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Reframing the Mammoth Steppe: Examining Mammoth Steppe Ecology Using Carbon and Nitrogen Isotopic Compositions of Megafauna Collagen

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Graduate Program in Geology A thesis submitted in partial fulfillment of the requirements for the degree in Doctor of Philosophy © Rachel E. Schwartz-Narbonne 2016

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Abstract

The Pleistocene mammoth steppe was a vast biome that stretched from northwestern Europe to central Canada. A diverse set of megaherbivore and megacarnivore species lived within this biome and there was significant ecosystem faunal and floral homogeneity. At the end of the Pleistocene, this biome disappeared, with the extinction or extirpation of many of the megafaunal species that inhabited it. This thesis reconstructs the ecology of the mammoth steppe using the isotopic compositions of carbon and nitrogen from megafaunal collagen. The reconstruction is done at a variety of ecological scales, beginning with individual animal- and season-specific isotopic studies of antlers, and then comparison to bones from the same species. This provides a framework to understand the habitat and diet of antlered species through the Pleistocene and into the Holocene. Non-ruminant species ecology is assessed using the carbon and nitrogen isotopic compositions of the individual amino acids that comprise their bulk collagen. The compound-specific technique allows metabolic and habitat or dietary effects to be separated and diets to be classified. These studies indicate woolly mammoths ate a distinct diet, likely comprising decayed plants, and that some horses shared this dietary niche. The Pleistocene giant beaver consumed aquatic plants, while the mastodon consumed unmodified terrestrial plant material. Finally, the bulk collagen isotopic compositions measured in this work as well as reviewed from the literature are compiled and the mathematical tool SIBER (Stable Isotope Bayesian Ellipses in R) is used to define the isotopic niche for multiple megaherbivore species at different times and sites across the mammoth steppe. This, combined with the dietary and habitat information gleaned from the antler and amino acid isotopic measurements, allows an in-depth analysis of mammoth steppe ecology. Before the LGM (Last Glacial Maximum), most species occupied consistent isotopic niches between sites across the mammoth steppe, suggesting consistent diets or habitats during the pre-LGM period. These isotopic niche patterns changed during the LGM, and the patterns were not re-established post-LGM or in the Holocene. These changes suggest that the ecosystem suffered a major disturbance during the LGM, before the extinctions that occurred at the end of the Pleistocene.

Keywords

mammoth steppe, Pleistocene, stable isotopes, carbon isotopes, nitrogen isotopes, collagen, amino acid isotopes, SIBER, serial sampling, paleoecology

Co-Authorship Statement

Chapter 3 of this thesis was co-authored by Dr. Fred J. Longstaffe, Dr. Jessica Z. Metcalfe and Dr. Grant Zazula. F.J.L. funded the study, participated in study conception, sample collection, data reduction and interpretation and revised the manuscript. J.Z.M. participated in sample collection, data interpretation and provided substantive comments on the manuscript. G.Z. provided access to the samples and substantive comments on the manuscript.

Artwork for figures was commissioned from Katherine Allan, and her work is acknowledged in the figure captions.

Epigraph

This isotope is so dope I got hope Lookin' through my microscope On high power, Get a glower They're supervising; I'm socializing, minimizing the work that I'm doing And I'm reviewing my data, but my results are nada. I won't listen to the hate, Those who can't appreciate, Say this field ain't yo' fate, So I'll be showin' defiance with a paper in Science Yeah

- By Heather Schwartz-Narbonne

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Chapter 1

1 Introduction

1.1 Thesis objectives

During the Pleistocene, a vast biome existed, known as the mammoth steppe. The mammoth steppe was home to a wide array of megaherbivore and megacarnivore species. At the end of the Pleistocene, many of these species went extinct or were extirpated, and leading to the loss of the ecosystem as a whole. Understanding the individual-, population- and species-level behaviours that allowed this ecosystem to be maintained is vital to reconstructing Pleistocene ecology, as well as to understanding modern ecosystems that are facing significant changes from climate and anthropogenic effects. This thesis uses isotopic analysis of collagen in bone, teeth, tusk and antler to investigate megaherbivore and megacarnivore ecology. This is first studied over short time scales, such as a single season or a few years of life, to understand individual animal responses to changing environmental conditions. Species' diet and physiology are then investigated using the isotopic compositions of the individual amino acids that compose collagen. Finally, population-level responses are examined by comparing isotopic compositions of various species at multiple sites and time periods. This allows for a deeper understanding of the ecology of the mammoth steppe, and potentially the factors that might have contributed to its disappearance.

1.2 The mammoth steppe

1.2.1 The mammoth steppe ecosystem

The Pleistocene mammoth steppe was a highly diverse biome, with a range of megafaunal and floral elements that are not seen in association in modern ecosystems (Guthrie, 2001, 1990, 1982). The Pleistocene mammoth steppe has been reconstructed to have had animal and plant productivity similar to the African savannah (Zimov et al., 2012), and to have had more ecological connectivity than the modern African savannah (Pires et al., 2015). The mammoth steppe was the largest biome on Earth during the Pleistocene, spanning from Spain to the Yukon (Fig. 1.1; Guthrie, 2001, 1990, 1982).

Understanding the mammoth steppe is key to understanding Pleistocene paleoecology. Such insight also holds value for anticipating the ecological outcomes of modern climate change, as it can help to elucidate how species adapt to differences in climate and anthropocentric effects, both by comparing geographic locations across the mammoth steppe and examining ecosystem changes over time. Given the potential consequences of modern, anthropogenic climate change, and the prediction that the future will hold an increasing number of non-analogue faunal communities (Williams and Jackson, 2007), understanding the functioning of past ecosystems has become of growing importance.

The mammoth steppe biome was characterized by woolly mammoth, horse and bison dominated ecosystems (Druckenmiller, 2008; Guthrie, 1968; Mann et al., 2013; Mol et al., 2006; Zimov et al., 2012), as well as by herb-steppe-tundra flora (Bocherens, 2003; Guthrie, 2001, 1990, 1982). Pollen, ancient DNA and plant macrofossil studies have identified the mammoth steppe plants as primarily graminoids and forbs, with some willow present. Few records of trees were found during most of the Pleistocene (Blinnikov et al., 2011; Goetcheus and Birks, 2001; Höfle et al., 2000; Schweger et al., 2011; Willerslev et al., 2014). Rather than floral species being evenly distributed across the mammoth steppe, they formed a "vegetational mosaic" (Guthrie, 1982). However,

similar floral characteristics were seen at a broad scale between different sites on the mammoth steppe (Willerslev et al., 2014). Similar megaherbivore and megacarnivore species were also present across the mammoth steppe, including muskox, caribou, brown bear and grey wolf (Bocherens, 2015; Druckenmiller, 2008; Guthrie, 1968; Mann et al., 2013; Mol et al., 2006; Zimov et al., 2012). There were some differences between regions. For example, woolly rhinoceros has not been found in North America and shortfaced bear has not been found in Eurasia, suggesting that some species were unable to cross the Bering Land Bridge and fully disperse (Guthrie, 2001). Others co-existed only during specific time intervals. For example, elk was present in Europe throughout the Pleistocene, but did not migrate to North America until around $13,000$ ¹⁴C years BP (Guthrie, 2006; Meiri et al., 2014).

A combination of environmental factors generated a large, highly productive plant biomass on the mammoth steppe. The mammoth steppe was more arid than those regions are today (Edwards et al., 2001; Elias, 2000; Guthrie, 2001; Schweger et al., 2011). This led to decreased snowfall and thus an early spring melt, which increased the length of the growing season (Guthrie, 2001, 1982). Decreased precipitation promoted the growth of arid-adapted plants, which do not form a summer-season insulating cover over soil. This lack of insulating cover meant that the soil warmed more rapidly and warmer soils promoted nutrient turnover and soil fertility (Guthrie, 1982). The Pleistocene flora had an extended growing season causing increased plant productivity. Warmer soils also meant a deeper permafrost layer, so a significant proportion of plant biomass could be stored underground and the plants faced decreased risk from grazing herbivores. This meant they did not develop strong anti-herbivore defence mechanisms such as production of various alkaloids (Guthrie, 1990, 1982). The decreased snowfall also made the plants more accessible to several Pleistocene herbivores (Guthrie, 2001). The high plant biomass levels were also promoted by nutrient-rich soils (Goetcheus and Birks, 2001; Guthrie, 1982). Many Pleistocene soils were composed of loess, a fine-grained material that forms when glacial flow erodes the underlying rock. This glacial dust was carried by outwash streams and deposited by wind kilometres from the original glacier, forming the basis of a new soil layer (Goetcheus and Birks, 2001; Guthrie, 1990, 1982). These newly formed soils were rich in potassium, phosphate and calcium, which are necessary for

plant nutrition. The megafauna are suggested to have encouraged plant growth by trampling and grazing, both of which promoted the growth of fast-growing flora (Blinnikov et al., 2011; Guthrie, 1982; Willerslev et al., 2014; Zimov et al., 2012).

The Pleistocene had repeated cycles of glaciations and deglaciation, and the accompanying climatic changes had significant effects on the mammoth steppe. Woodlands became more prevalent in parts of the mammoth steppe during warmer periods (interglacials and interstadials; Castaños et al., 2014; Elias, 2000; Schweger et al., 2011). During the last glacial maximum (LGM), several species are posited to have been extirpated from parts of the mammoth steppe. For example, there are no post-LGM dates for the scimitar-tooth cat or the short-faced bear in central Alaska (Fox-Dobbs et al., 2008). The floral compositions of sites on the mammoth steppe changed during the LGM as well, with fewer species and less similarity of plant species among sites (Willerslev et al., 2014). The post-LGM warming and increase in mesic conditions may have been the factor that allowed elk to enter North America (Meiri et al., 2014).

1.2.2 Megafaunal extinctions on the mammoth steppe

A number of extinctions occurred at the terminal Pleistocene (12,000-10,000⁻¹⁴C BP). In North America alone, 35 genera of animals went extinct locally, and 29 of those went extinct globally (Faith and Surovell, 2009). The majority of the megaherbivore and megacarnivore species on the mammoth steppe were extirpated or went extinct. The exact timing of the extinctions is disputed and needs to be resolved on a species-byspecies basis (Faith and Surovell, 2009; Gill et al., 2009; Grayson and Meltzer, 2003; Guthrie, 2006). However, while the precise timing is not fully resolved, many of these extinctions were approximately synchronous with widespread climatic and vegetation change (Guthrie, 2006). The extinctions were also approximately synchronous with some of the earliest evidence for human habitation in North America, which is provided by the Clovis spear points (Faith and Surovell, 2009; Guthrie, 2006). Humans and their predecessors coexisted with Pleistocene megafaunal species for approximately 2 million years in the mammoth steppe in Eurasia, though anatomically modern humans likely arrived in Eurasia around 45,000 years ago (Barnosky et al., 2004; Koch and Barnosky, 2006). It is generally accepted that human hunting, climate change or a combination of

these two factors led to the extinctions and that the extent to which each of those factors is responsible varied globally (Barnosky et al., 2004; Cooper et al., 2015; Koch and Barnosky, 2006).

Overkill models are based on the concept that species were removed from the mammoth steppe by human hunting, leaving empty ecological niches (Barnosky et al., 2004; Koch and Barnosky, 2006; Sandom et al., 2014). The structure of mammoth steppe ecology may have made the ecosystem particularly vulnerable to disruption by human hunting (Pires et al., 2015). Some authors further suggest that the terminal Pleistocene vegetation change occurred because of the removal of mammoths, a keystone herbivore (Gill et al., 2009; Koch and Barnosky, 2006), and that these changes led to the extinction of further herbivore species. Radiocarbon dating of megafaunal remains, however, suggests that – in Alaska and the Yukon – mammoth extinctions followed rather than preceded the extinctions of most megafauna species (Guthrie, 2006), and this likely occurred at other places as well (Barnosky et al., 2004).

At the terminal Pleistocene, the climate changed to warmer, moister conditions (Edwards et al., 2001; Guthrie, 2006). Vegetation shifted from herb-steppe-tundra to bogs, wetlands, and forests (Guthrie, 2001, 1982). Mammoth steppe flora was replaced with highly zoned, low diversity floral communities, with high levels of anti-herbivore defences. Ungulates in general are unable to digest significant quantities of woody tissues, and non-ruminants (e.g. horse, mammoth) in particular require a diverse set of forage types. This vegetation shift is hypothesized to have disrupted the ability of these species to obtain the diverse types and quantity of forage that they required (Barnosky et al., 2004). This conclusion is supported by evidence that several species of megafauna experienced population decline or environmental stress as a result of climatic changes before the terminal Pleistocene, suggesting that while the extinction event occurred at the terminal Pleistocene, the species may have already been in decline (Faith, 2011; Guthrie, 2003; Shapiro et al., 2004).

1.3 Stable isotopes

1.3.1 Carbon isotopes

Plants can take up and fix carbon using a variety of mechanisms, each of which has implications for the $\delta^{13}C$ of the plant. The three major photosynthetic pathways are C_3 , C_4 and CAM (Crassulacean Acid Metabolism). C_3 plants tend to have much lower $\delta^{13}C$ (average -27% ; Koch, 2007), than C_4 plants (average -13% ; Koch, 2007), though in some circumstances, such as low pCO_2 , C_3 plants may utilize pathways more similar to C⁴ plants, which may cause their isotopic compositions to increase (Busch et al., 2013; Way et al., 2014). CAM plants tend to have isotopic compositions between the two (average –11‰; Marshall et al., 2007). No evidence for CAM plants has been found on the mammoth steppe. There is a limited quantity of modern C_4 plants on the area that was the Pleistocene mammoth steppe (Wooller et al., 2007). However, studies of the Pleistocene mammoth steppe have found only C_3 plants (Bocherens, 2015, 2003; Gaglioti et al., 2011; Kristensen et al., 2011; Wooller et al., 2007).

In modern tundra, shrubs generally have the lowest δ^{13} C, followed by forbs, graminoids, fungi and then lichens (Fig. 1.2; Barnett, 1994; Ben-David et al., 2001; Drucker et al., 2010; Kristensen et al., 2011). There is commonly significant overlap in the range of $\delta^{13}C$ of different plant types. Some of this overlap occurs because of varying isotopic compositions of different plant parts. For example, in trees there is a tendency for needles and leaves to have lower δ^{13} C than twigs (Ehleringer et al., 1992; Gebauer and Schulze, 1991; Tischler, 2004). Algae and C₃ macrophytes have a wide range of $\delta^{13}C$ (-47 to -8‰) encompassing the entire range of C_3 terrestrial plants (-32 to -22‰; Farquhar, 1989; Finlay and Kendall, 2007). While terrestrial plants use only atmospheric carbon, aquatic plants take up carbon from a variety of sources including dissolved inorganic carbonate from carbonate rocks, respiring organic matter and detritus, and atmospheric CO_2 , and each of these can impart a distinct δ^{13} C to the plant (Farquhar, 1989; Finlay and Kendall, 2007; Keeley and Sandquist, 1992; LaZerte and Szalados, 1982; Osmond et al., 1981). While several site-specific studies have found consistent differences between terrestrial and aquatic plants (Doucett et al., 1996; Fry, 1991; Tischler, 2004), these

cannot be generalized to global differences among plant types (Finlay and Kendall, 2007; France, 1995; Keeley and Sandquist, 1992).

Figure 1.2 Conceptual diagram illustrating the relative carbon and nitrogen isotopic compositions of common modern terrestrial tundra vegetation.

Climatic differences between habitats affect the δ^{13} C of terrestrial plants. When aridity increases, plants have higher water use efficiency, leading to higher $\delta^{13}C$ (de Bello et al., 2009; Farquhar, 1989; Tieszen, 1991; Wooller et al., 2007). An increase in altitude and temperature can also cause higher δ^{13} C, though these effects are disputed (de Bello et al., 2009; Diefendorf et al., 2010; Ehleringer and Cooper, 1988; Ehleringer et al., 1987; Farquhar, 1989; Heaton, 1999; Kohn, 2011, 2010; Stevens et al., 2006; Tieszen, 1991; Wooller et al., 2007). The role of temperature may vary with landscape, and temperature has been reported as a significant factor in plant δ^{13} C in Arctic environments (Iacumin et al., 2006). Plants that grow underneath a dense canopy obtain less light, and more recycled $CO₂$ from respiring plant tissue, than plants that grow in open areas. For this reason, they tend to have lower $\delta^{13}C$ (Adams and Grierson, 2001; Bocherens et al., 2011; Bonafini et al., 2013; Buchmann et al., 1997; Farquhar, 1989; Garten Jr and Taylor Jr,

1992; Heaton, 1999; Kohn, 2010; Tieszen, 1991). Sea spray can increase the $\delta^{13}C$ of plants (see Sykes et al., 2011 and references therein), as can higher levels of nutrients such as nitrogen or phosphorus (Heaton, 1999; Tieszen, 1991; Toft et al., 1989). Some authors have suggested during periods when the Earth had lower $pCO₂$, plants had higher δ ¹³C, and vice versa (Schubert and Jahren, 2015), but this has not been consistently observed in multiple studies (see discussions in Bocherens, 2003; Richards and Hedges, 2003; Stevens and Hedges, 2004). Once a plant has died, its carbon isotopic composition can also be changed by decay processes (Gleixner et al., 1993; Wynn, 2007).

The biochemical components within a plant have consistent differences in their δ^{13} C. Within a plant, lipids have the lowest δ^{13} C, followed by carbohydrates and then proteins (Boutton, 1996; Gleixner et al., 1993; Tieszen, 1991). The patterns of isotopic compositions of the amino acids that compose proteins vary with plant type, plant part, and kingdom (Fogel and Tuross, 2003; Larsen et al., 2013, 2012, 2011, 2009; Lynch et al., 2011; Smallwood et al., 2003). Since there are clear differences in the $\delta^{13}C$ patterns among groups such as aquatic plants, terrestrial plants, bacteria and fungi, linear discriminant analysis can be used to classify the group from which a protein originated by determining common trends in the δ^{13} C of the amino acids between groups (Larsen et al., 2013, 2012, 2009).

Bone, tooth, tusk and antler are composed of organic and inorganic components. The organic material consists primarily of the protein collagen and the inorganic component comprises bioapatite (Szpak, 2011). Collagen can be preserved over archaeological and paleontological time scales. There are well-defined criteria to assess the extent of collagen preservation prior to accepting its isotopic composition as representative of primary processes (Ambrose, 1990; DeNiro, 1985; van Klinken, 1999). The isotopic composition of an animal's collagen derives from the isotopic composition of the diet that it consumed. Because of a number of metabolic effects, however, an animal's collagen typically has a higher carbon isotopic composition ($\delta^{13}C_{\text{Bulk}}$) than the dietary materials from which it formed. Large herbivores are typically enriched in ¹³C by 5.1‰ \pm 0.3 % from diet to bone collagen (Drucker et al., 2008). The increase in $\delta^{13}C_{\text{Bulk}}$ from prey to predator is typically 1.2 ± 0.3 ‰ (Bocherens, 2015).

Collagen is composed of both essential and nonessential amino acids (Howland et al., 2003). Essential amino acids are routed directly from the diet, while nonessential amino acids can either be directly routed, or can be synthesized from the carbohydrate or lipid portion of the diet (Jim et al., 2006; Newsome et al., 2014). Which nonessential amino acids are routed and which are synthesized depends in part on the quantity of those amino acids in the diet (McMahon et al., 2010). When nonessential amino acids are synthesized, their isotopic composition depends on the isotopic composition of the biochemical portion of the diet from which they are synthesized (e.g. lipids, carbohydrates or protein) and on the isotopic separation induced by the metabolic process (Jim et al., 2006; Newsome et al., 2014). Amino acids that are directly routed with minimal changes in their δ^{13} C, such as essential amino acids, can be used to classify the dietary source of a consumer using linear discriminant analysis (LDA). In LDA, the characteristic $\delta^{13}C$ signatures of amino acids from defined groups such as terrestrial plants, aquatic plants, bacteria and fungi are entered into a program such as the MASS package in R (R Core Team, 2014; Venables and Ripley, 2002). This program defines the linear combination of features that vary between groups, and so is able to create a set of expected isotopic trends between amino acids for each group. These expected isotopic differences, or prediction functions, can then be used to classify unknown samples by checking the samples against the expected trends. This can be used to classify the diet of consumers by inputting amino acids from consumers and testing which dietary source they most closely resemble (Larsen et al., 2013, 2012, 2009). Herbivores consume significantly less protein than carnivores, and so some, or all, of their nonessential amino acids are expected to reflect the δ^{13} C of non-protein portions of the diet. Care must be taken, therefore, in selecting which amino acids are used in LDA to create the predictive functions.

The $\delta^{13}C_{\text{Bulk}}$ can also be affected by metabolic effects specific to an animal's physiology. For example, a nursing animal consumes a diet rich in lipids, which have lower $\delta^{13}C$ (Metcalfe et al., 2010). An animal suffering from winter starvation may rely on its fat reserves to survive, which again could cause it to have lower $\delta^{13}C_{\text{Bulk}}$ (Szpak et al., 2010). Hibernation may also have an effect on a species' $\delta^{13}C_{\text{Bulk}}$, but it is difficult to distinguish this from the effect of consuming body lipids to survive the winter (Bocherens, 2015; Nelson et al., 1998). Ruminant species produce and release large quantities of methane,

which has low δ^{13} C. This means that their δ^{13} C_{Bulk} may be higher than those of nonruminant species (Coltrain et al., 2004). Finally, different tissues are grown over different time periods. Teeth form at a single point in an animal's life, while bone is continuously remodelled and thus its isotopic composition reflects diet and metabolic and physiological processes over several years of an animal's life (Bocherens, 2015; Koch et al., 1994; Metcalfe et al., 2010). Antler forms over a single season (Chapman, 1975). Hence, the isotopic compositions of different tissues from the same individual can provide information on the physiology, diet and habitat at different points in the animal's life. Conversely, the isotopic composition of bone, a tissue that provides an averaged isotopic composition over several years, can be invaluable to look at population-level ecology.

