-basic pH (Dor Maar and Beaudoin 1991; Pennock et al. 2011), and overall good preservation of bone.

Taxonomy

Morphologically identifying zooarchaeological taxa beyond the family or genus rank can be challenging in degraded and fragmented specimens. This is particularly true within sympatric canids where intra-specific variability can be high (e.g., dogs), and hybridization can result in transitional morphologies (Allen 1920; Byrd et al. 2013; Callahan 1997). In these situations, aDNA can effectively discriminate among low taxonomic levels of Canidae (e.g., Witt et al. 2015), and can correct morphological misidentifications (Byrd et al. 2013). This analysis demonstrates the ability of a single, short DNA fragment from the mitochondrial control region to classify degraded and fragmentary archaeological canids with superior taxonomic resolution compared with morphological methods. For example, CD31 from Cluny (Figure 2) was initially misidentified as fox (*Vulpes* sp.) due to its small adult size, rather than as a potential European breed of domestic dog. Additionally, the FM Ranch canids had initially been identified as domestic dog. The two successful amplifications (CD20, CD21) reclassified these as grey wolf.

The potential for increased taxonomic accuracy is important for capturing the canid diversity that was present on the Plains, both before and after European contact. While previous studies relied on measurable traits and ethnographic accounts to classify domestic

dog remains into vague categories such as “medium”, “large”, and “wolf-like” (Allen 1920:442, 449), aDNA can help assess the extent of genetic relationships with other canids. Classifications such as “wolf-like” can be genetically evaluated as opposed to visually estimated. This analysis helps to expand our understandings of canid diversity at the Cluny and FM Ranch sites by reclassifying ambiguous specimens.

The locus targeted in this exploratory analysis was a short segment (198 bp) of the hypervariable D-loop region (Ishiguro et al. 2000), meaning that there is a small, yet highly variable set of polymorphic characters with which to differentiate populations. Our initial results hint at a higher degree of canid variability on the Northern Plains than previously identified. However, a larger portion of the mtDNA control region using overlapping primers, or, preferably, next-generation sequencing techniques targeting the whole mitogenome are necessary to further investigate the correlation of observed genetic variability in ancient *C.l. familiaris* with cultural-historic distinctions in the region.

Distinguishing Archaeological Entities

This analysis was unable to compare the FM Ranch samples with those of the Lake Midden (Mortlach phase) or Cluny (One Gun phase) due to the genetic reclassification of two of the FM Ranch samples as grey wolf. However, the data are suggestive of some degree of population genetic differences between One Gun and Mortlach dogs. A unique clade is present at Cluny that aligns well with contemporary Asian dogs, distinct from other ancient North American canid lineages identified to date (Figure 3). The set of SNPs that define this clade are not present in

clades A–D, as presented by Thalmann and colleagues (2013). This hints at the potential for delineating archaeological entities on the plains using dog palaeogenetics, although more research is needed with a larger genetic dataset to achieve sufficient statistical support. Further investigation is also needed to investigate whether this clade is supported with the increased character set of the mitogenome (ca. 16,000 bp), and to assess its geographic origin. To this end, mitogenomes could be compared from archaeological canids across the northern and central plains and adjacent regions, such as the northwestern forested mountains and boreal forest.

It remains unclear who the occupants of the Cluny Site were, and where they came from. One hypothesis involves a migration of horticultural groups from the Middle Missouri region (Bryne 1973; Forbis 1977; Walde 2008:53), which could be evaluated in a future aDNA study of archaeological dogs recovered across the Great Plains. This analysis would be reliant on two factors: some degree of genetic isolation, and that dogs accompanied the migrating One Gun peoples. Given the unique clade identified at Cluny, our preliminary investigation is suggestive of genetic isolation (acknowledging our small sample size). Also, as mentioned previously, dogs played an important role in transportation prior to, and even after, the introduction of the horse. Therefore, it is plausible that dogs were a component in the migration of One Gun peoples (Wilson 1924). Our results suggest that canid aDNA is a viable means of investigating the One Gun migration hypothesis; however, a sample set spanning a larger geographic area is needed to provide conclusive evidence, as is mitogenomic sequencing. Assessing whether genetic similarities from a region

are due to trade or migration could be evaluated with stable isotope analysis and further comparisons of material culture.

A recent study by Edwards et al. (2016) used carbon and nitrogen isotopes from dog bone collagen to find evidence of maize consumption at Cluny, which would indicate affiliation with populations from North Dakota (e.g., Hidatsa and the Middle Missouri people). The diet of the domestic dog was presumed to be representative of the human diet. Ultimately, their results were not consistent with maize consumption, and the authors concluded that the inhabitants had likely adopted a local diet (Edwards et al. 2016).

European Contact

Our analysis adds to the results of Verwoerd (2012) by identifying additional *C.l. familiaris* population variability in Late Period sites on the Northern Plains, and the presence of possible European dogs in the assemblages. The precise provenience of the FM Ranch and Lake Midden samples are unknown due to a lack of sensitivity in excavation methods at the FM Ranch, and the acquisition of Lake Midden materials from amateur collectors (Verwoerd 2012). However, the meticulous excavation methods employed at Cluny allows for stratigraphic consideration of the European lineages. CD31's depth (level 3) feasibly falls within the proto-contact component at Cluny; however, CD30 was recovered from level 4.3, placing it within the pre-contact, One Gun component. There are two possible explanations for this (excluding contamination, which is an omnipresent consideration for aDNA): (1) there may be a proto-contact element of One Gun related to an exchange of European dogs that had not been identified previously; or (2) cryo- and

bioturbation may have caused mixing of proto-contact and prehistoric components (Figure 4). While evidence of European contact, such as glass beads, metal buttons, and machine-cut nails, has been abundant in the upper component at Cluny, there has been no evidence for contact in the prehistoric component (Walde et al. 2013:36–37). For this reason, we believe that post-depositional disturbance is more likely. Additionally, level 4.3 represents the upper limit of the pre-contact component, making it more susceptible to mixing with the lower levels of the proto-contact component. The identification of European dogs in archaeological assemblages, occurring either through trade or interbreeding, could potentially present an additional line of evidence in differentiating pre- and proto-contact components on the Plains where diagnostic European trade goods are absent.