1.3.2 Nitrogen isotopes

Nitrogen used for plant amino acid synthesis can come from one of four sources: (i) direct uptake of soil amino acids, although most plants compete poorly for amino acids compared to soil microbes (Styring et al., 2014); fixation of atmospheric nitrogen by plants or associated microorganisms, and (iii) nitrate or (iv) ammonium uptake from soil (Amundson et al., 2003). Plants then convert this nitrogen into an amino acid by attaching it as an amide group to glutamate, forming glutamine. Glutamine can then be used a precursor to form the rest of the amino acids in the plant (Styring et al., 2014). The isotopic composition of a terrestrial plant partly depends on the source and $\delta^{15}N$ of the nitrogen used (Gannes et al., 1998; Nadelhoffer et al., 1996). Plants that fix nitrogen have δ^{15} N close to 0 ‰ (Amundson et al., 2003). If nitrogen is obtained from associated mycorrhizal fungi, the plant often has lower $\delta^{5}N$ than if it had obtained nitrogen directly from soil (Bocherens, 2003; Craine et al., 2009; Nadelhoffer et al., 1996). The rooting depth of a plant also affects its $\delta^{15}N$; deeper soil tends to have higher $\delta^{15}N$, which are passed on to the plant (Barnett, 1994; Handley and Raven, 1992; Kelly, 2000; Nadelhoffer et al., 1996). Nitrogen can also be lost from a plant by root exudations, or as gaseous nitrogen emissions from leaves, with an associated nitrogen isotopic fractionation (Dawson et al., 2002). All of these factors combine to produce the pattern of modern terrestrial plant isotopic compositions in tundra environments illustrated in

Figure 1.2. Fungi have the highest $\delta^{15}N$, followed by graminoids, forbs, lichens and shrubs (Ben-David et al., 2001; Drucker et al., 2010; Finstad and Kielland, 2011; Kristensen et al., 2011; Nadelhoffer et al., 1996). There is significant overlap in the $\delta^{5}N$ of different plant types, making clear differentiation based solely on the nitrogen isotopic composition of the plant difficult. There are also differences in the $\delta^{5}N$ of different plant parts. For examples, tree stems commonly have lower $\delta^{15}N$ than leaves or needles (Gebauer and Schulze, 1991; Kielland, 2001).

Global studies of aquatic plants report a wide range of $\delta^{15}N$, since there are a variety of sources that such plants can access, including dissolved inorganic nitrogen in lakes and rivers or nitrogen drawn from soils (Finlay and Kendall, 2007). The global range of aquatic plant $\delta^{5}N$ overlaps that of terrestrial plants (France, 1995). However, studies at specific sites commonly find higher $\delta^{15}N$ for aquatic than adjacent terrestrial plants (Delong and Thorp, 2006; Finstad and Kielland, 2011; Fry, 1991; Milligan et al., 2010; Tischler, 2004). This pattern, however, is not universally observed (Ben-David et al., 2001; McArthur and Moorhead, 1996).

Terrestrial habitats can be divided into "open" and "closed" ecosystems. An open habitat is usually warmer and more arid, and significant quantities of nitrogen are lost to the atmosphere or in removal of water from the system such as in run-off. Nitrogen is preferentially lost as ^{14}N , causing the remaining nitrogen to be enriched in ^{15}N , and the plants that grow in that habitat to have higher $\delta^{15}N$. Plants that grow in colder and more mesic environments tend to have lower $\delta^{5}N$ (Ambrose, 1991; Amundson et al., 2003; Drucker et al., 2003a; Heaton, 1987; Stevens and Hedges, 2004; Stevens et al., 2008). Salinity can increase the $\delta^{5}N$ of an ecosystem that experiences significant quantities of sea spray (see Sykes et al., 2011). Deeper winter snow can cause higher $\delta^{15}N$ in the plants that grow there (Blok et al., 2015). Finally, fertilization with organic material such as dung can increase the $\delta^{15}N$ of plants (Szpak et al., 2012).

The $\delta^{15}N$ of animal bone collagen ($\delta^{15}N_{\text{Bulk}}$) reflect the $\delta^{15}N$ of its diet plus an increase of 3.6 ± 0.9 % (Bocherens, 2015). The isotopic composition of an animal's collagen derives from a combination of the $\delta^{15}N$ of source amino acids, which tend to retain the isotopic

composition of the diet, and trophic amino acids, which are strongly influenced by metabolic effects and therefore increase in $\delta^{15}N$ with trophic level (McCarthy et al., 2007; McClelland and Montoya, 2002; Popp et al., 2007). Source amino acids can be used to determine the isotopic composition of food from the base of the food web, while trophic amino acids provide an indication of the trophic level and degree of metabolic isotopic enrichment occurring within an animal.

There are some physiological effects that can cause an increase in $\delta^{15}N_{\text{Bulk}}$. A nursing individual consumes tissue from its mother, and so nursing animals have a $\delta^{15}N_{\text{Bulk}}$ one trophic level higher than their mother (Metcalfe et al., 2010). Extreme nutritional stress has been posited to cause an animal to recycle its own tissues, causing an increase in $\delta^{15}N_{\text{Bulk}}$ (Gannes et al., 1998; Hobson et al., 1993; Kelly, 2000; Koch, 2007; Polischuk et al., 2011), although some research suggests that this only occurs at an extreme threshold of nutritional stress (Kempster et al., 2007). Aridity has also been suggested to cause increases in $\delta^{15}N_{\text{Bulk}}$ (Kelly, 2000; Koch et al., 1994; Sealy et al., 1987; Sponheimer et al., 2003). Hibernation has also been suggested to cause increases in $\delta^{15}N_{\text{Bulk}}$ of hibernators such as bears (see discussion in Bocherens, 2015).

1.3.3 Combined carbon and nitrogen isotopic analysis

A number of mathematical tools have been created that use the combination of $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ to better understand species' ecology. When considering a species at a single trophic level, evaluation of its carbon and nitrogen isotopic compositions in combination allows an "isotopic niche" to be defined. This isotopic niche can be defined to include the total area in isotopic space on a graph of δ^{13} C versus δ^{15} N (measured in per mil) covered by the all the isotopic compositions of a species (Layman et al., 2007), or it can be defined to include the core 40% of the isotopic compositions of the species on the graph (Jackson et al., 2011). Either method provides a distinctly shaped and sized isotopic niche for each species. The relative size of two isotopic niches can also be compared using Bayesian statistics. These statistics use a probabilistic framework to determine how likely it is that a species' niche is a given size. They can then compare the likelihood of each niche size for two groups to determine which species has a higher
proportion of expected niche sizes, and so is most probable to have the larger niche. (Jackson et al., 2011; Parnell et al., 2010). The size of the isotopic niche can provide information about the generalist versus specialist tendencies of a species. For example, a larger isotopic niche may indicate a species feeding on a more diverse set of resources or in a wider range of habitats, so a more generalist species. The amount of isotopic niche overlap is informative about the extent of competition for resources. SIBER (Stable Isotope Bayesian Ellipses in R) is one of the mathematical programs that perform this analysis (Jackson et al., 2011; Parnell et al., 2010).

Bayesian analysis can be used to elucidate the diet of a species when the isotopic compositions of plants and animals, and/or animals from multiple trophic levels are known. The isotopic compositions of potential dietary resources and the consumer can be used as the input to mixing models such as SIAR (Stable Isotope Analysis in R) to provide estimates of the most probable combination of dietary resources used (Parnell et al., 2010).

1.4 Previous isotopic investigations of collagen on the mammoth steppe

Isotopic compositions of collagen have been used in numerous studies to reconstruct the ecology of the mammoth steppe (e.g. Bocherens et al., 2011, 1994; Drucker et al., 2003a, b; Fizet et al., 1995; Fox-Dobbs et al., 2008; Iacumin et al., 2010; Mann et al., 2013; Metcalfe, 2011; Metcalfe et al., 2013; Raghavan et al., 2014; Stevens et al., 2009; Szpak et al., 2010). Reviews of isotopic results across the mammoth steppe have noted that the patterns of $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ among herbivores at a site tend to be relatively consistent (Bocherens, 2015, 2003), suggesting specific dietary niches for each species. For example, caribou are reconstructed as having consumed lichen (Bocherens, 2015; Castaños et al., 2014), and horse and bison as consuming graze (graminoids and forbs; Fox-Dobbs et al., 2008), with horses eating the shorter grasses and bison eating the taller grasses (Britton et al., 2012). Woolly mammoth had unusually high $\delta^{15}N_{\text{Bulk}}$, more similar to coeval carnivores than herbivores (Bocherens, 2003), which made their isotopic compositions difficult to interpret. This "woolly mammoth conundrum" suggests

that they had a distinct diet, habitat or physiological mechanism. A variety of explanations have been suggested, including consumption of plants that grew in more arid environments, consumption of plants that had been previously fertilized by dung, selection for specific plants or plant parts, seasonal starvation that caused $15N$ -enrichment and/or consumption of their own feces (Bocherens, 2003; Iacumin et al., 2000; Koch, 1991; Kuitems et al., 2012; Metcalfe et al., 2013; Szpak et al., 2010). The low $\delta^{5}N_{\text{Bulk}}$ of mastodon, by comparison, are suggested to reflect consumption of browse such as spruce trees (Metcalfe et al., 2013).

Changes have been noted in the isotopic compositions of herbivore species, both over time and between sites. Higher $\delta^{15}N_{\text{Bulk}}$ have been measured for woolly mammoths in Russia than in Alaska or the Yukon (Szpak et al., 2010), suggesting that Pleistocene Russia was more arid than the two other sites. A decline in the average $\delta^{15}N_{\text{Bulk}}$ of 2-3 ‰ in several herbivore species was observed in southwestern Europe and in Alaska after the LGM (Bocherens et al., 2011; Fox-Dobbs et al., 2008; Mann et al., 2013; Stevens et al., 2008), which may have been caused by changes in aridity and/or temperature. Variations in the pCO_2 of the atmosphere may have also affected the δ^{13} C of plants between glacial and interglacial cycles, and thus the animals that consumed these plants (Bocherens, 2003; Iacumin et al., 2006; Stevens and Hedges, 2004), though this difference is not observed at all sites (Fox-Dobbs et al., 2008). Alternatively, changes in $\delta^{13}C_{\text{Bulk}}$ between the post-LGM period and the Holocene in France have been posited to reflect an increase in canopy vegetation (Drucker et al., 2003a, 2008). Overlapping $\delta^{15}N_{\text{Bulk}}$ have been observed for horse and woolly mammoth in Ukraine and Germany during certain time periods, which may suggest that these species shifted their diet depending on resource availability and competition with other herbivores (Bocherens, 2015).

Fewer studies have been performed on carnivore isotopic compositions for the mammoth steppe megafauna, likely because fewer carnivore than herbivore specimens have been found (e.g. Mann et al., 2013). Bocherens (2015) and Yeakel et al. (2013) have reviewed the isotopic compositions of carnivore collagen from multiple mammoth steppe sites. Bocherens (2015) focussed on identifying the diet of individual species, and comparing those diets at differing sites or time periods across the mammoth steppe. Several species,

such as cave lion and brown bear, varied their diet among sites, potentially in response to competition with other carnivores for prey, as had been observed in similar studies of individual species (Barnes et al., 2002; Bocherens, 2015; Bocherens et al., 2011). Yeakel et al. (2013) used a Baynesian mixing model to identify the diets of carnivores at two sites over multiple time periods, and then compared the structure of the ecosystems based on this interpretive approach to collagen isotopic data. They found that the Alaskan site had more resource segregation between carnivores, consistent with the interpretation that this ecosystem was more isolated from neighbouring animal communities.

1.5 Dissertation

1.5.1 Goals of the dissertation

There is a growing body of work using isotopic compositions of megafauna to understand the ecology of the mammoth steppe. The majority of work on collagen in the mammoth steppe has focused on single sampling of bone or adult teeth. Bone provides a timeaveraged signal of the last several years of an animal's life (Balasse et al., 1999; Koch et al., 1994).

Teeth and tusk, by comparison, provide a "snapshot" view of an animal's life, as the collagen in teeth and tusk is deposited once and not remodelled over an animal's lifetime (Koch et al., 1994; Metcalfe et al., 2010). Measuring the isotopic composition of an adult tooth or tusk is also commonly used to assess the isotopic composition of the adult diet of the animal, in the same manner that bone collagen is used (e.g. Mann et al., 2013; Metcalfe et al., 2013; Szpak et al., 2010). This approach, however, is made more powerful by taking multiple samples, typically of smaller size, from an individual tusk or tooth to investigate seasonal or yearly changes. This approach is invaluable for investigating signals that are not generated year-round – for example, weaning happens once in an animal's lifetime, pregnancy occurs seasonally for species such as caribou (Finstad and Kielland, 2011) and many dietary resources are population-limiting seasonally rather than year-round (Adamczewski et al., 1988; Heggberget et al., 2002). In situations such as these, isotopic compositions can reveal dietary switching over time (Peterson and Fry, 1987). One study has examined the differences in the isotopic

composition of woolly mammoth teeth formed at different ages to assess the timing of nursing and weaning (Metcalfe et al., 2010), and another studied serially sampled increments of a juvenile mammoth's tusk to assess age of weaning (Rountrey et al., 2007). Moving beyond collagen as the tissue examined, still other studies have serially sampled woolly mammoth hair (Iacumin et al., 2006, 2005), horse tooth enamel (Bellissimo, 2013) and tusk enamel of woolly mammoths (Fox et al., 2007) to investigate seasonal changes in the species.

There remain, however, a number of unresolved questions concerning the ecology of the mammoth steppe:

- (1) Extensions of the serial sampling approach to other tissues, such as antler, and to other species should allow more exploration of seasonal changes within the mammoth steppe.
- (2) Isotopic work to date on the mammoth steppe has focused on bulk tissue isotopic analysis. While the isotopic compositions of both carbonate and phosphate components of bioapatite from mammoth steppe animals are now routinely measured and interpreted (e.g. Bellissimo, 2013; Fox et al., 2007), only bulk protein from keratin and collagen has been analysed for these animals. Individual amino acid analysis, by comparison, has proven invaluable for elucidating an individual's trophic level and the major components of their diet in a number of modern (e.g. Hannides et al., 2009; Miller et al., 2012; Popp et al., 2007; Sherwood et al., 2011) and archeological studies (e.g. Fogel and Tuross, 2003; Naito et al., 2010; Styring et al., 2010). This method has the potential to provide insight into the diet of several species from the mammoth steppe, and to better resolve their ecology. For example, its application to woolly mammoth collagen could resolve the "woolly mammoth conundrum". It could also help to better resolve the diet of a variety of herbivores, using the $\delta^{5}N$ of source amino acids (McCarthy et al., 2007; McClelland and Montoya, 2002; Popp et al., 2007) and linear discriminant analysis classification of amino acid δ^{13} C (Larsen et al., 2013, 2012, 2009).

(3) While there have been numerous studies of bulk collagen isotopic compositions of megaherbivores from the mammoth steppe (e.g. Bocherens et al., 2011, 1994; Drucker et al., 2003a, b; Fizet et al., 1995; Fox-Dobbs et al., 2008; Iacumin et al., 2010; Mann et al., 2013; Metcalfe, 2011; Metcalfe et al., 2013; Raghavan et al., 2014; Stevens et al., 2009; Szpak et al., 2010), reviews that integrate and explain the metadata arising from these studies are few (Bocherens, 2015, 2003). Several studies investigate multiple species, time periods or sites across the mammoth steppe. However, no single study has simultaneously examined the changes in published $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ for all megaherbivore species among different sites and time periods. As well, overlaps in the isotopic composition of species, such as those observed for the $\delta^{15}N$ of horse and mammoth in Germany and Ukraine (Bocherens, 2015), have not been quantified using models of isotopic niche. Mathematical tools such as SIBER (Jackson et al., 2011; Parnell et al., 2010) are being increasingly used in ecological work to provide insight into niche size and the degree of niche overlap between species, and thus the way that different species use and share resources (Layman et al., 2012). These tools could help to understand ecological patterns and changes over time, and between geographic areas.

To understand the mammoth steppe, the ecology of the species that inhabited it must be understood on both the individual and population levels. This thesis will accomplish this through applications of ecological techniques that have not been previously used in the mammoth steppe:

- (1) I examine seasonal changes and individual animal responses through changes in the isotopic composition over the length of an antler and comparison between this tissue and bone.
- (2) I use amino acid δ^{13} C and δ^{15} N to separate dietary and metabolic isotopic signals, allowing me to better understand and classify herbivore and carnivore diets.
- (3) I use SIBER analyses to understand the resource use of animal populations and competition between them.

Using these techniques, I am able to assess the typical megafaunal ecology of the mammoth steppe, as well as to assess ecological responses to climatic and anthropogenic changes over time and between geographic locations.

1.5.2 Organization of the dissertation

This thesis is composed of four distinct research chapters (Chapters 2 through 5), each of which is prepared as a stand-alone article for publication, plus this introduction (Chapter 1) and some broader conclusions (Chapter 6). Supplementary tables and figures for Chapters 2-5 are contained in the appendices.

Chapter 1 provides a general introduction to the mammoth steppe, carbon and nitrogen isotopic systematics of plants and animals, and a review of relevant previous isotopic investigations, with a focus on animal collagen.

Chapter 2 examines the carbon and nitrogen isotopic compositions of collagen from elk, moose and caribou antler and bone. As these tissues that have different growth periods, their isotopic compositions can provide a seasonal signal (antler) and an annual signal (bone). We serially sampled antler to investigate the changes in its isotopic composition over a single season, and compared antler isotopic compositions with those of bone to determine seasonal ecological differences as well as differences through the Late Pleistocene and Holocene. We establish that the isotopic compositions of antlers cannot be directly compared to those of bone when reconstructing a species' diet, and that each tissue provides a distinct set of ecological information concerning that species.

Chapter 3 examines the characteristic but anomalously high woolly mammoth bulk collagen $\delta^{15}N$ using a source (phenylalanine) and trophic (glutamate) amino acid. Using this approach, we established that the woolly mammoth ate a distinct diet or lived in a distinct habitat within the mammoth steppe. In some cases, this habitat may have been shared with horse. Understanding that the woolly mammoth's high $\delta^{15}N_{\text{Bulk}}$ arose from a dietary or habitat source provides insight into the ecology of a keystone herbivore of the mammoth steppe, which provides a starting point to investigate the rest of the megafaunal species.

Chapter 4 further investigates the isotopic compositions of amino acids in mammoth steppe herbivores and carnivores. The $\delta^{15}N$ of 8 amino acids are used to establish the trophic position of a variety of megaherbivores and megacarnivores, and to establish that there likely were differences in the plant types consumed by certain species or individuals. These differences are further evaluated using the δ^{13} C of 9 amino acids. We use LDA of the $\delta^{13}C$ for 7 of these amino acids to classify the diets of each herbivore individual, and of the herbivores consumed by the carnivores. Differences in $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ are linked to differences in diet, such as the consumption of aquatic plants by the giant beaver and decayed plants by horse and woolly mammoth.

Chapter 5 integrates data for $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ of megaherbivores from numerous sites across the mammoth steppe. Using SIBER (Jackson et al., 2011), isotopic niche spaces were defined for each herbivore at each site for four time periods (pre-LGM, LGM, post-LGM and Holocene). Species are shown to have had consistent niche positions and niche overlaps across the mammoth steppe before the LGM. These niches were disrupted during the LGM, and were not re-established post-LGM. This analysis suggests that a major ecosystem shift occurred during the LGM that weakened the ecosystem's stability as a whole, and made it more susceptible to changes from other climatic or anthropogenic effects.

Chapter 6 summarizes the previous chapters and discusses the implications of these new data for our understanding of the mammoth steppe as a whole.

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Chapter 2

2 Carbon and nitrogen isotopic analysis of antlers as a tool to investigate seasonal shifts in ecology

2.1 Introduction

2.1.1 Importance of investigating seasonal variation

Understanding modern and ancient ecology at multiple time scales is key for biological, archeological and paleontological work. Such information is particularly important in high latitude regions, where climate change can have significant impacts. For example, climate change has effects on caribou ecology that are an integral part of high latitude food webs, including food webs that contain humans (Heggberget et al., 2002; Sharma et al., 2009). Carbon and nitrogen isotopic studies of collagen have proven to be valuable methods for investigating Holocene and Pleistocene ecology (e.g. Bellissimo, 2013; Bocherens et al., 2011, 2005, 2001, 1997, 1996, 1994; Drucker and Henry-Gambier, 2005; Drucker et al., 2003a, b; Drucker et al., 2011; Fizet et al., 1995; Fox-Dobbs et al., 2008; Iacumin et al., 2010, 2000; Mann et al., 2013; Metcalfe et al., 2013, 2010; Stevens and Hedges, 2004; Stevens et al., 2009; Szpak et al., 2010). The majority of studies have focused on bone collagen, which provides an isotopic signal representing the past several years of an animal's life, but does not provide discrete information over a shorter time scale (Koch et al., 1994). Interspecies interactions and the level of ecological niche overlap can change seasonally, and a yearly average may not fully represent the variations within the system (Hansen and Reid, 1975; Leslie et al., 1984). Many resources are scarcer during the winter, and may be population-limiting only during this season (Adamczewski et al., 1988; Heggberget et al., 2002). As well, metabolic changes are commonly coordinated seasonally (e.g. pregnancy, birth). Knowing the specific conditions at these times is therefore important to understanding the long-term health of a population (Finstad and Kielland, 2011). Examining the isotopic compositions of tissues with different growth periods and turnover rates than bone provides such a tool.

Here, we focus on antlers, which have a short growth period and do not remodel, and hence should record and retain the isotopic signal of the diet and environment during this tissue's formation. Antlers are cast naturally, making it possible to sample this tissue in modern settings without injuring the animal. As well, antler material is found in some archeological and paleontological contexts (e.g. Madgwick et al., 2013; Miller et al., 2014; Stevens et al., 2008), and thus it has the potential to be valuable for zooarcheological and paleoecological reconstruction. In the present study, antler from elk (*Cervus elaphus*), moose (*Alces alces*) and caribou (*Rangifer tarandus*) was serialsampled to investigate the extent of isotopic variation along the growth length of this tissue. The isotopic compositions of coexisting antler and bone from several sites in Alaska and Yukon Territory (Fig. 2.1) were also determined to gain insight into seasonal and annual ecology and how it might have changed over several time periods during the Late Pleistocene and Holocene. These results were then compared with the ecological variation expected based on previous investigations in order to evaluate the viability of antler as a tool for investigating seasonal ecology and paleoecology.

Figure 2.1 Sites included in this study: ED. Edmonton; HI. Herschel Island; KD. Klondike; NS. North Slope; SK. Selawik. Darker shades of grey represent higher altitudes. Art by Katherine Allan.

2.1.2 Antler and bone growth

Antler growth is a continuous process, with multiple deposition stages spatially overlapping in the tissue (Banks and Newbrey, 1983). As a result, growth lines are not visible in the antler. Nonetheless, the general pattern of deposition occurs from the base to the tip of the antler (Fig. 2.2a; Banks and Newbrey, 1983). The inner tissue of an antler is composed of trabecular bone, and is composed of younger tissue, while the outer tissue is denser and represents a signal from later in the growth season (Fig 2.2b; Finstad and Kielland, 2011). The final stage of collagen deposition involves a layer of woven bone that is deposited over the outside of the basal portions of the antler (Gomez et al., 2013), but this layer is extremely thin (Fig. 2.2b; Kierdorf et al., 2013). During growth, nutrients are supplied through the antler skin, known as velvet. Once this skin is shed, the antlers become dead appendages and there is no remodelling of tissue material (Gomez et al., 2013; Wislocki, 1942). Antler growth does not occur at a continuous pace. On a cellular level, primary osteons in the lower and middle third of elk antlers take 30-40 days to complete growth, while those in the upper third take 20-30 days (Gomez et al., 2013). On a larger scale, antler growth in south-central Alaskan moose was observed to be slow until the first green forage became available in late May; antler development then accelerated, with 50% of antler growth occurring in June (Ballenberghe, 1983). Finstad and Kielland (2011) also note that more rapid caribou antler growth corresponds to months with higher nutrient availability. The precise timing of antler growth initiation and cessation varies between individuals, especially of different age groups, between populations of a species and between species (Chapman, 1975). In males, antler growth typically begins in the late spring and summer, and velvet is shed in the early autumn or late summer before the rut (Ballenberghe, 1983; Chapman, 1975). Caribou are the only species where females as well as males have antlers. The timing of female antler growth is delayed relative to males in some populations, although it tends to fall in the same general seasonal time frame (Chapman, 1975; Leader-Williams, 1988).

Figure 2.2 Sampling strategy: a. Conceptual model of the timing of tissue formation in cranial bone (right occipital condyle) versus antler. Art by Katherine Allan; b. Outermost, outer and inner antler tissue; c. An example of the sampling pattern (arrows) for a caribou skill and antler. Photograph by Tessa Plint.

In contrast to antler, bone forms by either endochondral or intramembranous ossification. Once formed, bone is then remodelled over a period of years, with the exact timing depending on the species. For this reason, bone records an isotopic signal averaged over many years of an individual's life (Balasse et al., 1999; Koch et al., 1994).

2.1.3 Modern seasonal diet and habitat

2.1.3.1 Caribou

Caribou (also known as reindeer) occupy an extremely diverse set of habitats, including forest, alpine and tundra environments. Within each of those regions, there are both migratory and sedentary populations of caribou (Sharma et al., 2009). The seasonal diets and habitats of caribou vary considerably depending on their habitat. Numerous studies have highlighted the role of lichen in caribou diet, both as a year-round food source and as the dominant, though never sole, forage during the winter (Boertje, 1984; Heggberget et al., 2002; Thomas et al., 1996; Thompson and McCourt, 1981). If snow is not overly deep, caribou are able to dig to access lichen (Guthrie, 1990). In areas with tree-cover, they can also access lichen growing on tree bark. Willow is often a large component of spring and summer diets, possibly because it helps caribou to recover their body protein after winter losses (Adamczewski et al., 1988; Bjørkvoll et al., 2009; Boertje, 1984; Shank et al., 1978; Thomas et al., 1996). Herbs, sedges and graminoids are also eaten in large quantities in the spring and summer in some environments (Bjørkvoll et al., 2009; Bjune, 2000; Thompson and McCourt, 1981). In caribou herds that migrated seasonally between tundra and forested environments, calving grounds, used during the spring, are commonly found in tundra regions, and the caribou then migrated into forests during the fall (Kelsall, 1968; Sharma et al., 2009).

2.1.3.2 Elk

Elk (also known as red deer or wapiti) are opportunistic mixed feeders that inhabit habitats ranging from steppe to boreal or temperate forests. Their diets vary with habitat, with the animals consuming graze in prairies and browse in dense forest, or migrating between the two habitats (Christianson and Creel, 2007; Drucker et al., 2008; Dumont et al., 2005; Gebert and Verheyden-Tixier, 2001; Hofmann, 1989; Jenkins and Starkey,

1991; Kufeld, 1973; Morgantini and Hudson, 1989; Prokešová, 2004). In addition to choosing their habitat to obtain the best quality forage, elk also choose dense forest rather than open steppe (i) when they face higher predation risk, (ii) for thermal cover in the winter, and (iii) to obtain forage not covered by heavy snowfall in harsh winters (Christianson and Creel, 2007; Jones and Hudson, 2002).

As elk inhabit highly varied habitats, it is difficult to assign a single diet type to all elk populations for each season. Commonly, spring and fall diets consist mainly of grasses (Jenkins and Starkey, 1991; Morgantini and Hudson, 1989; Stevens, 1966), and summer diets contain a high proportion of shrubs and forbs (Jenkins and Starkey, 1991; Morgantini and Hudson, 1989). Some populations consume higher proportions of conifers during the winter than during the rest of the year (Jenkins and Starkey, 1991), while others consume mainly grasses (Christianson and Creel, 2007; Morgantini and Hudson, 1989), and some shift from graze to browse (graminoids and forbs to trees and shrubs; Hobbs et al., 1981). Some elk populations consume winter diets sufficient to meet maintenance requirements (Hobbs et al., 1981) while others do not (Christianson and Creel, 2007; Morgantini and Hudson, 1989).

2.1.3.3 Moose

Moose (also called Eurasian elk) are browse specialists (Hofmann, 1989; Hörnberg, 2001; Stevens, 1970; Wam and Hjeljord, 2010), and the bulk of their diet is commonly composed of a small number of deciduous or coniferous browse, such as willow, birch, rowan and aspen (Hörnberg, 2001; Wam and Hjeljord, 2010). They tend to eat bark and new twigs and leaves of trees in the spring, and eat primarily dormant twigs during the winter (Belovsky, 1981; Edwards, 1983; MacCracken et al., 1997; Wam and Hjeljord, 2010). When aquatic plants are available in the moose's range, they tend to be a major part of the animal's diet from spring to midsummer (Fraser et al., 1982; MacCracken et al., 1993). Aquatic plant consumption generally declines by midsummer, though in some populations it continues until the fall (Fraser et al., 1982; MacCracken et al., 1993; Peek, 2007). Some studies report substantial forb consumption by moose in the spring and summer (Knowlton, 1960; LeResche and Davis, 1973). Winter maintenance diets have

lower nutrient levels and hence moose are at much higher risk of starvation during the winter than during the rest of the year (Edwards, 1983).

2.1.4 Stable Isotopes

Stable isotope compositions are reported using the δ -notation, which compares sample isotopic ratios to internationally accepted standard isotopic ratios, in units of per mil (‰). The reference standards are VPDB for carbon (Coplen et al., 2006), and AIR for nitrogen (Mariotti, 1983).

2.1.4.1 Plant *δ* ¹³C

Plants utilizing the C_3 photosynthetic pathway comprised the vast majority, and at times the entirety, of the vegetation in North American high latitude regions during the late Pleistocene and Holocene (Gaglioti et al., 2011; Kristensen et al., 2011; Wooller et al., 2007). There is significant overlap in the range of C_3 plant carbon isotopic compositions. Nonetheless, there is a difference in the average δ^{13} C of various plant groups of \geq 1.5 ‰ (Barnett, 1994). From lowest to highest, the average δ^{13} C of terrestrial plants tended to follow the order: shrubs, forbs, graminoids, fungi, lichens (see conceptual model Fig. 1.2; Barnett, 1994; Ben-David et al., 2001; Drucker et al., 2010; Kristensen et al., 2011). Isotopic compositions can also vary among tissues in a plant. In spruce trees, twigs were found to have higher δ^{13} C than needles, likely because of differences in their chemical makeup (Gebauer and Schulze, 1991). This pattern has also been observed for twigs and leaves of deciduous plants (Ehleringer et al., 1992; Tischler, 2004). This can have a seasonal effect on dietary carbon isotopic composition, as twigs of deciduous plants are more likely to be consumed in the winter when leaves are not available.

Evergreen trees usually have higher δ^{13} C than deciduous trees, but this is not universal (Brooks et al., 1997; Kloeppel et al., 1998). Variability in the carbon isotopic composition of a plant can also result from environmental effects. Increased aridity, higher altitudes and higher temperatures can all cause an increase in the $\delta^{13}C$ of a plant (de Bello et al., 2009; Diefendorf et al., 2010; Ehleringer and Cooper, 1988; Ehleringer et al., 1987; Farquhar, 1989; Kohn, 2010; Tieszen, 1991; Wooller et al., 2007). Plants growing under a dense canopy tend to have lower δ^{13} C than those growing in open

grasslands, deserts or tundra (Bocherens et al., 2011). Sea spray can also cause increases in the δ^{13} C of plants (see Sykes et al., 2011 and references therein); however, as this study compares populations within a site rather than between sites, it is unlikely to be a factor.

Freshwater aquatic plants have a much wider range of $\delta^{13}C$ (-47 to -8 ‰) than terrestrial C_3 plants (–32 to –22 ‰; Finlay and Kendall, 2007). This wide range occurs because freshwater algae and macrophytes take up carbon from a variety of sources including atmospheric $CO₂$ and dissolved inorganic carbon. Dissolved inorganic carbonate can originate from a wide range of sources including carbonate minerals, atmospheric carbon dioxide, respiring organic matter and detritus, each of which imparts a distinct $\delta^{13}C$ to the plant (Finlay and Kendall, 2007; Keeley and Sandquist, 1992; LaZerte and Szalados, 1982; Osmond et al., 1981). As well, the degree of isotopic fractionation between DIC and freshwater plants varies with species, the type of carbon taken up, and water velocity, though water velocity does not play a significant role in δ^{13} C of plant material in ponds (Finlay and Kendall, 2007; Finlay et al., 1999; Keeley and Sandquist, 1992; Osmond et al., 1981).

Although there is considerable overlap in the global δ^{13} C of terrestrial and aquatic plants (Finlay and Kendall, 2007; France, 1995; Keeley and Sandquist, 1992), several studies have demonstrated that they can have distinct carbon isotopic compositions at specific sites (Doucett et al., 1996; Fry, 1991; Tischler, 2004). Since moose consume aquatic plants and attached algae from lenthic (still-water) systems, isotopic differences between these aquatic plants and terrestrial plants should be reflected in moose' tissues. At Isle Royale National Park, Michigan, aquatic plants have higher δ^{13} C than terrestrial plants, although the degree of 13 C-enrichment varies because the aquatic plants exhibit a wide range of $\delta^{13}C$ (Tischler, 2004). Higher average $\delta^{13}C$ for aquatic than terrestrial plants has also been found in rivers and lakes in the Old Crow flats of the Yukon, the James Bay region of Quebec (Milligan et al., 2010), and the tundra and associated rivers and lakes at Koroc River, Quebec (Bunn et al., 1989). The same pattern is known for several other lakes (Chikaraishi and Naraoka, 2003; LaZerte and Szalados, 1982), although it is not

universal (France, 1995; Fry, 1991; Rau, 1980). At the majority of sites studied to date, however, aquatic plants consumed by herbivores have higher δ^{13} C than terrestrial browse.

There is also a large overlap in the C/N ratios of terrestrial and aquatic plants (Finlay and Kendall, 2007), but the situation is variable from site to site. At Isle Royale National Park, for example, aquatic plants have lower C/N ratios, and thus more protein, than terrestrial plants (Tischler, 2004). Among terrestrial plants, lichen are particularly poor in protein (Chapin and Shaver, 1988; Drucker et al., 2001).

2.1.4.2 Herbivore collagen *δ* ¹³C

Herbivores have a higher δ^{13} C than the food they eat. For large herbivores, there is generally an increase of ~5 ‰ between their bulk diet and their bone collagen (Drucker et al., 2008). Starvation and nursing can both affect the isotopic composition of an animal. Both involve greater utilization of lipids, either from the animal's own fat reserves (Szpak et al., 2010) or mother's milk (Metcalfe et al., 2010). Lipids have low $\delta^{13}C$ relative to other biological macromolecules, and their preferential utilization may be the cause of the low $\delta^{13}C$ of woolly mammoth collagen, given the cold environments with harsh winters inhabited by these animals (Szpak et al., 2010). It is possible that the species sampled in this study might have been similarly affected. Bones from juvenile individuals were not sampled in the present study, and extremely young animals would be unlikely to grow large antlers. Nursing effects are therefore not considered further in this study.

2.1.4.3 Plant **δ¹⁵N**

The typical pattern of average $\delta^{15}N$ for terrestrial plants encountered in tundra environments, from lowest to highest, is: shrubs, lichens, forbs, graminoids and fungi (Fig. 1.2; Ben-David et al., 2001; Drucker et al., 2010; Finstad and Kielland, 2011; Kristensen et al., 2011; Nadelhoffer et al., 1996). There is a large degree of overlap among them. Forbs in particular have a wide variety of nitrogen isotopic compositions, likely resulting from a large number of possible growth forms, and the existence of nitrogen-fixing forbs with $\delta^{15}N$ close to 0 ‰ (Nadelhoffer et al., 1996; Stewart et al., 2003). Some tissue-based differences have been observed for $\delta^{5}N$. In spruce trees, twigs

have lower $\delta^{15}N$ than needles (Gebauer and Schulze, 1991). Lower $\delta^{15}N$ for stems versus leaves are also known for several deciduous species (Kielland, 2001). Similarly to the pattern observed in carbon, therefore, the isotopic composition of plants consumed could vary seasonally, as browsing herbivores' winter diets consist of twigs rather than leaves. Environmental factors can also affect the $\delta^{5}N$ of a plant. When nitrogen is lost from an ecosystem, it tends to be lost as ^{14}N , causing the plants to become enriched in ^{15}N . The quantity of nitrogen lost from an ecosystem relates to the degree of nitrogen cycling, which is higher in an arid, hot ecosystem than a mesic, cool ecosystem (Ambrose, 1991; Amundson et al., 2003; Drucker et al., 2003a; Heaton, 1987; Stevens and Hedges, 2004; Stevens et al., 2008). Increased salinity, and sea spray, can also lead to higher $\delta^{15}N$ in plants (as discussed in Sykes et al., 2011), but is unlikely to be important in this study.

The δ^{15} N of aquatic plants is less well understood than their carbon isotopic compositions (Finlay and Kendall, 2007). Typical undisturbed freshwater ecosystems have a wide range of $\delta^{15}N$ from -1 to +7 ‰, with the higher and lower values associated with anthropogenic effects (Finlay and Kendall, 2007). Variations occur because of differences in the type and $\delta^{15}N$ of nitrogen dissolved in the water or available in the sediment, and differences in the isotopic fractionation during nitrogen uptake (Finlay and Kendall, 2007). Globally, the mode $\delta^{5}N$ of aquatic plants (+3 ‰) is higher than that of terrestrial plants (-1%) , but there is extensive overlap in nitrogen isotopic compositions (France, 1995). Discrete differences are evident at some sites, and in the majority of those cases, aquatic plants have higher $\delta^{15}N$ than terrestrial plants (Ben-David et al., 2001; Delong and Thorp, 2006; Finstad and Kielland, 2011; Fry, 1991; McArthur and Moorhead, 1996; Milligan et al., 2010; Tischler, 2004).

2.1.4.4 Herbivores collagen *δ* ¹⁵N

There is an increase of +2 to + 5 ‰ in the $\delta^{5}N$ from diet to consumer collagen (Gannes et al., 1998; Koch, 2007; Koch et al., 1994). Physiological changes can also affect the nitrogen isotopic composition of an animal, and $\delta^{15}N$ are expected to be higher for animals undergoing nutritional stress (Gannes et al., 1998; Hobson et al., 1993; Kelly, 2000; Koch, 2007; Polischuk et al., 2011), though this may only occur when animals

experience a threshold level of extreme starvation (Kempster et al., 2007). Increases in δ^{15} N are likewise expected for animals living in arid environments (Kelly, 2000; Sealy et al., 1987; Sponheimer et al., 2003). Nursing young also experience an increase in $\delta^{5}N$ (Metcalfe et al., 2010), but this trophic effect is not expected to be encountered in the present study.

There is some concern that antlers, being a rapidly growing tissue, would have a smaller nitrogen isotopic spacing ($\Delta^{15}N_{Tissue-Diet} = \delta^{15}N_{Tissue} - \delta^{15}N_{Diet}$) between antler collagen and diet than exists between bone and diet (Finstad and Kielland, 2011). Waters-Rist and Katzenberg (2010) reviewed previous studies that found such a decrease for several types of rapidly growing tissues, but did not observe it in their own investigation of bone, and it is unknown if this phenomenon occurs in antlers. Antler-specific studies have suggested other tissue-specific effects may occur. Towards the end of antler growth, there may be increased mobilization of protein from bones to the antler. In this case, the $\delta^{15}N$ of antler tips would to trend towards the $\delta^{5}N$ of bone. As well, if the protein mobilized from the bone is recycled through the body before being deposited in the antler, then a metabolic effect could cause an additional increase in antler $\delta^{5}N$ (Madgwick et al., 2013; Osborne, 2013).

2.1.4.5 Isotopic analysis of shifting diets

Changes in diet can be recognized when distinct differences in isotopic compositions exist among dietary sources, and animal tissues preserve this seasonal or life stage record (e.g. Peterson and Fry, 1987). Such changes in animal tissue $\delta^{13}C$ and $\delta^{15}N$ have been used previously to study caribou, moose and elk dietary and habitat change over seasons and years. Studies of moose using hoof keratin and blood isotopic compositions have confirmed higher aquatic plant and shrub- and tree-leaf consumption in summer, and higher twig consumption in winter, based on lower δ^{13} C and lower δ^{15} N during summer than winter (Ben-David et al., 2001; Kielland, 2001; Tischler, 2004). Temporal variations in the amplitudes of isotopic changes of hoof keratin, however, suggest a high degree of dietary mixing and individual dietary choice (Kielland, 2001). In the absence of substantial consumption of aquatic plants, moose hair showed no distinctive seasonal

isotopic shifts (Drucker et al., 2010). The study of caribou using the isotopic composition of tooth dentin has revealed that individual caribou within a population ate distinct diets with a high level of individual dietary choice (Drucker et al., 2012) and increased nitrogen recycling and lichen consumption during winter, which caused higher tissue δ ¹³C and δ ¹⁵N in winter and spring than summer or fall (Drucker et al., 2001). Higher δ ¹³C was also found for blood and hoof keratin that corresponded to winter, again suggesting more lichen consumption in winter and more vascular plant consumption during the rest of the year (Barnett, 1994; Ben-David et al., 2001). Caribou hoof keratin, however, had the highest $\delta^{5}N$ in fall, suggesting consumption of a forage source with high $\delta^{15}N$, such as mushrooms.

Archaeological and palaeontological studies have previously employed antler isotopic compositions, alongside those of bone, to understand species ecology and to construct an isotopic herbivore baseline (France et al., 2007; Kuitems et al., 2015; Madgwick et al., 2013; Osborne, 2013; Stevens et al., 2010, 2008; Sykes et al., 2011), while noting potential pitfalls in the comparison of different tissues. Some studies have used these differences to investigate the origin of deer antler in Roman times (Madgwick et al., 2013; Miller et al., 2014), though limited work has been undertaken to expressly compare the isotopic compositions of archaeological bone and antler (Miller et al., 2014; Osborne, 2013).

Isotopic variability within antler has been investigated previously for modern animals. A feeding study found no isotopic variation along the length of the antler for deer fed a consistent diet (Darr and Hewitt, 2008). The $\delta^{5}N$ of inner and outer antler tissues of Alaskan female caribou were used to investigate the timing and proportion of shrub use (Finstad and Kielland, 2011). Lower $\delta^{5}N$ for spring than summer antler tissue was related to a higher proportions of shrubs in the spring diet. Higher shrub use in spring correlated to poorer body condition at the end of the winter, making this a potential technique to investigate the health of a population. A study of wild deer investigated the extent to which a single sample of antler could be used to assess the isotopic composition of the whole (Miller et al., 2014; Osborne, 2013). Within the limited isotopic variability that was observed, changes in δ^{13} C were attributed to dietary shifts during the growing

season, and higher $\delta^{5}N$ towards the tip of the antler to increased nitrogen supply from bone. These studies found that deer antler had higher $\delta^{3}C$ and lower $\delta^{5}N$ than bone (Miller et al., 2014; Osborne, 2013).

2.2 Methods

2.2.1 Sample selection

Caribou, elk and moose specimens were obtained from the Edmonton area (Edmonton), the Klondike area (Klondike), Herschel Island (Hershel Island) and the Selawik Wildlife Refuge and Surround Areas (Selawik) (Fig. 2.1). Information about sample location and age is summarized in Appendix A. Stable isotopic data for antlers that were serially sampled (sampled several times along the growing length) are listed in Appendix B. The dimensions of the antler are also listed in Appendix B, as well as whether the antler was broken along the length that that it was sampled, or was a complete specimen. All stable isotopic data, including previously reported data for antler and bone for the North Slope (Mann et al., 2013) and Selawik (Druckenmiller, 2008), are also summarized in Appendix C.

2.2.2 Collagen extraction

For specimens from which only a single sample was taken, this tissue was removed using a Dremel $^{\circledR}$ cutting wheel. Sampling along the length of an antler specimen was performed using a 0.625 cm drill core attached to a drill press. These samples were taken every 10 cm along one side of one beam of the antler, with the base of the antler designated as 0 cm (Fig. 2.2b). Cancellous bone was removed from bone samples to allow for sampling of purely cortical bone. Outer antler tissue was preferentially sampled when the antler was thick. The surfaces of antler and bone were removed using a carbide burr attachment to the Dremel[®], and the new surface then washed with deionised water and dried at room temperature.

Lipid extraction was performed on a subset of seven samples using a modified Bligh and Dyer method (Bligh and Dyer, 1959). Prior to collagen extraction, these samples were treated three times each with a 2:1 chloroform:methanol solution (v:v) for 15 minutes.

The samples were then dried at room temperature. Comparison of unextracted versus lipid-extracted fractions showed that the isotopic compositions obtained from the two approaches differ by a maximum of \pm 0.1 ‰ (SD) for both $\delta^{13}C$ and $\delta^{15}N$ (Appendix D). For this reason, unextracted and lipid-extracted fractions are considered to be isotopically equivalent in any discussion that follows.

Collagen extraction was performed at room temperature following the modified Longin method (see method in Metcalfe et al., 2010). Samples were dissolved for 24 hours in 0.25 M and subsequently in 0.5 M HCl with the acid changed every 1-3 days until the samples were demineralized. Samples were then rinsed 3 times with deionized water. Humic substances were removed by treatment with 0.1 M NaOH for 20 minutes at room temperature, which was repeated until the liquid remained colourless. The samples were then rinsed seven times with deionized water, and the pH was adjusted to less than 3. They were then placed in a 90°C oven for approximately 16 hours to solubilise the collagen. The solubilised collagen was decanted and dried at 90°C before being weighed for analysis.