Use of Small Dogs

During the pre-contact period, little to no historic or archaeological evidence exists on the presence of small dogs on the Northern Plains. The most com-

monly occurring breeds residing in this region were medium to large sized, as documented by Allen (1920). Smaller breeds were reportedly more popular with canoe-using tribes, as they were easier to transport on canoes. Additionally, they were considered superior beaver hunters (as they could fit into smaller spaces), and some even used them as pets (Allen 1920:467). Wilson (1924:204) reports a more recent occurrence of small dogs among the Hidatsa being the result of admixture of their “pure” Hidatsa breed with other breeds, including European.

Given the identification of CD31 (the small-sized, fully-developed mandible) as a domestic dog with SNPs similar to European terriers, consideration must be given to the presence of small dogs at Cluny. There is no evidence of canoe use or beaver hunting (Walde 2008; Walde and Evans 2014; Walde et al. 2011, 2013), hence the inhabitants would have had other motives for keeping smaller breeds of dogs. Due to CD31’s presence in the proto-contact component, it is possible that dogs were a European trade commodity on the plains; however, to

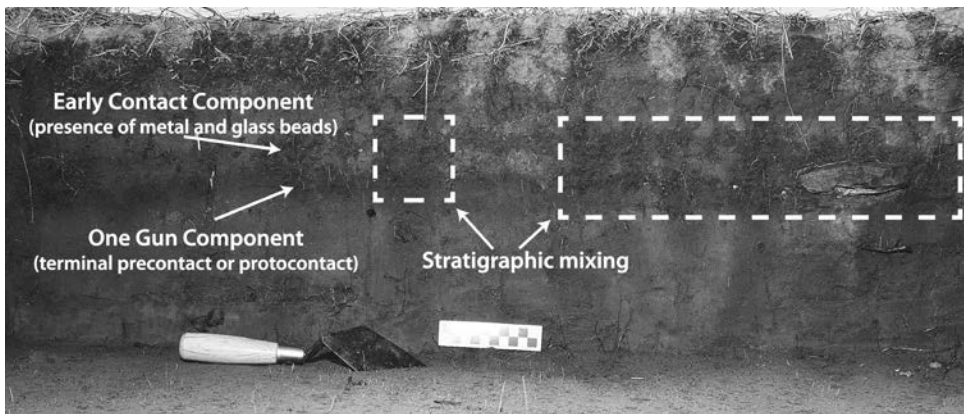


FIGURE 4. Unit profile (142E 81S) west wall (east facing) from the Cluny site indicating examples of stratigraphic mixing.

our knowledge, there is no evidence of this in the historic record.

On British ships, such as the *Mary Rose* and the *Earl of Abergavenny*, terriers and other small-sized dogs were often used as ratters to combat vermin, protect trade goods on long sea voyages, and act as companions for the crew (Gardiner and Allen 2013:615). In many areas of the world where trade with the British was common, dogs of similar characteristics and skills have often been found. Further research is needed to identify whether European dogs were traded during proto- or post-contact periods on the plains and, if they were, what their use was for First Nations.

Conclusions and Future Directions

Our results are consistent with our original hypothesis that genetic variability exists in North American dogs, which may be correlated with distinct cultural-historic events and phases. The unique clade present at Cluny is suggestive of this, however, it remains to be seen whether this is a result of the small sample size and a small set of genetic data. We demonstrated the complexity involved with morphological identification and genetically reclassified three of the 11 specimens. Furthermore, the amenable conditions for survivability of DNA molecules in this region of the Plains were demonstrated by the successful extraction of DNA from 10 of 11 specimens (and replication of nine), which illustrates the promise for future genetic research in this area.

Many gaps exist in the archaeological record of the Plains where domestic dogs may serve as analytically valuable cultural proxies, particularly given the lack of human remains for a direct investigation (see also Edwards et al. 2016). With the long history of dog domestication

in the Americas, having been initially brought across Beringia during the first migrations (Byrd 2013), analyzing canid genetics from a number of different cultural entities on the Canadian Plains may be a viable means of teasing apart inter-regional culture-historic developments through time. Other applications of aDNA analysis could include investigations into preference and utility of American dog breeds. Byrd and colleagues (2013) suggest that domestic dogs may have held a more prominent social role for past populations in western North America than has been previously considered, with aDNA being a suitable method for investigating this prominence. This work was intended as a preliminary exploratory analysis, and we hope that it will serve as a catalyst for future research into the diverse applications of canid remains for archaeological research on the Plains.

Acknowledgments. We wish to thank Dr. Brian Kooyman and Dr. Dale Walde for their guidance and support throughout the project, as well as the Department of Anthropology and Archaeology (University of Calgary) for their financial support.

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Manuscript received June 13, 2016.
Final revisions February 7, 2017.