2.2.3 Stable isotope measurements

The carbon and nitrogen isotopic compositions of the collagen were measured using a Costech elemental combustion system (ECS 4010) attached to a Thermo-Scientific Delta V stable isotope ratio mass spectrometer (IRMS) operated in continuous-flow mode. The results are presented in Appendices B (serial samples) and C (single samples). The samples were measured over a total of eleven analytical sessions. The carbon isotopic data were calibrated to VPDB using a two-point scale anchored by either NBS-22 (± 0.0) % one standard deviation (SD), $n = 24$; accepted $\delta^{13}C = -30.03$ %; Coplen et al., 2006), and IAEA-CH-6 (\pm 0.1 ‰ SD, n = 37; accepted δ^{13} C = -10.45 ‰; Coplen et al., 2006) or USGS-40 (\pm 0.1 ‰ SD, n = 44; accepted $\delta^{3}C = -26.39$ ‰; Coplen et al., 2006) and USGS-41 (\pm 0.2 ‰ SD, n = 35; accepted $\delta^{3}C = +37.63$ ‰; Coplen et al., 2006). The nitrogen isotopic data were calibrated to AIR using a two-point scale anchored by USGS-40 (\pm 0.1 ‰ SD, n = 43; accepted $\delta^{5}N = -4.52$ ‰; Qi et al., 2003) and either IAEA-N2 $(\pm 0.2 \text{ % SD}, n = 35; \text{ accepted } \delta^{15}N = +20.39 \text{ % }$, Qi et al., 2003) or USGS-41 ($\pm 0.4 \text{ % }$

SD, n = 33; accepted $\delta^{15}N = +47.57 \%$; Qi et al., 2003). These standards were also used for calibration of the carbon and nitrogen contents and C/N ratio of each sample. When these standards were not used in the calibration curve, they were used measured as unknowns. IAEA-CH-6 (measured δ^{13} C = -10.5 ‰), USGS-40 (measured δ^{13} C = -26.4 %o), USGS-41 (measured $\delta^{13}C = +37.8$ %o, measured $\delta^{15}N = +47.0$ %o), IAEA-N1 (measured $\delta^{15}N = +0.5 \%$; accepted $\delta^{15}N = +0.43 \%$; Qi et al., 2003) and IAEA-N2 (measured $\delta^{15}N = +20.4 \%$) all had similar isotopic compositions to their accepted values. Every analytical session also included an internal keratin laboratory standard (MP Biomedicals Inc., Cat. No. 90211, Lot No. 9966H) for which the following average results (SD) were obtained (n = 72): $\delta^{13}C = -24.1 \pm 0.1 \%$, $\delta^{15}N = +6.4 \pm 0.1 \%$, C = 48 \pm 2 wt.%, N = 15 \pm 1 wt.%, and atomic C/N ratio = 3.7 \pm 0.2. These compare well with accepted values of $\delta^{13}C = -24.0 \%$, $\delta^{15}N = +6.4 \%$, $C = 46.8$ wt.%, $N = 14.6$ wt.% and atomic $C/N = 3.7$. A subset of samples ($n = 25$) were analyzed in duplicate or triplicate; reproducibility (SD) ranged from \pm 0.0 to \pm 0.2 ‰ for $\delta^{13}C$, and from \pm 0.0 to \pm 0.3 ‰ for δ^{15} N, with an average for both of \pm 0.1 ‰.

2.2.4 Radiocarbon dating

Radiocarbon dates were obtained for a subset of samples. Collagen was extracted, combusted, graphitized and dated at the University of Arizona Accelerator Mass Spectrometry (AMS) Laboratory. Dates are presented as uncalibrated radiocarbon years before present (1950), and are listed in Appendices A, B and C alongside previously published dates (Druckenmiller, 2008; Kristensen and Heffner, 2011; Mann et al., 2013; Meiri, 2010; Zazula, pers. comm., 2015).

2.2.5 Mathematical treatment

Antler-bone pairs were tested to determine if the populations were statistically identical using the Mann-Whitney-Wilcoxon test, as this test does not assume parametric populations (Bauer, 1972). Carbon and nitrogen isotopic compositions were tested separately, and the data sets were assumed to be independent. A *p*-value of 0.05 was selected. The test was run in R version 3.1.1 (R Core Team, 2014) using the R Studio interface version 0.98.1083, and the results are summarized in Table 2.1.
The Herschel Island caribou bone and antler samples postdate the Industrial Revolution (post-bomb period; Appendix A). A Suess effect correction was therefore made for the lower carbon isotopic composition of the atmosphere resulting from the burning of fossil fuels following the method of Long et al. (2005). Because the exact date for this specimen is not known, the mid-point (1987) between the start of the post-bomb time period (1964) and the time of collection (2009) was used to make the Suess effect correction.

2.3 Results

2.3.1 Preservation

Applying the preservation criterion for bone to both bone and antler samples, all samples are considered well preserved (see Appendices B and C). The collagen extraction yield ranges from 5.7 to 19.4 % for bone, and 1.4 to 44.2 % for antler, above the 1% limit below which original isotopic compositions may be affected (van Klinken, 1999). A higher yield of collagen from antler than bone was expected, as antler contains more organic matter than bone (Chapman, 1975). The sample with the lowest yield was obtained midway along the length of a serially sampled antler, and its $\delta^{13}C$ and $\delta^{15}N$ are consistent with other samples from the same antler. The C/N ratios of the samples range from 3.0 to 3.4, within the accepted range of 2.9-3.6 for well-preserved bone samples (Ambrose, 1990; DeNiro, 1985; van Klinken, 1999). The carbon and nitrogen contents range from 33-46 wt.% and 12-17 wt.%, respectively, which also meet the preservation criterion of \geq 13 wt.% for carbon and \geq wt.4.8 % for nitrogen (Ambrose, 1990; DeNiro, 1985; van Klinken, 1999).

2.3.2 Collagen stable isotope compositions

2.3.2.1 Intra-tissue variation

Carbon and nitrogen isotopic compositions have been measured along the length of an antler for eight specimens (one Herschel Island caribou, three Klondike caribou, two Klondike elk and two Klondike moose; see Figs. 2.3; 2.4; Appendix B). For all antlers, the observed isotopic variation is greater than typical analytical error for at least one of

Figure 2.3 (left) Carbon isotopic compositions of serially sampled antler collagen (Herschel Island; Klondike): a. caribou antler, post-bomb; b. caribou antler; c. caribou antler, >41,100 ¹⁴C BP; d. caribou antler, 29,570±970 ¹⁴C BP; e. elk antler, 11,675±45 ¹⁴C BP and h. moose antler, 1,363±35 and 1,197±27 ¹⁴C BP. Black stars represent samples from Herschel Island; blue diamonds represent samples from the Klondike.

Figure 2.4 (right) Nitrogen isotopic compositions of serially sampled antler collagen. Description as in Figure 2.3.

the two isotopic systems considered (\pm 0.2 ‰ for δ ¹³C, \pm 0.3 ‰ for δ ¹⁵N, as estimated using the maximum SD of sample replicates).

Four of the antlers (three Klondike caribou and one moose) exhibit generally decreasing *δ* ¹³C from the base of the antler to its tip, with the total change ranging from *–*0.4 ‰ to *–* 1.1 ‰ between the base and the tip of the antler (Figs. 2.3b-d, g). Two antlers (one Herschel Island caribou and one moose) have δ^{15} N that increases by 0.8 ‰ from the antler base to its tip (Figs. 2.4a, g) and two antlers (one Klondike caribou, one elk) have δ ¹⁵N that decreases by 0.4 ‰ from the base to the tip (Figs. 2.4d, f). Two antlers (Klondike caribou and moose) display variations both in δ^{13} C and δ^{15} N (Figs. 2.3d, g; 2.4d, g) and two antlers (moose and elk) show no isotopic variation along the length of the antler (Figs. 2.3e, h; 2.4e, h). The change in isotopic composition with length along the antler is not always smooth, but a between-serial sample variation from the general isotopic trend that is larger than analytical error occurs for only once specimen (Fig. 2.4g). While the majority of the antlers are not complete tissues (Appendix B), sufficient tissue was preserved for isotopic shifts to be observed in the majority of antlers, even in cases where much of the antler was lost (e.g. Fig. 2.4f). The two antlers without isotopic shifts from base to tip both have long sampling lengths intact. While it is possible that isotopic shifts occurred during antler growth but were lost when the specimen was broken, it is more likely that the individuals had consistent diet and habitat during the period of antler growth.

2.3.2.2 Inter-tissue variation

Paired antler and bone specimens were available for one Klondike moose and one Herschel Island caribou. To allow for more analysis, comparisons were also made between antler and bone of populations composed of multiple individuals from a single site (see Fig. 2.5 and Appendix C). The difference in average carbon or nitrogen isotopic compositions between bone and antler for a population of one species at one site was calculated as $\delta_{\text{Bone}} - \delta_{\text{Antler}}$ ($\Delta_{\text{Bone-Antler}}$). The Mann-Whitney-Wilcoxon test was also used to check for significant differences between the isotopic compositions of bone and antler for a population (Table 2.1).

Figure 2.5 Isotopic compositions of antler and bone collagen: a. caribou; b. elk, and c. moose. Paired antler and bone samples for a single individual are joined by a line. The number of specimens in each group is listed in parentheses in the legend.

			p -value		p -value
		$\Lambda^{13}C_{(Bone-)}$	(Bone,	$\Delta^{15}N_{(Bone-)}$	Bone,
Species	Site	Antler)	Antler)	Antler)	Antler)
Caribou	Edmonton	0.2	1.00	1.0	0.51
Caribou	Herschel Island	1.4	N/A	1.3	N/A
Caribou	Klondike	0.6	0.21	2.7	0.04
Caribou	Selawik	0.6	0.05	-0.5	0.39
Elk	Klondike	-0.7	0.12	-0.4	0.13
Moose	Klondike	-0.3	0.17	0.9	0.06
Moose	North Slope	0.7	0.07	1.6	0.12
Moose	Selawik	0.1	N/A	2.2	N/A

Table 2.1 Comparison of the isotopic composition of bone and antler in a population for various species and sites. The difference in carbon isotopic composition between bone and antler for one species at one site, or $\delta^{13}\rm{C}_{\rm{Bone}}$ - $\delta^{13}\rm{C}_{\rm{Antler}},$ is given as $\boldsymbol{\Delta}^{13}\boldsymbol{\mathrm{C}}_{\text{(Bone-Antler)}}$. The significance of a Mann-Whitney-Wilcoxon test between the two **tissues is given as p value (Bone, Antler), with differences** $p \leq 0.05$ **treated as significant and shown in bold.**

The $\delta^{15}N$ of Klondike caribou and the $\delta^{13}C$ of the Selawik caribou are the only groups that have significantly different isotopic compositions between bone and antler at $p \leq$ 0.05. Despite the lack of statistical significance, however, there appears to be some trends in the data, which are generally consistent within a species. The Herschel Island caribou specimen has higher δ^{13} C and δ^{15} N in bone than antler, as is also observed for the populations of caribou at Edmonton and the Klondike and carbon isotopic compositions at Selawik. The Klondike elk specimens have lower δ^{13} C and δ^{15} N in bone than antler. Moose show no strong pattern of $\Delta^{13}C_{\text{Bone-Antler}}$ across the Klondike, North Slope and Selawik sites. Moose bone, however, has higher $\delta^{5}N$ than antler at all three of these sites. These patterns are generally consistent with the result for the Klondike moose boneantler pair (Appendix C).

2.3.3 Isotopic variation over time

There are several dated specimens for each site and species considered here (see Appendices A and C and Figs. 2.6-2.8). Caribou specimens span an age range from $>41,100$ ¹⁴C BP (infinite) to post-bomb. Elk specimens have dates ranging from 12,100 to 9,064 14 C BP, which spans the transition from the Pleistocene to the Holocene. Radiocarbon dates for the moose specimens range from 10,790 to 80⁻¹⁴C BP, with the majority of the specimens being younger than 3.000^{14} C BP.

Statistical testing for changes in stable isotopic composition of antler or bone over the time periods considered here is impossible without additional dated specimens. Nonetheless, the existing data can still be examined for general trends. No strong patterns in δ^{13} C are observed for caribou or moose; instead, the majority of isotopic variation appears to be site- or tissue-specific, rather than time-dependent (Figs. 2.6a; 2.8a). Collagen δ^{13} C for elk antler and bone appear to decrease from oldest to youngest during the Terminal Pleistocene to Holocene transition (Fig. 2.7a). Caribou $\delta^{15}N$ reaches a maximum between $25,000-30,000$ ¹⁴C BP, and decreases thereafter (Fig. 2.6b). No timedependent trend is apparent in $\delta^{15}N$ for elk or moose (Figs. 2.7b; 2.8b).

2.4 Discussion

2.4.1 Antler-specific physiological factors

There is general agreement that the δ^{13} C of antlers relates to the isotopic composition of the food consumed by the animal during the antler growth period (Darr and Hewitt, 2008; Osborne, 2013). Some authors suggest that dietary changes during antler growth are also a main control on their nitrogen isotopic compositions (Finstad and Kielland, 2011). Antler-specific physiological factors, however, may also play a defining role in determining antler $\delta^{15}N$. Increasing levels of resorption and routing of bone protein to antler during the growth season would cause antler isotopic compositions to be more similar to bone towards the antler tip (Osborne, 2013). If routing was the primary control on the nitrogen isotopic composition of antlers, however, the observed shifts would all be of a similar magnitude and direction within a species, as was observed previously (Miller et al., 2014; Osborne, 2013). In the present study, one Klondike caribou antler has

Figure 2.6 Isotopic compositions of caribou collagen from specimens younger than 45,000 ¹⁴C BP: a. δ^{13} C; b. δ^{15} N. The number of specimens in each group is listed in **parentheses in the legend.**

Figure 2.7 Isotopic compositions of elk collagen from specimens younger than 15,000 ¹⁴C BP: a. δ ¹³C; b. δ ⁵N. The number of specimens in each group is listed in **parentheses in the legend.**

Figure 2.8 Isotopic compositions of dated moose collagen from specimens younger than 15,000 ¹⁴C BP: a. δ^{13} C; b. δ^{15} N. The number of specimens in each group is **listed in parentheses in the legend.**

decreasing nitrogen isotopic compositions from the base to the tip of the antler (Fig. 2.4d), other Klondike specimens have unchanging nitrogen isotopic compositions along the antler length (Figs. 2.4b, c), and Herschel Island caribou antler has pattern of increasing $\delta^{15}N$ (Fig. 2.4a). In both Klondike and Herschel Island populations, caribou bone has higher average $\delta^{15}N$ than antler. Collectively, these data suggest that routing from bone is not a primary control on the nitrogen isotopic composition within antler.

We suggest instead that isotopic changes in diet are the main control on antler $\delta^{5}N$. Nonetheless, the differences between the isotopic composition of bone and antler observed in this study are generally not statistically significant, and in the case of the δ^{15} N of Selawik caribou, do not always follow the same pattern for a species. This may reflect the lack of strong temporal control on these specimens. Previous work has suggested that the isotopic compositions of plants have changed over the Pleistocene and Holocene (Bocherens et al., 2011; Drucker et al., 2003a; Fox-Dobbs et al., 2008; Mann et al., 2013; Stevens and Hedges, 2004; Stevens et al., 2008), and the specimens analysed here do not all date to the same time period. Some of the variation may also relate to individual dietary choices within a population, as observed by the differences in the amount of variation observed along the length of an antler within a species. Future feeding studies are needed to elucidate the exact controls on the isotopic compositions of each species. In general, however, it appears that the model shown in Figure 2.2a fairly represents the isotopic signals that can be obtained from antler and bone tissue.

The typically non-linear change in carbon and nitrogen isotopic compositions of serially sampled antler along the antler length has been observed previously (Miller et al., 2014; Osborne, 2013). There are a number of possible explanations for this behaviour. (1) There may be increased dietary routing from if forage is less available. As discussed earlier, however, this is unlikely to be the main process, since the Klondike moose antler for which this change is most prominent (Fig. 2.5g) shifts away from the average $\delta^{5}N$ of Klondike moose bone as growth continued. (2) Depending on the forage available in an animal's habitat, multiple shifts in diet could occur. Also, antler growth does not occur at a continuous pace. Shifts in diet, therefore, will be less represented during slower than faster growth by evenly spaced serial sampling. (3) Collagen deposition occurs both

along the length and across the width of the antler. Differences in the amounts of inner tissue included in the sample, either because of changes in antler width or variations in the extent of weathering of outer antler tissue, could affect the bulk isotopic signal. More detailed sampling of antler from a population with a known diet, and guided by histological mapping of the tissue, is needed to evaluate these possibilities more fully.

2.4.2 Seasonal, yearly, and inter-annual variation

2.4.2.1 Caribou

The caribou antler from Herschel Island, which increases in $\delta^{15}N$ along the length of the antler (Fig. 2.4a), is likely from a female or a juvenile male, based on the relatively small antler size. Modern studies of caribou highlight the importance of browse as one component of spring and summer diets, in conjunction with herbs, sedges and graminoids (Adamczewski et al., 1988; Bjørkvoll et al., 2009; Bjune, 2000; Boertje, 1984; Shank et al., 1978; Thomas et al., 1996; Thompson and McCourt, 1981). However, the proportion of each dietary source used may have changed over the antler growth period. Finstad and Kielland (2011) previously reported female Alaskan caribou to have increasing antler δ^{15} N over the growth period, which they attributed to consumption of less browse and more graminoids and forbs. While there are no trees on Herschel Island, this caribou may have consumed substantial amounts of ground shrubs during the late spring, but decreased its use of this forage over the summer.

Of the three caribou antlers from Klondike, two show decreases in $\delta^{13}C$ from antler base to tip, with no shift in $\delta^{15}N$ (Figs. 2.3b-c; 2.4b-c). One was from was from a female or juvenile male (Figs. 2.3b; 2.4b) and the other was from an adult male which dated to $>41,100$ ¹⁴C BP (Figs. 2.3c; 2.4c), as identified based on their size (Appendix B). This δ ¹³C pattern may arise from reduced consumption of lichen as other, more nutrient-rich forage became available, but as lichen is protein-poor (Chapin and Shaver, 1988; Drucker et al., 2001), it may not have contributed substantially to the $\delta^{15}N$ signal. The decreasing δ ¹³C and δ ¹⁵N along the length of the third antler (Figs. 2.3d; 2.4d), which is from an adult male, likely indicates a dietary shift to consumption of more browse (ground shrubs) and fewer graminoids and forbs, and, perhaps for carbon, lichen (see Fig. 1.2).

The lower δ^{13} C is unlikely to indicate a canopy effect; this antler was dated to \sim 29,570 ¹⁴C BP, at which time there was limited tree cover in the Klondike (Zazula et al., 2014). The decreasing δ^{13} C and δ^{15} N could also indicate an increase in aridity during antler growth. Isotopic analysis of modern antlers for years of known seasonal changes in aridity could be used to test this idea. The higher $\delta^{15}N$ and $\delta^{13}C$ of bone than antler in the paired caribou specimen from Herschel Island and more generally for this species (Fig. 2.5a; Table 2.1) mirrors that reported by (Drucker et al., 2001) and likely has the same cause, that is, bone acquires higher $\delta^{13}C$ from lichen in their winter diet and higher $\delta^{15}N$ from winter food shortages that led to increasing nitrogen recycling. In short, these data support the idea that lichen use was most important during the winter and decreased during the rest of the year.

Caribou were present in North American high latitude environments over the entirety of the time measureable using radiocarbon methods (Guthrie, 2006; Mann et al., 2013), and sampled over this range in the present study (Fig. 2.6). The Herschel Island caribou samples are not included in these comparisons because of the uncertainty associated with the Suess effect correction. The caribou collagen δ^{13} C for this limited number of samples is relatively constant over time (Fig. 2.6a). The peak in caribou δ^{15} N at ~30,000 to 25,000 14° C BP and subsequent decrease towards the Pleistocene/Holocene transition and into the Holocene (Fig. 2.6b) have been observed in multiple studies of megafaunal herbivore bone (Bocherens et al., 2011; Drucker et al., 2003b; Fox-Dobbs et al., 2008; Mann et al., 2013; Stevens and Hedges, 2004; Stevens et al., 2008) and may indicate a difference in available forage, such as an increase in browse, or an increase in moisture from the melting of permafrost (Guthrie, 2006; Stevens and Hedges, 2004; Stevens et al., 2008; Zazula et al., 2014).

2.4.2.2 Elk

The decrease in $\delta^{15}N$ of the elk antler from 9,064 ¹⁴C BP over the growth period potentially corresponds to a shift from a graze to a browse diet (Fig. 2.4f), as has been observed for several modern elk populations (Hobbs et al., 1981). Given that the collagen δ ¹³C did not change (Fig. 2.3f), this animal may have consumed a range of plant types

that grew in similar habitats. The elk antler from $11,675$ ¹⁴C BP, which shows no notable changes in collagen isotopic composition along the length of the antler (Figs. 2.3e; 2.4e), may have had a smaller range that limited access to wide a variety of plant or habitat types. Variability in the diet of ancient elk individuals is not unexpected, given the opportunistic and varied feeding patterns of modern populations (Christianson and Creel, 2007; Drucker et al., 2008; Dumont et al., 2005; Gebert and Verheyden-Tixier, 2001; Hofmann, 1989; Jenkins and Starkey, 1991; Kufeld, 1973; Morgantini and Hudson, 1989; Prokešová, 2004).

The higher average nitrogen isotopic compositions of antler than the bone in elk from the Klondike (Fig. 2.5b; Table 2.1) likely relate to seasonal differences in diet. As elk are mixed-feeders, they may consume more graminoids and forbs than browse during the fall and winter than during the spring and summer, consistent with some modern elk populations (Christianson and Creel, 2007; Morgantini and Hudson, 1989). It is interesting that the spring and summer diets have lower $\delta^{15}N$ than the fall and winter diets, opposite to that generally observed for caribou and moose (Fig. 2.5; Table 2.1). The caribou and moose nitrogen isotopic variation may indicate winter starvation, as discussed earlier. The lack of such an isotopic signal in elk may suggest they did not experience high levels of winter starvation in the Klondike during the Pleistocene/Holocene transition. Winter diets that meet maintenance requirements have been observed for some modern elk populations (Hobbs et al., 1981).

Elk are suggested to have entered North America across the Bering Land Bridge around $13,000$ ¹⁴C years BP and to have moved southward after the Pleistocene/Holocene transition (Guthrie, 2006; Meiri et al., 2014). This is consistent with the dated individuals examined in the present study (Fig. 2.7). There is a strong pattern of decreasing $\delta^{13}C$ in elk bone and antler collagen from \approx 15,000 to 10,000⁻¹⁴C BP (Fig. 2.7a), whereas no pattern is apparent in $\delta^{15}N$ (Fig. 2.7b). The change in $\delta^{13}C$ may relate to increasing consumption of plants that grew in dense canopy cover, consistent with the rise of boreal forests in these environments at this time (Zazula et al., 2014), as has been suggested to have occurred in other environments (Drucker et al., 2003a; Drucker et al., 2008). Alternatively, it may reflect variations in the $pCO₂$ of the atmosphere, which caused

changes in the δ^{13} C of the plants at the base of the food web (see discussions in Bocherens, 2003; Iacumin et al., 2006; Stevens and Hedges, 2004). As there are limited dated specimens available, and the dated specimens include both antler and bone, this pattern may also arise in part from seasonal differences between the two tissues, as we suggested for the differences in average elk $\delta^{15}N$. This seems a less parsimonious explanation, however, as both antler and bone show the same trend of decreasing $\delta^{13}C$ values over time, and no such temporal trend was seen in $\delta^{15}N$.

2.4.2.3 Moose

The increase in collagen $\delta^{15}N$ from base to tip of the moose antler dated to 1,197 ¹⁴C BP (Fig. 2.4g) likely corresponds to a seasonal increase in the consumption of aquatic plants, which often have distinct isotopic compositions from terrestrial plants, as hypothesized in previous isotopic studies of moose (Kielland, 2001; Tischler, 2004). Aquatic plants typically have higher protein contents than browse, which would further accentuate the increase in δ^{15} N. The concomitant decrease in δ^{13} C (Fig. 2.3g) could indicate a habitat where aquatic plants had lower δ^{13} C than browse, or a diet involving increased consumption of leaves relative to twigs (Tischler, 2004). The lack of significant variation in collagen δ^{13} C or δ^{15} N between the base and tip of the antler of the other moose specimen (Figs. 2.3h; 2.4h) suggests invariant forage over the antler growth period, and perhaps the lack of access to aquatic plants within this individual's range.

Higher $\delta^{15}N$ was observed for bone than antler both for the paired moose specimen and for the populations at all sites (Fig. 2.5c; Table 2.1). None of the typical dietary or habitat shifts of the moose are expected to produce a higher $\delta^{15}N$ for fall and winter than spring and summer. For example, an increase in aquatic plant or leaf consumption (rather than twigs) in spring and summer would be expected to increase the $\delta^{5}N$ of the antler. The higher $\delta^{15}N$ of the bone may be a metabolic signal, indicating that moose are undergoing sufficient winter dietary restrictions to cause increased nitrogen recycling that drove $\delta^{15}N$ to higher values in their bones.

The dated moose specimens cover the range expected for entry into North American high latitude environments at the end of the Pleistocene (Guthrie, 2006; Mann et al., 2013). There is no significant pattern of isotopic variation from \sim 10,000⁻¹⁴C BP to pre-industrial revolution times, despite a larger dataset than for caribou or elk. This time period may have undergone fewer changes in the isotopic composition of plants, moose might have selected plants whose isotopic compositions tended not to change over time, or the wider range of isotopic compositions known for aquatic plants may obscure other variation that has occurred.

2.5 Conclusion

The main controls on the carbon and nitrogen isotopic composition of antler collagen are diet and the physiological state of the animal. Antler-specific metabolic effects do not exert a primary control on antler collagen isotopic composition. Such isotopic measurements of antler are therefore useful for investigating seasonal ecology. At a minimum, sampling of the base and tip of an antler can provide information about the spring and summer ecology of that animal. Isotopic variation over the length of the antler can have multiple causes: (1) individual dietary choice, potentially related to the relative nutrient levels of available forage, as reflected in decreased lichen consumption of some caribou during summer; (2) habitat differences such as access to aquatic plants during summer, as suggested for one moose, and (3) environmental differences, such as increased levels of aridity over summer, as was suggested for one caribou.

Comparisons between bone and antler collagen isotopic compositions demonstrate differences in the ecology of the species between summer and the rest of the year. The carbon isotopic compositions of bone versus antler highlight the varied diet between the summer and the rest of the year, in particular, the substantial contribution of lichen to the winter diet of caribou. The nitrogen isotopic compositions of the Holocene moose and Holocene and Pleistocene caribou both suggest that these species faced high levels of winter stress, almost certainly from starvation. Interestingly, elk from the Pleistocene/Holocene transition did not seem to have faced the same high levels of winter starvation.

The ability to pinpoint ecological differences over annual time periods is particularly useful for ecological reconstruction. Hence further investigation of the information held by the isotopic composition of antler tissues represents a fruitful direction for learning more about seasonal variations in diet and habitat, and more broadly climate-related changes that may have contributed to the extirpation or extinction of Pleisotocene and Holocence megaherbivores.

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Chapter 3

3 Solving the woolly mammoth conundrum: amino acid 15 N-enrichment suggests a distinct forage or habitat¹

3.1 Introduction

 \overline{a}

Woolly mammoths (*Mammuthus primigenius*) were keystone herbivores in the Pleistocene mammoth steppe (Owen-Smith, 1987; Zimov et al., 1995). This megacontinental biome was inhabited by a now-extinct community of mammals, dominated by woolly mammoth, horse and bison. The mammoth steppe reached from north-western Canada, across the exposed Bering Isthmus, to Western Europe (Bocherens, 2003; Guthrie, 1982). The ecological role of woolly mammoths within this ecosystem has been a subject of vigorous investigation (Bocherens, 2003; Haynes, 1991; Putshkov, 2003). Reconstructions of woolly mammoth behaviour and physiology have been largely based on morphology (Haynes, 1991). Isotopic studies of bulk tissues have provided independent tests of morphology-based hypotheses, as well as suggesting new ones (Bocherens, 2003; Bocherens et al., 1994; Iacumin et al., 2010, 2000; Szpak et al., 2010). Compound-specific isotopic studies can provide a further level of understanding of ecosystem functioning within the mammoth steppe.

Bulk collagen nitrogen isotopic compositions ($\delta^{5}N_{\text{Bulk}}$) are commonly used in ecological studies to reveal the diet and trophic level of a species, as these values typically reflect the isotopic compositions of the plants at the base of the food web plus a 2-5 ‰ increase with each trophic level (Koch et al., 1994). As a result, the $\delta^{15}N_{\text{Bulk}}$ of mammoth-steppe herbivore collagen are commonly $~+6$ % where the values of carnivores ($~+9$ %) are

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higher, reflective of this trophic enrichment (Bocherens, 2003). The carnivore- rather than herbivore-like $\delta^{15}N_{\text{Bulk}}$ of woolly mammoth collagen (~+8 ‰; Bocherens, 2003), known as the "woolly mammoth conundrum" are seemingly problematic and therefore require examination. The various hypotheses to explain this phenomenon (unique diet, niche feeding in a special habitat or distinct metabolic processes; Bocherens, 2003; Bocherens et al., 1996, 1994; Fox-Dobbs et al., 2008; Iacumin et al., 2010, 2000; Koch, 1991; Metcalfe et al., 2013; Szpak et al., 2010; Tahmasebi, 2015) have different implications for our understanding of the now-vanished mammoth steppe ecosystem, woolly mammoth ecology, and related factors that contributed to extirpation of the woolly mammoth in this region.

Woolly mammoths may have consumed plants with higher $\delta^{15}N$, such as graminoids and herbs rather than woody vegetation (Koch, 1991; Metcalfe et al., 2013; Szpak et al., 2010), as suggested by the morphology of their enamel plates (Haynes, 1991). However, an herbaceous diet alone is not sufficient to fully explain the woolly mammoth's high δ^{15} N; some further form of habitat or plant selection is also required (Matheus et al., 2003). While modern Arctic graminoids and forbs from some sites have a $\delta^{15}N$ range of – 0.3 to +10 ‰, the average value of these species ranges from $-+1$ to $-+4$ ‰ (Barnett, 1994), and still other studies have reported maximum $\delta^{15}N$ for sedges of +2 ‰ (Nadelhoffer et al., 1996) and for herbs of +5.3 ‰ (Ben-David et al., 2001). The majority of these plants, therefore, are not sufficiently enriched in ^{15}N to explain the woolly mammoth $\delta^{15}N_{\text{Bulk}}$. Plants growing in drier habitats, however, have higher $\delta^{15}N$ than plants from a more mesic environment (Szpak et al., 2010), and woolly mammoths may have eaten plants experiencing water-stress (Bocherens, 2003; Iacumin et al., 2000). Water stress can also cause 13 C-enrichment of plants (Wooller et al., 2007). This enrichment, however, is unlikely to be directly observable in woolly mammoth collagen, because its carbon isotopic composition is likely dominated by the low $\delta^{13}C$ of fat reserves used to survive the winter (Szpak et al., 2010).

Several other factors could also have contributed to high $\delta^{15}N$ for woolly mammoth collagen. Woolly mammoths that had small ranges, or repeatedly travelled the same routes, could have deposited significant quantities of faeces in those areas (Metcalfe et al., 2013), thus causing $15N$ -enrichment in plants arising from this dung fertilization (Szpak et al., 2012). Partially decayed plant material can also have higher $\delta^{15}N$ than the original living plant (Tremblay and Benner, 2006). Woolly mammoths may have removed snow and ice cover by trampling and (or) with their tusks (Putshkov, 2003), allowing them to forage on winter-killed plants generally not utilized by other large herbivores that did not share the mammoth ecological niche (Tahmasebi, 2015). It has also been proposed that woolly mammoths had distinct metabolic processes, such as increased levels of nitrogen recycling associated with winter starvation (Hobson et al., 1993; Polischuk et al., 2011) or poor quality food with low protein levels (Bocherens, 2003; Bocherens et al., 1996, 1994; Fox-Dobbs et al., 2008; Iacumin et al., 2010, 2000; Koch, 1991; Szpak et al., 2010), or that woolly mammoths engaged in coprophagy (Metcalfe et al., 2013).

The nitrogen isotopic compositions of the individual amino acids in collagen, as opposed to bulk collagen, enable discrimination between 15 N-enrichment occurring at the base of the food chain prior to consumption (source amino acids) versus that associated with mammoth metabolic processes (trophic amino acids) (Fig. 3.1). Phenylalanine (Phe) and glutamate (Glu) have been identified as characteristic of source and trophic amino acids, respectively (McClelland and Montoya, 2002; Styring et al., 2010). The $\delta^{5}N_{\text{Phe}}$ reflects the isotopic composition of those amino acids in plants at the base of the food web, while the $\Delta^{15}N_{\text{Glu-Phe}}$ spacing $(\delta^{15}N_{\text{Glu}} - \delta^{15}N_{\text{Phe}})$ serves as a proxy for metabolic enrichment of 15 N in the consumer's body (Styring et al., 2010).

3.2 Methods

3.2.1 Bulk collagen nitrogen isotope analysis

Collagen for $\delta^{15}N_{\text{Bulk}}$ analysis was extracted at the Laboratory for Stable Isotope Science (LSIS) following previously published methods (Metcalfe et al., 2010), or was previously extracted and analyzed for another study (see Appendix F; Metcalfe, 2011; Metcalfe et al., 2010). The $\delta^{15}N_{\text{Bulk}}$ was obtained using a Costech Elemental Combustion System (ECS 4010) attached to a Thermo-Scientific Delta Plus XL IRMS or to a

Figure 3.1 Simplified pathway for nitrogen incorporation from soil to animal protein. Arrows represent: uptake (dashed line), chemical transformations (solid line), and metabolic processes (solid curves). a. Plant NO³ - uptake; b. NO³ converted to glutamine (Styring et al., 2014); c. NH⁴ ⁺uptake; d. NH⁴ + converted to glutamine by attachment to glutamate (Styring et al., 2014); e. Glutamine supplies \mathbf{n} itrogen for synthesis of other amino acids. The associated shift in $\delta^{15}\mathbf{N}$ depends on **the specific amino acid, plant part and plant type (Styring et al., 2014); f. Consumption of amino acids by the animal; g. Source amino acids are minimally** i nvolved in metabolic processes, undergoing small changes in δ^{15} N (e.g. increases in $\delta^{15}N_{\text{Phe}}$ from diet to consumer tissue are commonly ≤ 2 %; (McClelland and **Montoya, 2002); h. Trophic amino acids are heavily involved in metabolic processes,** ${\bf u}$ ndergoing enrichment in $^{15}{\rm N}$ (e.g. increases in $\delta^{15}{\rm N}_{\rm Glu}$ from diet to consumer tissue **are commonly 6-7 ‰; McClelland and Montoya, 2002). Katherine Allan drew the images of grass and mammoth.**

Thermo-Scientific Delta V Plus IRMS. The $\delta^{15}N_{\text{Bulk}}$ was measured over three analytical sessions. In the first two analytical sessions, $\delta^{5}N$ was calibrated to AIR using USGS40 (L-glumatic acid; accepted value *–*4.52 ‰; Qi et al., 2003) and IAEA-N2 (ammonium sulfate; accepted value +20.3‰; Brand et al., 2014), while the third analytical sessions substituted USGS41 (L-glumatic acid; accepted value +47.57 ‰; Qi et al., 2003) for IAEA-N2. The same standards were used to create calibration curves for determining carbon and nitrogen contents (wt%) of each sample, from which C/N ratios were calculated. Keratin (MP Biomedicals Inc., Cat No. 90211, Lot No. 9966H) was used as an internal standard in each analytical session. For a total of 18 keratin measurements over the three analytical sessions, average values (mean \pm 1 SD) were $\delta^{15}N$ = +6.4 \pm 0.2 % (accepted value = $+6.4$ %), and C/N = 3.6 ± 0.4 (accepted value = 3.7). The standard deviation of a sample analyzed as an instrumental duplicate was $\delta^{15}N_{\text{Bulk}} = \pm 0.0$ ‰, and $CN = \pm 0.1$ (1 SD). The standard deviations (1 SD) for method duplicates of $\delta^{5}N_{\text{Bulk}}$ ranged from 0.0 to 0.2 ‰, and for C/N ratios, from 0.0 to 0.3. All samples were considered to be well preserved based on their extraction yields, C/N ratios, and carbon and nitrogen contents (Ambrose, 1990; van Klinken, 1999). Eight samples had high carbon and/or nitrogen contents, but this anomaly likely arises from a weighing error as they were well preserved by other measures.

3.2.2 Amino acid nitrogen isotope analysis

Using collagen first extracted for $\delta^{15}N_{\text{Bulk}}$ measurements, amino acids were hydrolysed, derivatized to their N-acetyl-methyl ester derivative, and their individual $\delta^{15}N_{\text{Amino Acid}}$ measured using an Aligent 6890N-Thermo-Scientific Gas Chromatograph-Combustion 3- Thermo-Scientific Delta Plus XL IRMS. An Agilent Technologies VF-23MS column was used in the GC. We followed published methods (Corr et al., 2007; Styring et al., 2010) with only slight modifications: (i) the quantity of collagen hydrolysed was increased from 2 to 6 mg, and the quantity derivatized was increased from 0.25 to 1.5 mg; and (ii) the initial GC column temperature was set at 60 $^{\circ}$ C instead of 40 $^{\circ}$ C, and its final temperature of 250 °C was held for 15 min instead of 20 min. A representative chromatogram is shown in Appendix G. Three reference gas pulses were introduced into the IRMS at the beginning of each analytical session and one pulse was introduced at the end of each

session. The isotopic composition of the reference gas was calibrated using four amino acid standards. Three of these standards, alanine, leucine and phenylalanine, were purchased as their NACME derivative from Sigma Aldrich. The fourth, proline, was purchased as an amino acid and derivatized in-house. The nitrogen isotopic compositions of the derivatized standards were established by multiple measurements performed in the same manner as used for isotopic analysis of bulk collagen, and calibration to AIR using international standards. The amino acid reference standards were injected every three to five runs. All samples were analyzed a minimum of three times, and the average variation was ± 0.7 ‰ (1 SD) for phenyalanine, and ± 0.7 ‰ (1 SD) for glutamate, with a range of 0.0-3.9 ‰. An internal standard, norleucine, was also analyzed. Its nitrogen isotopic compositions were offset from expected values by an average of +1.3 ‰.

3.2.3 Radiocarbon dating

Radiocarbon dates for six woolly mammoths discussed here have been published previously (Metcalfe, 2011; Metcalfe et al., 2010). A further subset of samples was dated for this study; these included two other herbivores and two carnivores (see Appendix E). Collagen was extracted, combusted, graphitized and radiocarbon dated at the University of Arizona Accelerator Mass Spectrometry (AMS) Laboratory. All dates are presented as uncalibrated radiocarbon years before present (mean \pm 1SD).

3.3 Results

Eight Pleistocene megafauna species were analyzed in this study. These included four herbivore species: woolly mammoth (*Mammuthus primigenius*), mastodon (*Mammut americanum)*, horse (*Equus* sp.) and giant beaver (*Castoroides ohioensis*), and four carnivore species: brown bear (*Ursus arctos*), scimitar cat (*Homotherium serum*), wolf (*Canis lupus*), and short-faced bear (*Arctodus simus*) (see Appendix E). All samples were obtained from specimens collected near Old Crow, Yukon, Canada (latitude: 67.6; longitude: -139.8). A subset of these specimens was dated, including both herbivores and carnivores. Two horse specimens were dated to 18,370 and 27,180⁻¹⁴C years BP. The rest of the specimens yielded effectively non-finite radiocarbon dates $\geq 37,200^{14}$ C yr BP, and one specimen was dated by context to \sim 140,000 years BP (see Appendix E; Metcalfe,

2011; Metcalfe et al., 2010). All collagen samples were considered well preserved based on their collagen yields, C/N ratios, and carbon and nitrogen contents (see Appendix F; van Klinken, 1999).

The $\delta^{15}N_{\text{Bulk}}$ for the Old Crow samples follows the pattern previously observed for Pleistocene megafauna (Bocherens, 2003; Fox-Dobbs et al., 2008; Iacumin et al., 2000); woolly mammoth collagen generally has $\delta^{15}N_{\text{Bulk}}$ similar to the carnivores and higher than the other herbivores, with some overlap with horses (Fig. 3.2a). The $\delta^{15}N_{\text{Phe}}$ of woolly mammoth collagen, however, is higher than those of the carnivores and most of the other herbivores (Fig. 3.2b); horses with high $\delta^{15}N_{\text{Bulk}}$ for collagen show the most overlap with the $\delta^{5}N_{\text{Phe}}$ of woolly mammoths. Woolly mammoth $\Delta^{15}N_{\text{Glu-Phe}}$ spacings overlap those of the other herbivores but are lower than the $\Delta^{15}N_{\text{Glu-Phe}}$ spacings of the carnivores, extending to negative values for most samples (Fig. 3.2c). Negative $\Delta^{15}N_{\text{Glu}}$. Phe spacings have observed in terrestrial herbivores previously (Chikaraishi et al., 2011; Styring et al., 2010) and may be the result of relatively high $\delta^{15}N_{\text{Phe}}$ in vascular plants (Styring et al., 2014).

3.4 Discussion and conclusion

The high $\delta^{15}N_{\text{Phe}}$ of the woolly mammoth implies that they selectively consumed plants more enriched in ¹⁵N than forage consumed by most of the other herbivores. The fact that the $\delta^{15}N_{\text{Phe}}$ of woolly mammoths is higher than those of carnivores suggests that the latter consumed herbivores subsisting on less ${}^{15}N$ -rich forage than consumed by woolly mammoths. In short, the carnivores did not consume significant quantities of woolly mammoth. Partial overlap between horse and woolly mammoth $\delta^{^{15}\rm N_{Bulk}}$ and $\delta^{^{15}\rm N_{Phe}}$ likely indicates that horses exploited a similar niche to the woolly mammoth in some cases. The low $\Delta^{15}N_{\text{Glu-Phe}}$ spacings of woolly mammoths indicate that their $\delta^{15}N_{\text{Bulk}}$ arises from the higher $\delta^{15}N$ of the plants they consumed, and not from a specialized metabolic process.

It seems that woolly mammoths occupied a specialized dietary or habitat niche. A dietary niche implies that woolly mammoths selected particular herbaceous plants or consumed

Figure 3.2 Nitrogen isotopic compositions of Pleistocene Old Crow megafauna: a. Bulk collagen nitrogen isotopic compositions ($\delta^{\text{15}}\text{N}_{\text{Bulk}}$). Results for woolly **mammoths are displayed in blue, other herbivores in purple, and carnivores in red; b. Phenyalanine (source) amino acid nitrogen isotopic compositions (** $\delta^{15}\text{N}_{\text{Phe}}$ **) of each species; c. Difference between the nitrogen isotopic composition of glutamate and** \mathbf{ph} enylalanine ($\boldsymbol{\varDelta}^{15}\mathbf{N}_{\mathrm{Glu-Phe}}$) for each species.

large quantities of decayed plants in winter, while a habitat niche suggests that woolly mammoths occupied more arid habitats, or lived in distinct ranges where they left considerable quantities of dung that fertilized the plants growing there. While some Old Crow horses appear also to have exploited such a niche, it was not generally shared by other mammoth steppe megafauna. The Old Crow samples likely represent various time intervals through the late Pleistocene and potentially varied climate regimes. The fact that the relative differences in average $\delta^{15}N_{\text{Bulk}}$ among herbivore species are generally consistent across the mammoth steppe (Bocherens, 2003) suggests that most herbivore species ate the same forage types regardless of climatic differences or time period. This implies that mammoth steppe herbivores targeted specific forage types.

Two significant conclusions arise from these observations. First, the woolly mammoth occupied a distinct niche from other contemporaneous herbivores. This unique habitat or forage existed across the entirety of the mammoth steppe, although its size may have varied with changing climate across geographic or temporal zones. Other evidence of the woolly mammoth's dependence on a specialized niche may be provided by the retraction of woolly mammoth populations into small, isolated refugia during the last interglacial warm period (MIS 5e, 130-116 kyr BP), and the subsequent re-expansion upon return to glacial conditions(Palkopoulou et al., 2013). An investigation of the isotopic compositions of woolly mammoths from a variety of time periods and sites across the mammoth steppe could reveal the extent of adaptability of the woolly mammoth to disruptions in its niche, such as may have occurred with the onset of climatic shifts at the end of the Pleistocene (Willerslev et al., 2014).

Second, the horse $\delta^{15}N_{\text{Bulk}}$ and $\delta^{15}N_{\text{Phe}}$ overlap those of the woolly mammoth and the other herbivores. This implies that horses fed from a wide diversity of habitats or forage types, including the woolly mammoths' niche. Such behaviour would suggest that the mammoth steppe ecosystem supported herbivores with a variety of ecological adaptations, and that even in the Pleistocene Arctic, resources were sufficiently abundant to support both specialist and generalist strategies.
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Chapter 4

4 Ecology of Pleistocene Old Crow revealed by amino acid carbon and nitrogen isotopic compositions

4.1 Introduction

4.1.1 Mammoth steppe ecology

The Pleistocene mammoth steppe was a megacontinental biome stretching from northwestern Canada to western Europe. It supported a highly diverse ecosystem, with faunal associations not seen in modern ecosystems (Guthrie, 2001, 1990, 1982). Understanding the diets of these species is a key part of understanding species interactions, and thus how this vast ecosystem was able to thrive throughout the Pleistocene. The climatic and environmental change from the Pleistocene to the Holocene is known to have caused changes in plant species across the mammoth step (e.g. Willerslev et al., 2014). There is also significant interest in understanding the responses of megafauna species to this change, including those that survived the Pleistocene-Holocene transition, and how their diet and habitat use may have changed over this time.

Previous work on this topic has interpreted the diet of herbivores and carnivores using a variety of techniques including direct analysis of plant remains in digesta and teeth of frozen animals (e.g. Guthrie, 2001; Ukraintseva, 2013), macro and microwear analysis of teeth (e.g. Rivals and Solounias, 2007; Rivals et al., 2007) and isotopic studies of animal tissues (e.g. Bocherens, 2003; Bocherens et al., 1996; Fizet et al., 1995; Fox-Dobbs et al., 2008; Iacumin et al., 2000). These studies have revealed a number of dietary traits. Horse and mammoth were grazers, feeding on some combination of grasses, sedges and herbs (Bocherens, 2003; Fox-Dobbs et al., 2008). Mastodons were browsers, consuming trees and shrubs (Metcalfe, 2011; Metcalfe et al., 2013). The North American Pleistocene giant beaver may have consumed primarily aquatic plants, unlike the modern beaver's primarily browse diet (Perkins, 2009; Stirton, 1965; Stuart-Williams et al., 1997). The diet of the carnivore species varied with location and time period. At Fairbanks, Alaska, the gray wolf ate a wide range of prey (Feranec et al., 2010; Fox-Dobbs et al., 2008)

leading Fox-Dobbs et al. (2008) to speculate that it was a scavenging species. However, in Marillac, France, wolves were found to specialize on caribou (Fizet et al., 1995). The brown bear was generally omnivorous or herbivorous (Barnes et al., 2002; Feranec et al., 2010; Fox-Dobbs et al., 2008; Matheus, 1995), with some populations specializing on caribou at some points in time (Fox-Dobbs et al., 2008). Most morphological and all isotopic studies of the short-faced bear classify it as a hypercarnivore or scavanger (Barnes et al., 2002; Bocherens et al., 1995; Burns and Young, 1994; Matheus, 1995), and isotopic dietary reconstructions determined that short-faced bears were caribou specialists in the region near Fairbanks, Alaska (Fox-Dobbs et al., 2008). Previous work has classified various North American felid predators as generalists consuming multiple prey types (Coltrain et al., 2004; Fox-Dobbs et al., 2008).

Examining the carbon and nitrogen isotopic compositions of individual amino acids, rather than the bulk protein collagen, can reveal environment, physiology and diet of a species masked using other methods. Previous work on woolly mammoths from this site (Schwartz-Narbonne et al., 2015; Chapter 3) used amino acid $\delta^{15}N$ of two amino acids, phenylalanine and glutamate, to determine that the woolly mammoth consumed a diet drawn from a distinct habitat or forage niche. Several hypotheses were suggested for what made the diet distinct, such as extreme aridity, dung fertilization, consumption of decayed plants, plant selection for distinct plants, or a combination of these signals. The use of δ^{15} N in a greater number of amino acids, in combination with amino acid δ^{13} C, has the potential to discriminate among these possibilities, thus shedding futher light on the diets of mammoth steppe animals.

4.1.2 Nitrogen isotopic compositions

4.1.2.1 Plant **δ**¹⁵N

Within a trophic level, differences in $\delta^{15}N$ can arise from the plant type consumed, as seen in Figure 1.2. In a tundra environment, $\delta^{15}N$ of plants tends to vary, from lowest to highest in the following order: shrubs, lichens, forbs, graminoids, fungi (Ben-David et al., 2001; Drucker et al., 2010; Finstad and Kielland, 2011; Kristensen et al., 2011; Nadelhoffer et al., 1996). There is a great deal of overlap between categories. As well,

different parts of the same plant can have different $\delta^{15}N$. For examples, stems and twigs commonly have lower $\delta^{15}N$ than needles or leaves of trees (Gebauer and Schulze, 1991; Kielland, 2001). The $\delta^{15}N$ of aquatic plants are not as well understood as terrestrial plants (Finlay and Kendall, 2007). In general, the global average $\delta^{15}N$ of aquatic plants is higher than that of terrestrial plants (France, 1995), and higher values have been found for aquatic plants than terrestrial plants at several specific sites (Delong and Thorp, 2006; Finstad and Kielland, 2011; Fry, 1991; Milligan et al., 2010; Tischler, 2004). Many of these studies, however, compared the nitrogen isotopic composition of browse to aquatic plants and did not compare the $\delta^{15}N$ of aquatic plants to graminoids or forbs.

The δ^{15} N of plants can also be affected by climatic conditions. A site with a more open nitrogen cycle – one with greater nitrogen lost – will tend to have higher $\delta^{15}N$ in the plants that grow there. Warmer and drier environments tend to have more open nitrogen cycles (Ambrose, 1991; Amundson et al., 2003; Drucker et al., 2003; Heaton, 1987; Stevens and Hedges, 2004; Stevens et al., 2008).

4.1.2.2 Bulk collagen δ¹⁵N

Physiological factors can influence the $\delta^{15}N$ of an animal's collagen ($\delta^{15}N_{\text{Bulk}}$). As there is a 2-5 ‰ increase in the $\delta^{15}N$ of collagen with trophic level (Koch et al., 1994), higher δ^{15} N can commonly be used to distinguish carnivores from herbivores. Nutritional stress can also cause an increase in $\delta^{15}N_{\text{Bulk}}$ (Gannes et al., 1998; Hobson et al., 1993; Kelly, 2000; Koch, 2007; Polischuk et al., 2011), as can living in arid environments (Kelly, 2000; Sealy et al., 1987; Sponheimer et al., 2003). Nursing can also increases the $\delta^{15}N$ value of an infant's tissue (Metcalfe et al., 2010); however, samples of juvenile megafauna were not examined in this study.

Within the mammoth steppe, the "woolly mammoth conundrum" arose because of seemingly inconsistent evidence from woolly mammoths $\delta^{15}N_{\text{Bulk}}$, which is more similar to coeval carnivores than herbivores (Bocherens, 2003; Schwartz-Narbonne et al., 2015). This conundrum underscores a general problem in ecological and paleoecological isotopic studies when using $\delta^{15}N_{\text{Bulk}}$ to understand the isotopic compositions of an

animal. Environmental, dietary and metabolic factors can affect $\delta^{15}N_{\rm Bulk}$, making it difficult to pinpoint which factor is responsible for any observed isotopic variation. For this reason, this study examines the isotopic compositions of the individual amino acids that comprise collagen. Previous work (Schwartz-Narbonne et al., 2015; Chapter 3) examined two amino acids, glutamate and phenylalanine, and determined that the cause of high mammoth bulk collagen $\delta^{15}N$ was a distinct dietary or habitat niche, and that this niche was shared by some horses on the mammoth steppe. However, Schwartz-Narbonne et al. (2015) were not able to determine if this niche resulted from mammoths consuming: (i) plants that grew in more arid environments, (ii) plants that were fertilized by dung, (iii) specific plants or plant parts, or (iv) partially decayed plants. The present study examines the nitrogen and carbon isotopic compositions of multiple amino acids to help answer these remaining questions, and to provide further insight into the diet, habitat and trophic level of several megafaunal species from the Old Crow site, Yukon Territory, Canada (Fig. 4.1).

Figure 4.1 Location of samples. Samples were collected in Old Crow (OC), Yukon Territory, Canada. Higher altitudes are represented by darker shades of grey. The map was drawn by Katherine Allan.

4.1.2.3 Amino acid δ¹⁵N

Nitrogen used for plant amino acid synthesis can be drawn from several sources. It can come from direct uptake of soil amino acids, although most plants compete poorly for amino acids compared to soil microbes, and so this is not a primary mechanism of acquiring nitrogen for most plants (Styring et al., 2014). Plants, or associated microorganisms, can fix nitrogen, or plants can uptake nitrate or ammonium ions from soil. Plants then convert the nitrogen compound into an amino acid by attaching it as an amide group to glutamate, thus forming glutamine (Styring et al., 2014). Two of these processes are illustrated in Figure 3.1.

Since different plants synthesize and use amino acids with varied enzymes and in varied reactions, the pattern of amino acid $\delta^{15}N$ can vary among different plant types. This pattern has been referred to as the amino acid isotopic "fingerprint" (Larsen et al., 2009), though it has primarily been used for interpretation of carbon isotopic rather than nitrogen isotopic compositions (Arthur et al., 2014; Larsen et al., 2013, 2012, 2009). Chikaraishi et al. (2010) found the amino acid nitrogen fingerprint varied among aquatic, C_3 and C_4 plants, but did not propose a mechanism for this difference. Differences among plants' growth environments and nitrogen uptake strategies may be responsible. Bol et al. (2002) suggested that differences in amino acid $\delta^{15}N$ of plants may be related to their functional nitrogen strategy, which means there is potential for them to distinguish the source of nitrogen in an ecosystem. As one of the plant types studied by Bol et al. (2002) lived in a particularly wet environment with less access to inorganic nutrients, environmental factors may also play a role. Other studies have also found amino acidspecific differences in $\delta^{15}N$ of plants that correlate with environmental effects such as the limiting nutrient in an environment (Smallwood et al., 2003). There may also be plantpart differences. Styring et al. (2014) suggested that nitrogen is transported to certain plant tissues, such as legume seeds, in the form of aspargine rather than as glutamine, which could lead to different $\delta^{15}N$ fingerprints in different tissues of the same plant. Decayed plants may have a different nitrogen isotopic amino acid fingerprint than the living plant. Several studies have investigated the potential of degradation to change the δ^{15} N of amino acids, particularly glycine, in primary producers (Calleja et al., 2013;

Fogel and Tuross, 1999; Smallwood et al., 2003). More work is necessary to be able to interpret with confidence the plant amino acid $\delta^{15}N$ fingerprint in terms of plant type, plant part or ecosystem. Once this is done, such data may be more useful in helping to characterize the diet or habitat of consumers.

When considering the nitrogen isotopic composition of individual amino acids in consumers, the amino acids can be divided into two groups: source and trophic amino acids (McCarthy et al., 2007; Popp et al., 2007). The source amino acids measured in this study are glycine (Gly), phenylalanine (Phe) and threonine (Thr). The trophic amino acids measured are alanine (Ala), glutamate (Glu), leucine (Leu), proline (Pro) and valine (Val). Source amino acids experience little nitrogen isotopic variation from diet to the consumer's tissues. The feeding study of McClelland and Montoya (2002) found a 0 to $+2$ ‰ variation in the $\delta^{15}N$ of phenyalanine moving up one trophic level; this shift was smaller than the change in $\delta^{15}N$ observed in the bulk material. Threonine was found to have a slightly lower $\delta^{15}N$ with increasing trophic level (Chikaraishi et al., 2007; Popp et al., 2007). Trophic amino acids undergo larger ¹⁵N-enrichments (e.g. $+6$ to $+7$ ‰ for glutamate) upon moving up a trophic level (McClelland and Montoya, 2002). This process is illustrated in Fig. 3.1. Glutamate, which showed the largest trophic enrichment in feeding studies (Hare et al., 1991; McClelland and Montoya, 2002), plays a substantial role in nitrogen transport through the body (McCarthy et al., 2013), likely accounting for its significant enrichment in ¹⁵N during metabolic processes.

Since source amino acids experience little $15N$ -enrichment over their isotopic compositions at the base of the food web, they have been used to identify differences in dietary preferences and to track the changing isotopic compositions of plants with time or location (Hannides et al., 2009; Lorrain et al., 2009; McClelland et al., 2003; Ogawa et al., 2012; Pakhomov et al., 2004; Popp et al., 2007; Ruiz-Cooley et al., 2013; Seminoff et al., 2012; Sherwood et al., 2011). Source amino acids have the potential to be used to examine the nitrogen amino acid fingerprint of plants that were consumed, though this has not yet been done. The trophic amino acids have also been used to determine the degree of trophic enrichment of an organism. This measurement is typically performed by subtracting the $\delta^{15}N$ of a source amino acid from a trophic amino acid ($\Delta^{15}N_{\text{Trophic}-}$

 $_{\text{Source}}$), which accounts for varying $\delta^{15}N$ at the base of the food chain (e.g. Chikaraishi et al., 2014, 2007).

4.1.3 Carbon isotopic compositions

4.1.3.1 Plant δ¹³C

North American high latitude regions have been found to contain almost entirely C_3 plants, and no C⁴ plants have been found for these regions from the Pleistocene (Gaglioti et al., 2011; Kristensen et al., 2011; Wooller et al., 2007). There are some isotopic differences among plant types of C_3 plants, as displayed in Figure 1.2. From lowest to highest, the carbon isotopic composition of plant types rank as follows: shrubs, forbs, graminoids, fungi and lichens (Barnett, 1994; Ben-David et al., 2001; Drucker et al., 2010; Kristensen et al., 2011). As for plant nitrogen isotopic compositions, there are differences in the δ^{13} C of plant parts, with twigs having higher δ^{13} C than needles or leaves (Ehleringer et al., 1992; Gebauer and Schulze, 1991; Tischler, 2004). Typical δ¹³C for aquatic plants are difficult to define, as these plants have a much wider range of isotopic compositions than terrestrial C_3 plants (Finlay and Kendall, 2007).

Environmental factors can play a role in changing the δ^{13} C of a plant. For example, factors such as decreased aridity, lower altitudes, lower temperatures and growing underneath a dense canopy all tend to cause lower δ^{13} C in plants (Bocherens et al., 2011; de Bello et al., 2009; Diefendorf et al., 2010; Ehleringer and Cooper, 1988; Ehleringer et al., 1987; Farquhar, 1989; Kohn, 2010; Tieszen, 1991; Wooller et al., 2007).

4.1.3.2 Bulk collagen δ¹³C

Higher trophic levels, nutritional stress and nursing can all change the carbon isotopic composition of an animal's collagen. The collagen of large herbivores has been found to have ~5‰ higher δ^{13} C than their diet (Drucker et al., 2008). For carnivores, the increase in collagen $\delta^{13}C$ ($\delta^{13}C_{\text{Bulk}}$) with trophic level ranges from 0 to 2 ‰ (Bocherens and Drucker, 2003). During periods of nutritional stress, an animal may rely on stored lipids, which have a relatively low $\delta^{13}C$ (Szpak et al., 2010). Milk produced during nursing also has a large quantity of lipids, and so could also cause collagen from a juvenile animal to

have lower than expected $\delta^{13}C_{\text{Bulk}}$ (Metcalfe et al., 2010). As described earlier, however, none of the specimens sampled in this study are expected to show a nursing signal.

There are a number of environments where conventional isotopic analysis is not sufficient to determine the dietary sources for humans or animals. For example, understanding food webs in C_3 plant-only environments using carbon isotopes is challenging because of the relatively narrow range of C_3 plant $\delta^{13}C$ (e.g. Fox-Dobbs et al., 2008). As well, isotopic modelling studies that attempt to separate the dietary sources utilized by a carnivore using bulk collagen compositions are hindered by the fact that one cannot uniquely determine the proportions of $n + 1$ diet sources using *n* isotopes (Fox-Dobbs et al., 2008). Bayesian statistics such as used in SIAR (Stable Isotope Analysis in R) are helping to overcome these limitations (e.g. Parnell et al., 2010; Yeakel et al., 2013). These incorporate the isotopic compositions of the diet and of the consumer into a probabilistic model and produce estimates of the most likely diet, or combination of resources, used by the consumer.

Woolly mammoths generally had slightly lower collagen $\delta^{13}C_{\text{Bulk}}$ than the other herbivores at a site (e.g. Bocherens, 2003; Bocherens et al., 1996; Iacumin et al., 2010; Mann et al., 2013; Matheus et al., 2003). Mastodons tended to have similar or slightly higher $\delta^{13}C_{\text{Bulk}}$ than mammoths (Mann et al., 2013; Metcalfe, 2011; Metcalfe et al., 2013). Stomach content and teeth morphology suggest that their diets were distinct, with mammoths eating graminoids and forbs, and mastodons eating browse (Haynes, 1991). Proboscideans are nonruminants, and so produce less methane than ruminant species. Methane tends to have low δ^{13} C. The preferential loss of 12 C via methane emissions from the body would reduce the available ${}^{12}C$ reservoir for incorporation into collagen. This process could explain the higher $\delta^{13}C_{\text{Bulk}}$ of ruminant species such as caribou and bison compared to mammoth and mastodon, although it would not explain differences between proboscidean and horse $\delta^{13}C_{\text{Bulk}}$ (Mann et al., 2013). Alternatively, animals relied on fat reserves in order to survive the low forage levels available during the Pleistocene Arctic winter, and mammoths had thick fat deposits (Guthrie, 1990). Fat tends to be depleted of $13¹³C$, and so extensive use of fat reserves by Pleistocene proboscideans could explain their low $\delta^{13}C_{\text{Bulk}}$ values (Szpak et al., 2010). This explanation, however, requires that

proboscideans relied more heavily on their fat reserves than did other Pleistocene animals. In a different explanation, Iacumin et al. (2010, 2000) suggested that differences between the $\delta^{13}C_{\text{Bulk}}$ of reindeer and mammoths are related to dietary differences, such as incorporation of lichens into reindeer diets and woody vegetation into some mammoths' winter diets. A combination of these factors may be responsible for the $\delta^{13}C_{\text{Bulk}}$ of Pleistocene herbivores.

4.1.3.3 Amino acid $δ¹³C$

While plants can uptake amino acids from soil, amino acids are generally synthesized *de novo* from organic compounds produced as intermediates in the plant's metabolic cycle (Styring et al., 2014). Organisms synthesize amino acids by specific pathways associated with particular enzymes. Accordingly, several studies have focused on determining δ^{13} C for individual amino acids of a specific plant type, leading to a carbon isotopic "fingerprint". Different kingdoms, plant species, and even different plant parts have been shown to have different amino acid carbon isotopic fingerprints (Fogel and Tuross, 2003; Larsen et al., 2013, 2012, 2011, 2009; Lynch et al., 2011; Smallwood et al., 2003). While these fingerprints can vary with environmental conditions, they are useful as a baseline (Fig. 4.2). Further work is necessary to determine the amino acid carbon isotopic variation between plant types and plant parts in more detail. Lynch et al. (2011) was able to find differences between the δ^{13} C fingerprints of tree and nettle leaves, and grain seeds. At present, only limited research has been conducted on the carbon isotopic fingerprints of plant or bacterial types that would have been found on the mammoth steppe. Some carbon isotopic fingerprints are available for aquatic plants, bacteria, fungi and terrestrial plants (Larsen et al., 2012, 2009), but further differences likely exist among graminoids, forbs and trees, and among types of bacteria.

When considering the carbon isotopic composition of a consumer's amino acids, the amino acids can be divided into two broad categories: essential and nonessential. Essential amino acids cannot be produced by the animal, while nonessential amino acids can be biosynthesized by the animal or taken directly from the diet, depending on their availability in the diet and metabolic demand (Fig. 4.2; Jim et al., 2006). The essential amino acids analyzed in this study are leucine, phenylalanine, threonine and valine, and

the nonessential amino acids measured are alanine, glutamate, glycine, hydroxyproline and proline (Howland et al., 2003), though the classification of an amino acid into one of these categories can vary among species and age groups (Jim et al., 2006). As essential amino acids are taken directly from the diet, limited isotopic fractionation is expected to occur when they are incorporated into body proteins. In particular, the essential amino acids leucine and phenylalanine tend to retain isotopic compositions characteristic of diet, with leucine showing ¹³C enrichment of +0.5 \pm 1.2 ‰, and phenylalanine varying from the diet by -0.6 ± 0.6 % (Howland et al., 2003).

Caption on facing page.

Figure 4.2 Simplified pathway for carbon incorporation from plant biochemicals to animal protein. Arrows represent: uptake (solid lines) and metabolic processes (solid curves). **a.** Typical plant δ^{13} C fingerprint for each plant type. The specific **fingerprint for the essential and non-essential amino acids depends on the biosynthetic pathways used by the plant to produce and store amino acids. The amino acid carbon isotopic fingerprints are adapted from Larsen et al. (Larsen et al., 2013, 2012, 2009); b. Essential amino acids are taken up from the plant to animal; c. Non-essential amino acids are taken up from the plant to animal. d. Plant lipids are taken up from the plant to animal; e. Carbohydrates are taken up from the plant to animal; f. Animals can synthesize lipids from their diet; g. These lipids can be used by the animal during times of nutritional stress; h. Essential amino acids are generally routed directly from the diet with minimal changes in their isotopic composition (Jim et al., 2006); i. Non-essential amino acids can be routed directly from the diet. They can also be synthesized out of the entire diet, from precursors such as proteins, plant carbohydrates, plant lipids and animal lipids. The** difference in δ^{13} C of a nonessential amino acid in the diet and in the body depends **on the degree of routing versus** *de novo* **synthesis, the difference in isotopic composition between the amino acid in the diet and the portion of the diet from which the amino acid is synthesized, and the isotopic shift induced by biochemical synthesis. Katherine Allan drew the grass, aquatic plant, giant beaver and mastodon images. The grass image was published previously (Schwartz-Narbonne et al., 2015).**

Linear discriminant analysis (LDA) can be used to classify the diet of consumers based on the δ^{13} C of amino acids whose isotopic compositions are similar to those in the diet. The δ^{13} C of those amino acids in a variety of dietary sources were measured in previous work (Larsen et al., 2013, 2012, 2009). The common isotopic trends within a dietary group, or the linear combination of features for each dietary group (e.g. aquatic plants, bacteria, terrestrial plants) are defined based on the inputs from previous work. When an unknown sample is input, it can be compared to the linear combinations of features of each dietary group and it can be classified as most similar to one of the dietary groups. If the isotopic compositions of the amino acids in a consumer are similar to their isotopic composition in the diet, this technique can be used to identify what a consumer is eating

(Larsen et al., 2013, 2012, 2009).

When nonessential amino acids are synthesized *de novo* in the body, the biochemical processes involved can result in significant differences in the amino acid isotopic composition from diet to bone collagen. The feeding study of Jim et al. (2006), for example, was able to induce a glutamate variation of *–*7 to +13 ‰ from the diet to the consumer tissue. This variation occurred partially because of metabolic fractionations associated with the synthesis and degradation of amino acids, but largely because the nonessential amino acids were synthesized out of a carbon pool that was experimentally designed to have an extremely different isotopic composition to that of the essential amino acids. Some variation would also be expected in a natural system, as nonessential amino acids can be synthesized from carbohydrates, lipids or protein depending on the diet and metabolic state of the animal. Each of these compounds has a distinct $\delta^{13}C$ that will affect the δ^{13} C of the resulting amino acid, as has been demonstrated both for lipids (Newsome et al., 2014) and carbohydrates (Jim et al., 2006). The situation is further complicated by the fact that nonessential amino acids can also be routed directly from the diet. The degree of routing depends on the diet's protein content. An animal consuming a diet containing more than 5-12% protein will route some of their nonessential amino acids directly from the diet, and more routing appears to occur as the quantity of protein in the diet increases (Jim et al., 2006; Newsome et al., 2014, 2011). Which amino acids are routed, and which are *de novo* synthesized, seems to depend on the amino acid requirements of the consumer (McMahon et al., 2010). For extremely low protein diets, it has been suggested that the amino acid δ^{13} C are overprinted by the isotopic compositions introduced by enzymatic reactions of gut microflora (Arthur et al., 2014; Newsome et al., 2011). This process might be particularly pertinent for ruminants, as they digest a large portion of their food using gut microflora.

4.1.4 Inter-tissue variation

Previous work has observed some variation in $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ between different tissues of Old Crow mammoths (Metcalfe, 2011). Dentin from adult mammoths had higher $\delta^{15}N_{\text{Bulk}}$ (on average by 1.2 ‰), and slightly higher $\delta^{13}C_{\text{Bulk}}$ (on average by 0.2 ‰), than cementum. Mammoths from other locations, however, did not consistently

display the same offsets among their tissues, and some inter-tissue variation observed for mammoths from other locations, such as higher $\delta^{15}N_{\text{Bulk}}$ for tooth dentin than tusk dentin or bone in mammoths from Ontario, was not observed in the Old Crow mammoths (Metcalfe, 2011). Metcalfe (2011) suggested several explanations for these tissue-specific isotopic differences, including metabolism, diet, and age-related isotopic shifts resulting from variations in growth rates between tissues.

Amino-acid specific measurements have been used to examine tissue-specific differences in isotopic composition, with varying results and interpretations. In one study, the bulk protein of various non-collagen tissue types had different isotopic compositions but the individual amino acids did not, suggesting that variations among the amino acid profiles (relative abundances of individual amino acids) of the different tissues were responsible for the isotopic differences (Chikaraishi et al., 2011). Another study examined two tissues that had the same amino acid profile but different turnover rates and different amino acid δ ¹³C, and related the difference to a shift in diet over time (Corr et al., 2009). A third study (Schmidt et al., 2004) found differences in both the amino acid profile and the amino acid isotopic compositions of the krill digestive gland region, abdominal segment and remaining body tissues, which were related to internal metabolic processes. The present study examines the existence and origin of differences in the isotopic composition of the woolly mammoth using both the amino acid profiles and the differences in $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ of various collagenous tissues.

4.1.5 Site

A number of aquatic and semi-aquatic species, as well as tree trunks, suggest that there were shallow pools and lakes, and a spruce-larch forest in the Beringian Old Crow Basin region during the last interglacial (Fig. 4.1; Harington, 2011). Isotopic studies of mammoth collagen have suggested that the Old Crow was as colder and more arid than Alaskan and Yukon sites during the Late Pleistocene, although warmer and wetter than Siberian sites of similar ages (Metcalfe et al., 2010; Szpak et al., 2010). Appendix E and H present the longitude and latitude of sample collection for those specimens for which this information is available.

4.2 Methods

4.2.1 Sample selection

The herbivore species analysed include woolly mammoth (*Mammuthus primigenius*), mastodon (*Mammut americanum)*, horse (*Equus* sp.) and giant beaver (*Castoroides ohioensis*). The carnivore species analysed are brown bear (*Ursus arctos*), scimitar cat (*Homotherium serum*), wolf (*Canis lupus*), and short-faced bear (*Arctodus simus*). The majority of the samples used in this work have been utilized for other purposes in previous studies (Chapter 3; Metcalfe, 2011; Metcalfe et al., 2010; Schwartz-Narbonne et al., 2015). Two additional specimens, bones from a brown bear and a giant beaver, were added to this study, and are described in Appendix H.

4.2.2 Collagen extraction and measurement

Samples were taken using a Dremel tool equipped with a cutting wheel. Surfaces and cancellous bone were removed using a burr Dremel attachment and then the remaining sample was cleaned with deionised water and dried in air. A test lipid extraction was performed on one sample using a modified Bligh and Dyer method (Bligh and Dyer, 1959). A 2:1 chloroform:methanol solution (v:v) was applied for 15 minutes 3 times. As was the case for test samples reported elsewhere (Chapters 2 and 5), the $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ were similar for this sample before and after lipid-extraction (an absolute difference of 0.0 ‰ for $\delta^{13}C$ and 0.5 ‰ for $\delta^{15}N$ was found in this study). Accordingly, the isotopic results for lipid-extracted and untreated collagen samples described below are considered to be equivalent.

The collagen utilized for the majority of the samples reported here was extracted in previous work (Chapter 3; Metcalfe, 2011; Metcalfe et al., 2010; Schwartz-Narbonne et al., 2015). Collagen from the two additional samples described above was extracted using the same modified Longin method (Longin, 1971). The $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ for the mammoth and mastodon collagen have been reported previously (Metcalfe, 2011; Metcalfe et al., 2010), and the $\delta^{15}N_{\text{Bulk}}$ of all but the two additional samples were also reported in (Chapter 3; Schwartz-Narbonne et al., 2015).

The additional bulk collagen isotopic compositions were measured in continuous flow mode using a Costech elemental combustion system (ECS 4010) connected to a Thermo-Scientific Delta V stable isotope ratio mass spectrometer (IRMS) over a total of four analytical sessions. The carbon isotopic compositions were calibrated to VPDB using a two-point curve anchored either by NBS-22 (accepted value *–*30.03 ‰, (Coplen et al., 2006) and IAEA-CH-6 (accepted value *–*10.45 ‰, (Coplen et al., 2006), or USGS-40 (accepted value *–*26.39 ‰, (Coplen et al., 2006) and USGS-41 (accepted value +37.63 ‰, (Coplen et al., 2006). Calibration of $\delta^{15}N$ to AIR was performed using a two point curve anchored by USGS-40 (accepted value *–*4.52 ‰, (Qi et al., 2003) and either IAEA-N2 (accepted value +20.3 ‰) or USGS-41 (accepted value +47.57 ‰, (Qi et al., 2003). Elemental compositions were calculated with the same standards (NBS-22, $C = 86.3$ %; IAEA-CH-6, C = 42.1 %; USGS-40, C = 40.7%, N = 9.5 %; USGS-41, C = 40.7%, N = 9.5%; IAEA-N2, $N = 21.5\%$). Keratin (MP Biomedicals Inc., Cat No 90211, Lot No. 9966H) was used as an internal standard. Over 24 measurements, average values (\pm standard deviation, SD) were: -24.0 ± 0.1 % for $\delta^{13}C$; $+6.3 \pm 0.1$ % for $\delta^{15}N$; 48 ± 1 % for C wt.%; 16 ± 1 % for N wt.%, and 3.6 ± 0.4 for C/N ratio. These results compared well with accepted values of $\delta^{13}C = -24.0$ ‰, $\delta^{15}N = +6.4$ ‰, C wt.% = 46.8%, N wt.% = 14.6% and $CN = 3.7$. Precision was also assessed for each standard. Over 8 to 14 measurements, the δ ¹³C of NBS-22, IAEA-CH-6, USGS-40 and USGS-41 varied by \pm 0.1 to 0.2 ‰ (SD). Over 12 to 14 measurements, the $\delta^{15}N$ of USGS-40, IAEA-N2 and USGS-41 varied by \pm 0.1 to 0.3 ‰ (SD). For 3 samples analyzed in duplicate or triplicate, the variation (SD) ranged from 0.0 to \pm 0.1 ‰ for $\delta^{13}C$, 0.0 to \pm 0.5 ‰ for δ^{15} N, 0 to ± 3 % for C wt.%, 0.0 to \pm 1 % for N wt.%, and 0.0 to \pm 0.3 for C/N.

4.2.3 Hydrolysis, derivatization and measurement of amino acid isotopic compositions

The majority of samples were hydrolysed, derivatized to their N-acetyl-methyl ester derivative, and their amino-acid specific nitrogen isotopic compositions were measured for a previous study (Chapter 3; Schwartz-Narbonne et al., 2015). A typical gas chromatogram of the nitrogen isotopic measurements is found in Appendix G. The additional brown bear sample (YT83) was treated using the same method and analysed

using an Aligent 6890N-Thermo-Scientific Gas Chromatograph-Combustion 3-Thermo-Scientific Delta Plus XL IRMS, equipped with an Agilent Technologies VF-23MS column.

The present study reports $\delta^{15}N$ for 8 amino acids (Ala, Glu, Gly, Hyp, Phe, Pro, Thr and Val; Table 4.1). Peaks with intensities less than 100 mV are not reported. Samples were injected in triplicate, and the standard deviation (SD) of the triplicate measurement for all amino acids ranged from 0.0 to ± 3.9 ‰, with an average standard deviation of ± 0.7 ‰. Norleucine was used as an internal standard, for which an average isotopic composition of +13.3 \pm 1.0 ‰ was obtained, as compared to a δ^{15} N of +14.5 ‰ as measured using a Costech elemental combustion system (ECS 4010) connected to a Thermo-Scientific Delta V IRMS. Two amino acids produced $\delta^{15}N$ that should be considered with caution. Threonine was regularly determined to have very low $\delta^{5}N$, down to -22.0 ‰, whereas the four in-house standards used for calibration to AIR (Ala, Leu, Pro and Phe) had a minimum value of *–*4.6 ‰. This means that the threonine data lie outside of the range of the calibration curve. This is the only amino acid for which this situation arose. Second, the glycine peak partially overlapped with the leucine peak, as is visible from the gas chromatogram (Chapter 3; Schwartz-Narbonne et al., 2015). This overlap is more significant for measurements of nitrogen isotopic composition than carbon isotopic composition. Each amino acid has fewer nitrogen atoms than carbon atoms, and the IRMS system is less sensitive to nitrogen than to carbon, so more sample has to be injected than when measuring carbon isotopic composition, leading to more overlap of the amino acid peaks. The overlap is generally $< 25\%$, for which reliable isotopic compositions can still be obtained, but it is recommended that such peaks are measured at multiple amplitudes (Evershed et al., 2007), which was not possible for all samples.

The δ^{13} C of 9 amino acids are reported in this paper (Ala, Glu, Gly, Hyp, Leu, Phe, Pro, Thr and Val; Table 4.2). The same methods were used as for measurement of the nitrogen isotopic compositions, except that a liquid nitrogen trap was not used to trap the $CO₂$, and samples were analyzed in duplicate rather than triplicate. A representative gas chromatogram is provided in Appendix I. The carbon isotopic compositions were corrected for kinetic isotopic effects and added carbon during derivatization following the

Table 4.1 continues on next page.

Table 4.1 ¹⁵N for bulk collagen and individual amino acids. The nitrogen isotopic compositions of the specimens' amino acids (Ala = alanine, Val = valine, Gly = glycine, Leu = leucine, Thr = threonine, Pro = proline, Glu = glutamate, Phe = phenylalanine and Hyp = hydroxyproline) and bulk collagen are listed for all samples, along with the standard deviation (SD) for triplicate measurements of each amino acid. The average ¹⁵N (and SD) for each species or group of animals is also provided. Peaks that did not give reliable isotopic compositions are listed as ND (not determined). Except for sample YT83, the phenyalanine, glutamate and bulk collagen isotopic compositions were previously reported (Metcalfe, 2011; Metcalfe et al., 2010; Schwartz-Narbonne et al., 2015). RD = root dentin, D = crown dentin, B = bone, C = cementum and T = tusk.

methods of Corr et al. (Corr et al., 2007a, 2007b). The measurement error, and the compounding of this error introduced by the measurements used to correct for the carbon added during derivatization, is calculated following the methods of Docherty et al. (Docherty et al., 2001). The SD of duplicate measurements of individual amino acids ranged from ± 0.1 to ± 2.4 ‰, with an average SD of ± 0.6 ‰. The average $\delta^{13}C$ of the internal standard norleucine over all analytical sessions was *–*28.2 ± 0.6 ‰ (SD). A value of *–*27.8 ‰ was obtained for the same standard using a Costech elemental combustion system (ECS 4010) connected to a Thermo-Scientific Delta V IRMS.

The δ^{13} C of 9 amino acids are reported in this paper (Ala, Glu, Gly, Hyp, Leu, Phe, Pro, Thr and Val; Table 4.2). The same methods were used as for measurement of the nitrogen isotopic compositions, except that a liquid nitrogen trap was not used to trap the $CO₂$, and samples were analyzed in duplicate rather than triplicate. A representative gas chromatogram is provided in Appendix I. The carbon isotopic compositions were corrected for kinetic isotopic effects and added carbon during derivatization following the methods of Corr et al. (Corr et al., 2007a, 2007b). The measurement error, and the compounding of this error introduced by the measurements used to correct for the carbon added during derivatization, is calculated following the methods of Docherty et al. (Docherty et al., 2001). The SD of duplicate measurements of individual amino acids ranged from ± 0.1 to ± 2.4 ‰, with an average SD of ± 0.6 ‰. The average $\delta^{13}C$ of the internal standard norleucine over all analytical sessions was *–*28.2 ± 0.6 ‰ (SD). A value of *–*27.8 ‰ was obtained for the same standard using a Costech elemental combustion system (ECS 4010) connected to a Thermo-Scientific Delta V IRMS.

4.2.4 Amino acid profiles

Amino acid profiles were obtained at the Advanced Protein Technology Centre, located in the Sick Kids Hospital, Toronto, Canada. The collagen samples were hydrolysed using a Waters Pico-Tag Workstation. The amino acids were derivatized, and measured using a Waters Acquity Ultra Performance Liquid Chromatography System.

Lab ID	Species	Ala	Glu	Gly	Hyp	Leu	Phe	Pro	Thr	Val	$\delta^{13}\text{C}_{\text{Bulk}}$
YT											-21.5
1RD YT	Mammoth	$-25.2+0.8$	-18.4 ± 0.2	-15.4 ± 1.1	-21.2 ± 0.4	-26.2 ± 0.6	$-28.5+0.3$	$-22.5+0.4$	-15.2 ± 1.1	$-28.7+0.4$	
2RD	Mammoth	$-25.6 + 0.7$	$-17.9+0.2$	-14.7 ± 1.0	$-22.0+0.3$	-27.4 ± 0.4	$-28.4+0.4$	$-23.6+0.3$	$-16.5 + 1.1$	$-29.9+0.2$	-21.4
YT 3D	Mammoth	-25.1 ± 1.1	$-19.5+0.3$	-11.2 ± 1.0	$-21.7+0.5$	-25.8 ± 1.0	$-28.0+0.4$	$-23.0+0.5$	-13.6 ± 1.4	$-29.6+0.8$	-20.9
YT ₄ B	Mammoth	-22.6 ± 0.8	$-19.3 + 0.7$	-13.1 ± 0.6	-22.0 ± 0.4	$-27.8+0.4$	$-27.6 + 1.1$	$-22.8+0.3$	-14.5 ± 1.1	$-27.9+0.2$	-21.8
YT 5RD	Mammoth	$-23.9+0.6$	$-17.9+0.3$	-11.3 ± 1.3	-21.3 ± 0.6	$-25.7+0.5$	$-27.8+0.2$	$-22.0+0.5$	$-13.8 + 1.0$	$-28.2+0.3$	-21.4
YT ₆ C	Mammoth	$-22.5+0.7$	-19.3 ± 0.5	$-12.4+0.6$	$-21.5+0.3$	$-29.5+0.5$	$-27.9+0.5$	-22.6 ± 0.3	$-14.7+0.9$	$-28.7+0.1$	-21.7
YT _{7B}	Mammoth	$-24.5+0.8$	$-19.6 + 0.1$	$-16.5+0.7$	$-23.2+0.4$	-28.1 ± 0.3	$-28.6+0.4$	-24.2 ± 0.1	-18.9 ± 1.0	$-31.9+0.2$	-21.4
YT ₉ C	Mammoth	$-24.9+0.7$	$-20.5+0.1$	$-13.5+0.5$	-22.4 ± 0.3	$-26.5+0.5$	-29.4 ± 0.3	-23.4 ± 0.1	$-17.8 + 1.0$	-30.1 ± 0.6	-21.5
YT 10RD	Mammoth	$-24.9+0.6$	-18.5 ± 1.3	$-16.2+0.7$	$-21.9+1.2$	$-26.7+0.4$	-28.2 ± 1.6	$-23.0+0.3$	-15.1 ± 1.9	-28.1 ± 0.6	-21.5
YT 11C	Mammoth	$-24.9+0.6$	$-20.0+0.4$	-16.1 ± 0.9	$-22.6+0.4$	-27.6 ± 0.7	$-28.5+0.3$	$-23.5+0.3$	-17.6 ± 1.0	-30.1 ± 1.3	-21.5
YT 11RD	Mammoth	$-26.6+0.6$	$-20.7+0.2$	$-16.7 + 0.7$	-23.1 ± 0.3	-28.1 ± 0.4	$-29.5+0.3$	$-24.2+0.4$	-19.4 ± 1.2	$-31.5+0.7$	-21.5
YT											-20.7
51T	Mammoth	$-24.9+0.6$	$-16.8+0.3$	$-13.8 + 1.0$	$-20.8+0.5$	$-27.5+0.8$	-28.1 ± 0.4	-21.4 ± 0.3	-16.4 ± 1.0	-29.2 ± 0.2	
	Mammoths	-24.6 ± 1.1	$-19.0 + 1.1$	-14.2 ± 2.0	-22.0 ± 0.7	-27.2 ± 1.1	-28.4 ± 0.6	$-23.0+0.8$	-16.1 ± 2.0	$-29.5+1.3$	-21.4 ± 0.3
AMNH											
$\mathbf{1}$	Giant beaver	-14.6 ± 0.6	$-14.0+0.8$	$-6.0+0.6$	$-17.0 + 0.7$	$-21.8+0.5$	$-23.0+0.5$	$-18.6+0.5$	$-9.0+0.9$	$-23.0+0.2$	-18.8
YT ₈ D	Mastodon	-24.3 ± 1.1	$-18.6 + 0.3$	-13.2 ± 1.0	-22.1 ± 0.5	-27.5 ± 1.0	-27.4 ± 0.4	$-22.8+0.5$	$-12.9 + 1.4$	$-29.5+0.8$	-20.6

Table 4.2 continues on next page.

Lab ID	Species	Ala	Glu	Gly	Hyp	Leu	Phe	Pro	Thr	Val	$\overline{\delta^{13}}\overline{\text{C}}_{\text{Bulk}}$
YT129B	Horse	$-19.9+0.6$	-17.1 ± 0.1	$-9.6+0.8$	-17.1 ± 0.9	$-22.0+0.6$	$-27.9+0.3$	$-21.3+0.1$	$-11.9+1.4$	-24.7 ± 1.5	-20.8
YT130B	Horse	-20.4 ± 0.9	-17.2 ± 1.7	-7.0 ± 1.1	-18.3 ± 1.1	-21.7 ± 1.0	-26.8 ± 1.7	-21.9 ± 1.3	-11.3 ± 1.0	-28.2 ± 0.8	-21.1
YT131B	Horse	-22.1 ± 0.6	-17.3 ± 0.1	$-14.6+2.4$	$-19.6+0.4$	-23.8 ± 1.3	$-27.0+0.3$	$-22.4+0.1$	-12.9 ± 1.0	$-30.7+0.6$	-20.7
YT132B	Horse	-22.1 ± 0.6	$-18.0+0.3$	$-12.7+0.8$	-19.6 ± 0.3	-24.3 ± 0.2	$-26.5+0.2$	$-22.6+0.2$	-13.7 ± 1.1	-32.6 ± 0.8	-21.2
YT133B	Horse	-22.2±0.8	-18.0 ± 0.2	$-12.7{\pm}1.0$	-19.8±0.3	$-24.9+0.3$	-26.4 ± 0.3	$-22.7+0.2$	-13.8 ± 1.0	$-32.0+0.9$	-20.9
	Horses	-21.4 ± 1.1	-17.5 ± 0.4	-11.3 ± 3.0	$-18.9+1.2$	-23.4 ± 1.4	$-26.9+0.6$	-22.2 ± 0.6	$-12.7+1.1$	$-29.7+3.2$	$-20.9+0.2$
YT 68B	Brown bear	$-20.8+0.8$	$-18.3+0.2$	-6.0 ± 0.6	-17.2 ± 0.3	-24.2 ± 0.2	-25.4 ± 0.6	-19.9 ± 0.6	$-10.7+0.9$	$-23.8+0.2$	-18.8
	Short-faced										
YT 81B	bear	$-23.9+0.6$	$-18.8+0.2$	$-8.7+0.7$	-19.3 ± 0.3	$-22.8+0.3$	$-26.8+0.2$	-21.3 ± 0.2	-11.4 ± 1.0	$-25.4+0.2$	-19.7
	Homotherium										
YT 82B	serum	$-20.9+0.6$	$-18.0+0.2$	-9.5 ± 0.6	$-18.8+0.4$	$-23.7+0.2$	-27.1 ± 0.3	-21.4 ± 0.1	-13.0 ± 1.0	-25.4 ± 0.2	-19.0
YT 84B AMNH	Brown bear	-22.4 ± 0.6	-17.1 ± 0.1	$-8.7+0.7$	$-18.6+0.4$	$-23.9+0.2$	-26.4 ± 0.3	$-21.5+0.1$	-11.9 ± 1.0	$-26.2+0.5$	-19.8
3B	Canid	-21.3 ± 0.7	-19.6 ± 0.6	$-10.0+0.7$	$-19.8+0.4$	$-25.7+0.2$	-27.4 ± 0.3	$-22.0+0.3$	$-11.9+0.9$	$-25.0+0.5$	-19.7
	Carnivores	-21.8 ± 1.3	-18.4 ± 0.9	$-8.6{\pm}1.6$	-18.7 ± 1.0	-24.1 ± 1.1	-26.6 ± 0.8	-21.2 ± 0.8	-11.8 ± 0.8	$-25.2+0.9$	-19.4 ± 0.4
	Holocene										
YT 83B	brown bear	-17.5 ± 1.0	-17.1 ± 0.1	-4.7±0.6	-17.3 ± 0.3	$-22.8+0.5$	$-25.6+0.4$	-19.8 ± 0.2	-12.5 ± 1.0	$-24.7+0.4$	-18.2

Table 4.2 ¹³C for bulk collagen and individual amino acids. The carbon isotopic compositions of the specimens' amino acids and bulk collagen are listed for all samples, along with the SD of duplicate measurements for the amino acids. Amino acids and tissues are labelled as in Table 1. The average $\delta^{\!3}\rm{C}$ (and SD) for each species or group of animals is also provided. The **bulk collagen isotopic compositions of the mammoths and mastodons were previously reported (Metcalfe, 2011; Metcalfe et al., 2010)**

4.2.5 Radiocarbon dating

The majority of samples were dated previously (Chapter 3; Metcalfe, 2011; Metcalfe et al., 2010; Schwartz-Narbonne et al., 2015). Radiocarbon dates for the two additional samples included in the present study were obtained following the same procedure at the University of Arizona Accelerator Mass Spectrometry (AMS) Laboratory, and are reported in Appendix H. All dates are reported as uncalibrated radiocarbon years before present (1950).

4.2.6 Mathematical treatment

Previous work has established isotopic "fingerprints" for aquatic plants, bacteria, fungi and terrestrial plants using their carbon isotopic compositions (Larsen et al., 2013, 2012, 2009). As the samples from Larsen et al. (2012, 2009) were collected in 2007, a Suess effect correction of +1.67 ‰ was applied to the 2007 data to correct it to the Pleistocene data using the formula from Long et al. (2005). LDA was then applied to the Larsen et al. dataset to separate the four groups based on the δ^{13} C values of 7 amino acids (Ala, Glu, Leu, Phe, Pro, Thr, Val). Samples were included only when all seven amino acid carbon isotopic compositions were measured. Each herbivore and carnivore sample from this study was then classified using LDA to predict its membership in each group. The MASS package (Venables and Ripley, 2002) was used to perform the LDA in R version 3.1.1 (R Core Team, 2014) using the R Studio interface version 0.98.1083.

4.3 Results

4.3.1 Evaluation of collagen extraction and hydrolysis technique

Amino acid profiles were obtained for tissues at a variety of stages of preparation: whole tissue, extracted collagen and hydrolysed collagen (Fig. 4.3; Appendix J). These tissues included a modern cow bone (KFC), an archaeological human bone, (REG97), and mastodon crown dentin, (YT8D). The amino acid profiles for the human bone sample were presented previously by Olsen et al. (2010). The data were compared to previously published amino acid profiles of mammal bone (Szpak, 2011) to assess the integrity of the collagen extraction and hydrolysis technique. The whole bone has substantially

different amino acid profiles than collagen. The extracted and hydrolysed collagen, however, have the expected amino acid profiles. This outcome indicates that the collagen extraction successfully removed the non-collagenous proteins, and that hydrolysis did not cause preferential loss of some amino acids.

4.3.2 Sample preservation

The preservation of the collagen from the two additional samples used in this analysis was considered following the typical criteria. Samples are considered well-preserved if they have a collagen yield >1%, a C/N ratio between 2.9 to 3.6, carbon content \geq 13 wt.% and nitrogen content ≥4.8 wt.% (Ambrose, 1990; DeNiro, 1985; van Klinken, 1999). The brown bear sample met these criteria, but the collagen yield for the giant beaver was too low (Appendix H). An infinite radiocarbon date was obtained for the giant beaver sample. As previously suggested for Old Crow by Harington (2011), such a date could suggest that the giant beaver lived in this area during an interglacial period, as has also been interpreted from infinite radiocarbon dates obtained for Beringian mastodons (Zazula et al., 2014).

4.3.3 Bulk collagen stable isotope compositions

The $\delta^{13}C_{Bulk}$ and $\delta^{15}N_{Bulk}$ are displayed in Figure 4.4. The general pattern of $\delta^{15}N_{Bulk}$ has been described previously (Chapter 3; Schwartz-Narbonne et al., 2015). Mastodon has the lowest $\delta^{15}N_{\text{Bulk}}$. Beaver and some horse samples also have low $\delta^{15}N_{\text{Bulk}}$, while other horse samples and all woolly mammoths have high $\delta^{5}N_{\text{Bulk}}$. Three of five horse specimens were dated. The horse with the lowest $\delta^{5}N_{\text{Bulk}}$ has an infinite date, whereas the horse dated to 27,180¹⁴C BP has a $\delta^{15}N_{\text{Bulk}} \sim 3$ % higher. The horse with the highest $\delta^{15}N_{\text{Bulk}}$ was dated to 18,370 ¹⁴C BP. The mastodon and woolly mammoth samples have infinite dates, precluding investigation of radiocarbon date-dependent patterns in isotopic composition.

Two of the carnivore specimens, the canid and the scimitar cat, have infinite radiocarbon dates. The short-faced bear specimen was not dated, but this species went extinct by the end of the Pleistocene (Barnes et al., 2002). Brown bears were present in high latitudes

Figure 4.3 Amino acid profiles of samples after a variety of treatments. The modern bone measured was a cow femur. The archeological bone is a human rib bone and its amino acid profile was presented previously by (Olsen et al., 2010). The average mammal bone amino acid profile and SD is taken from (Szpak, 2011). Amino acid profiles are presented as the percentage of the tissue comprising each amino acid.

through the Pleistocene and Holocene (Barnes et al., 2002). A date of $5,941^{14}C$ BP was obtained for one brown bear sample, but radiocarbon dates for the other two samples have not yet been obtained. The undated carnivores and those dated to the Pleistocene have high $\delta^{5}N_{\text{Bulk}}$, similar to the woolly mammoth. The Holocene brown bear, however, has a lower $\delta^{15}N_{\text{Bulk}}$ than any other carnivore or woolly mammoth sample described in this paper. The two undated brown bears have the highest and lowest $\delta^{15}N_{\text{Bulk}}$ of the other carnivores.

The woolly mammoths tend to have the lowest $\delta^{13}C_{\text{Bulk}}$ of all the species, followed by horse and then mastodon. Of the three dated horses, the horse having an infinite radiocarbon date has the lowest $\delta^{13}C_{\text{Bulk}}$, while the other two horses have virtually identical carbon isotopic compositions. The giant beaver has a higher $\delta^{13}C_{\text{Bulk}}$ than any of the other herbivores, and is the only herbivore whose $\delta^{13}C_{\text{Bulk}}$ overlaps with those of the

carnivores. Of the carnivores, the Holocene brown bear has the highest $\delta^{13}C_{\text{Bulk}}$, whereas the undated brown bears have the highest and lowest $\delta^{13}C_{\text{Bulk}}$ of the remaining carnivores.

Figure 4.4 $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of bulk collagen for all samples. Values in parentheses in **the legend indicate the number of specimens.**

4.3.4 Inter-tissue differences

For most species, only a single tissue type (bone or crown dentin) was analyzed. Previous work (Metcalfe, 2011), however, suggested that there might be differences in isotopic compositions of woolly mammoth collagen from different tissues at some sites. Therefore, five tissue types were measured for the woolly mammoth (Appendix J), including tusk, root dentin, cementum and bone from adult mammoths. Root dentin from a juvenile mammoth, for which he $\delta^{13}\text{C}_{\text{Bulk}}$ and $\delta^{15}\text{N}_{\text{Bulk}}$ was reported previously by Metcalfe et al. (2010), and dentin from a mastodon were also examined (Appendix J). The amino acid profiles of these samples were obtained to determine if differences in

 $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ were related to variation in the amino acid profile of the collagen (Fig. 4.5). There was little variation in the amino acid profile among these tissues, or from average mammalian bone collagen amino acid profiles (Szpak, 2011). Hence, differences in isotopic composition among the collagen from the various tissues do not result from atypical amino acid profiles.

Woolly mammoth tusk has higher $\delta^{15}N_{\text{Bulk}}$ than the other tissues (Fig. 4.6a; Table 4.1). Crown dentin and root dentin have higher average $\delta^{5}N_{\text{Bulk}}$ than cementum. Tusk also has the highest average $\delta^{15}N$ for Ala, Glu, Gly, Hyp and Pro, but it does not have the highest value for Phe, Thr or Val. Crown dentin has higher average $\delta^{15}N$ than cementum for Ala, Glu, Phe, Pro, Thr and Val, lower average $\delta^{5}N_{\text{Gly}}$, and overlapping $\delta^{15}N_{\text{Hyp}}$ (within SD) with cementum $\delta^{15}N_{\text{Hyp}}$. Root dentin $\delta^{15}N$ and cementum have the same $\delta^{15}N$ (within SD) for most amino acids, though the root dentin has higher $\delta^{15}N$ for Thr and Val.

Figure 4.6 Amino acid: a. $\delta^{13}C$; b. $\delta^{15}N$ in a variety of woolly mammoth tissues. **Values in parentheses in the legend are the number of tissues measured. Error bars (whiskers) show SD.**

There are no large isotopic differences in $\delta^{13}C_{\text{Bulk}}$ between tissues (Fig. 4.6b; Table 4.2). The tusk has the highest $\delta^{13}C_{\text{Bulk}}$ and the crown dentin the lowest, with the other three tissues having values that overlap (within SD). In most cases, individual amino acids also have δ^{13} C that overlap (within SD) with the same amino acids in the other tissues. The only exceptions are tusk $\delta^{13}C_{\text{Glu}}$, $\delta^{13}C_{\text{Hy}}$, and $\delta^{13}C_{\text{Pro}}$, which are higher than $\delta^{13}C_{\text{Glu}}$, $\delta^{13}C_{\text{Hy}}$, and $\delta^{13}C_{\text{Pro}}$ of other tissues, and crown dentin $\delta^{13}C_{\text{Gly}}$, which is higher than $\delta^{13}C_{\text{Gly}}$ of other tissues.

4.3.5 Amino acid δ¹⁵N

Three source amino acids were analyzed in this study: Gly, Phe and Thr (Figs. 4.7a-c;

Table 4.1). The results for phenylalanine have been presented previously (Chapter 3; Schwartz-Narbonne et al., 2015). The woolly mammoth generally has higher $\delta^{15}N_{\text{Bulk}}$ than the other herbivores and carnivores, with some overlap with horse and one carnivore (Fig. 4.7a). The undated brown bear with the highest $\delta^{5}N_{\text{Bulk}}$ of the carnivores shows overlap in $\delta^{15}N_{\text{Phe}}$ with the woolly mammoth having the lowest $\delta^{15}N_{\text{Phe}}$. Four of five horses show overlap in $\delta^{15}N_{\text{Phe}}$ with woolly mammoths. The horse with the lowest $\delta^{15}N_{\text{Bulk}}$ and an infinite radiocarbon date also has the lowest $\delta^{15}N_{\text{Phe}}$.

All Pleistocene and undated carnivore samples have lower $\delta^{15}N_{\text{Thr}}$ than the Pleistocene herbivores (Fig. 4.7b). The Holocene brown bear is the only carnivore with a higher $\delta^{15}N_{\text{Thr}}$ than at least one herbivore, being higher than that of the mastodon and one woolly mammoth. There was complete overlap between horse and the woolly mammoth $\delta^{15}N_{\text{Thr}}$. These two species have the highest $\delta^{15}N_{\text{Thr}}$ of all species examined in this study.

Woolly mammoths have the highest $\delta^{15}N_{\text{Gly}}$, with some overlap with mastodon and horse (Fig. 4.7c). The two horse samples (undated, 18,370⁻¹⁴C BP) with the highest $\delta^{5}N_{\text{Bulk}}$ also have the highest $\delta^{15}N_{\text{Gly}}$, overlapping those of mammoth. Carnivore $\delta^{15}N_{\text{Gly}}$ is generally lower than that of woolly mammoth, mastodon, giant beaver and some horse samples. The only exception is for the brown bear with the highest $\delta^{15}N_{\text{Bulk}}$; it also has a high $\delta^{5}N_{\text{Gly}}$, overlapping those of woolly mammoth. The Holocene brown bear had the lowest $\delta^{15}N_{\text{Gly}}$ of any of the specimens sampled here.

The trophic position of each species was examined by as follows:

$$
\delta^{15}
$$
N_{Trophic Amino Acid} – δ^{15} N_{Source Amino Acid} = Δ^{15} N_{Trophic-Source}

Glutamate was always used as the trophic amino acid, and results for the three source amino acids compared. There is a range of several per mil in $\Delta^{15}N_{\text{Glu-Phe}}$ and $\Delta^{15}N_{\text{Glu-Thr}}$ of the herbivores and carnivores, but no overlap between them (Figs. 4.7d-e). There is overlap in $\Delta^{15}N_{\text{Glu-Gly}}$ between herbivores and carnivores (Fig. 4.7f). Woolly mammoth and mastodon have the lowest $\Delta^{15}N_{\rm Glu\text{-}Gly}$. The woolly mammoth with the largest $\Delta^{15}N_{\rm Glu}$ Gly overlaps with those of the giant beaver and two horse samples, including one horse

with an infinite radiocarbon date, but the rest of the horse samples have higher $\Delta^{15}N_{\text{Glu-Gly}}$ than the woolly mammoth. Carnivore $\Delta^{15}N_{\text{Glu-Gly}}$ is generally higher than herbivore, but the brown bear with the highest $\delta^{15}N_{\rm Bulk}$ and $\delta^{15}N_{\rm Gly}$ has lower $\Lambda^{15}N_{\rm Glu-Gly}$ than any other carnivore, and overlaps the $\Delta^{15}N_{\text{Glu-Gly}}$ of some horses.

When considering all the herbivores together, the $\delta^{15}N_{\text{Bulk}}$ correlates positively with the δ^{15} N of phenylalanine, threonine and glycine (Fig. 4.8). These trends are not strong, with $R^2 = 0.4$ -0.5. However, they are significant, with *p* values ≤ 0.01 .

4.3.6 Amino acid δ¹³C

Values of δ^{13} C have been measured for four essential amino acids (Leu, Phe, Thr and Val; Table 4.2) and five nonessential amino acids (Ala, Glu, Gly, Hyp and Pro; Table 4.2). Larsen et al. (Larsen et al., 2009) highlighted leucine, isoleucine and lysine as the three most informative essential amino acids for classification of samples such as bacteria, plants or fungi using LDA. Because of analytical limitations, the $\delta^{13}C$ of isoleucine or lysine were not measured in the present study. To accurately classify groups, however, LDA requires that the amino acid δ^{13} C inputs are sufficiently distinct and informative between groups. As two of the most informative essential amino acids could not be included, it was considered beneficial to add nonessential amino acids to the classification. Addition of nonessential amino acids to the LDA analysis, however, requires that those amino acids had been directly routed from the diet and so would have a similar isotopic composition to their δ^{13} C in the diet.

Determining which amino acids were most likely directly routed from diet, and which were strongly affected by metabolic processes was accomplished by normalizing all amino acids carbon isotopic compositions in a specimen to its $\delta^{13}C_{\text{Bulk}}$ (Figs. 4.9a-d; Table 4.3):

 $\delta^{13}C_{\text{Amino Acid}} - \delta^{13}C_{\text{Bulk}} = \varDelta^{13}C_{\text{Amino Acid-Bulk}}$

This approach serves to remove the effects of consumption of plants with varying $\delta^{13}C$. The amount of variation in $\Delta^{13}C_{\text{Amino Acid-Bulk}}$ for a given amino acid can then be compared

within and between species (Table 4.3). Since most animals within a species are expected

Caption on facing page.

Figure 4.7 Nitrogen isotopic compositions of amino acids and amino acid pairs. Results for woolly mammoths are displayed as blue circles, other herbivores are displayed as purple triangles, and carnivores are displayed as red squares: a. Phenyalanine (source) amino acid nitrogen isotopic compositions ($\delta^{45}\text{N}_{\text{Phe}}$ **) of each species. These data have been presented previously (Chapter 3; Schwartz-Narbonne et al., 2015); b. Threonine (source) amino acid nitrogen isotopic compositions (¹⁵NThr) of each species; c. Glycine (source) amino acid nitrogen isotopic** compositions $(\boldsymbol{\delta}^{15}\text{N}_{\text{Gly}})$ of each species; d. Difference between the nitrogen isotopic composition of glutamate and phenylalanine ($\varDelta^{15} \rm N_{Glu\text{-}Phe}$) for each species. These **data have been presented previously (Chapter 3; Schwartz-Narbonne et al., 2015); e. Difference between the nitrogen isotopic composition of glutamate and threonine (¹⁵NGlu-Thr) for each species; f. Difference between the nitrogen isotopic composition** of glutamate and glycine $(A^{15}N_{\rm Glu\text{-}Gly})$ for each species.

to have eaten similar plants, more variation (i.e., larger SD) is predicted for the $\Delta^{13}C_{Amino}$ Acid-Bulk affected by metabolic processes than for amino acids that were directly routed from diet. Of the nine amino acids, glycine shows the greatest variation for woolly mammoth, and the second largest variation for horse (after valine), and was tied for alanine for the highest variation within the carnivores. Across all species, $\Lambda^{13}C_{Amino\,\rm Acid}$ B_{Bulk} for glycine has second highest variation among the amino acids. Valine and alanine also have high variability of $\Delta^{13}C_{\text{Amino Acid-Bulk}}$, but not for all groupings of species. Based upon variation in $\Delta^{13}C_{\text{Amino Acid-Bulk}}$, glycine appears to be the amino acid, overall, that is most affected by metabolic processes. This suggests that glycine should not be used in the LDA. Since $\delta^{13}C_{\text{Gly}}$ is not considered in the LDA, its isotopic composition is examined individually. Woolly mammoth tends to have lower $\delta^{13}C_{\text{Gly}}$ than any of the other groups of species, followed by mastodon, which has the next lowest $\delta^{13}C_{\text{Gly}}$ (Table 4.2).

The δ^{13} C values of 8 amino acids other than glycine were measured (Ala, Glu, Hyp, Leu, Phe, Pro, Thr, Val). Of these, only the δ^{13} C of hydroxyproline was not measured in plants (Larsen et al., 2012, 2009). As mentioned earlier, only essential amino acids would

normally be used in LDA. The small degree of variability in the δ^{13} C of the nonessential amino acids other than glycine, however, suggests retention of isotopic composition from the diet. With this assumption in place, the dietary sources were first classified and defined using the δ^{13} C of these 7 amino acids, and then these linear functions were used to classify the diets of the consumers. The LDA classifications for the diet of each

Figure 4.8 δ^{45} N of individual amino acids versus δ^{45} N_{Bulk} for all herbivores: a. $\delta^{45}\rm{N}_{\rm{Phe}}$; b. $\delta^{45}\rm{N}_{\rm{Thr}}$; c. $\delta^{45}\rm{N}_{\rm{Gly}}$. Trendline, R^2 and p value include data for all **herbivores. Individual herbivores have distinct symbols and colours so that speciesspecific deviations from linearity can be observed.**

Figure 4.9 Normalized carbon isotopic compositions of amino acids $(A^{13}C_{\Lambda{\rm mino\,acid}}$ $B_{\text{bulk}} = \delta^{13}C_{\text{Amino acid}} - \delta^{13}C_{\text{Bulk}}$): a. Average for species or groups of species; b. woolly **mammoth; c. horse; d. carnivore.**

Table 4.3 \varDelta^{13} C of individual amino acids normalized to bulk collagen δ^{13} C. Δ^{13} **C**_{Normalized = δ^{13} **C**_{Amino Acid – δ^{13} **C**_{Bulk}. The average Δ^{13} **C** and SD for each species or}} group of animals is also listed. The average SD of the average $\varDelta^{13}C$ for each species **is also listed.**

individual animal are presented in Table 4.4, along with the posterior probabilities for

each classification. The posterior probabilities give a measure of how well the specimens fit into the group that they were assigned. With the exception of one brown bear, the various species are all considered to be well-classified, with posterior probabilities of \geq 78 %. Ten of the twelve mammoth specimens are classified as bacterial consumers, with the remaining two specimens classified as terrestrial plant consumers. These two mammoths do not have distinct $\delta^{15}N_{\text{Bulk}}$ from the other woolly mammoths, but they have the two lowest $\delta^{13}C_{\text{Bulk}}$. The mastodon is classified as a terrestrial-plant consumer. All horses are classified as bacterial consumers. The giant beaver is classified as an aquatic plant consumer.

Since carnivores consume primarily protein, it is assumed that the δ^{13} C of their amino acids reflects the amino acids of the herbivores they consumed, and thus the plants consumed by those herbivores. Using LDA, the majority of the carnivores are classified as having consumed animals that had consumed bacterial inputs, while the canid and one brown bear are classified as having consumed herbivores that had consumed terrestrial plants. The $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ of the canid are within the range of the other carnivores. However, this brown bear is more distinct. This brown bear has the highest $\delta^{13}C_{\text{Bulk}}$ and lowest $\delta^{5}N_{\text{Bulk}}$ of the undated brown bears. As well, its classification as a terrestrial plant consumer is not strong (posterior probability of terrestrial plants was 48%), making LDA a poor method of categorizing its diet.

4.4 Discussion

4.4.1 Inter-tissue variation

Variation in $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$ of different woolly mammoth tissues almost certainly arises from differences in the isotopic composition of the component amino acids, since all tissues have similar amino acid profiles. The nitrogen isotopic variation observed between bulk collagen of different mammoth tissues is generally small (Fig. 4.6a; Table 4.1). In every case where $\delta^{15}N_{\text{Bulk}}$ differences are observed among tissues, these effects are also observed for both source and trophic amino acids. This result suggests that a metabolic effect was not the primary cause of these isotopic differences. Differences in growth rates, amino acid routing or other metabolic changes do not seem to be

controlling differences in $\delta^{15}N_{\text{Bulk}}$ among tissues. Instead, it seems that certain tissues may record $\delta^{15}N_{\text{Bulk}}$ from different plants or plant parts, or from plants grown in different environments.

There are minimal differences in the bulk collagen or individual amino acid $\delta^{13}C$ among tissues, and the ranges measured for most δ^{13} C of individual amino acids overlap among the tissues (Fig. 4.6b; Table 4.2). There are also no clear tissue-dependent patterns in plant consumption, as identified using LDA (Table 4.4). Tusk has the largest $\delta^{15}N_{\rm Bulk}$ difference among these tissues, but only one tusk was sampled. As well, there is only one individual for which more than one tissue was sampled. This dataset is too small to demonstrate whether consistent isotopic differences exist between tissues or to explore the causes of these putative differences. Since the isotopic compositions are similar among tissues, all tissues are considered to be equivalent for the remainder of this discussion.

4.4.2 Dietary patterns suggested by *δ* ¹⁵N

The general dietary patterns suggested by $\delta^{5}N_{\text{Phe}}$ and $\Delta^{15}N_{\text{Glu-Phe}}$ (Figs. 4.7a, d) have been discussed previously by (Chapter 3; Schwartz-Narbonne et al., 2015). Woolly mammoth consumed a diet of plants with high $\delta^{15}N$, which reflected a distinct dietary or habitat niche. Mammoth $\delta^{15}N_{\text{Phe}}$ is higher than those of mastodon, giant beaver, and most carnivores, and similar to those of horse, suggesting a shared dietary or habitat niche with some horses. Herbivore $\Delta^{15}N_{\text{Glu-Phe}}$ is lower than measured for carnivores, consistent with a trophic enrichment in ¹⁵N of the carnivores. The negative $\Lambda^{15}N_{\text{Glu-Phe}}$ of some herbivores has been reported in previous terrestrial studies (Chikaraishi et al., 2011; Ishikawa et al., 2014).

The low $\delta^{15}N_{\text{Bulk}}$ and $\delta^{15}N_{\text{Phe}}$ of the mastodon (Figs. 4.4; 4.7a) are consistent with previous interpretations that it ate mainly browse (Metcalfe, 2011; Metcalfe et al., 2013). Its $\delta^{15}N_{\text{Bulk}}$ and $\delta^{15}N_{\text{Phe}}$ are lower than those of the giant beaver, which fits the interpretation that the giant beaver consumed aquatic plants with higher $\delta^{15}N$ than browse (Milligan et al., 2010; Perkins, 2009; Stuart-Williams et al., 1997). These two animals are

species that likely lived in Old Crow during interglacial periods when more browse and more aquatic vegetation would have been available (Harington, 2011; Grant D Zazula et al., 2014).

Table 4.4 Linear discriminant analysis (LDA) classification of herbivore and carnivore diets. The most probable diet of each specimen is indicated, along with the posterior probabilities of these classifications.

Among the source amino acids, the patterns observed for $\delta^{15}N_{\text{Thr}}$ (Fig. 4.7b) and $\Delta^{15}N_{\text{Glu}}$. $_{\text{Thr}}$ (Fig. 4.7e) are generally consistent with those suggested by $\delta^{15}N_{\text{Phe}}$. Overlap between woolly mammoth and horse $\delta^{15}N_{\text{Thr}}$ further suggest that woolly mammoth and horse shared a dietary or habitat niche that had high plant $\delta^{5}N$, and the lower values for

mastodon $\delta^{15}N_{\text{Thr}}$ again suggest that it consumed plant types such as browse that had lower $\delta^{5}N$. Consistent with the $\Delta^{15}N_{\text{Glu-Phe}}$ pattern, there is clear differentiation between the $\Delta^{15}N_{\text{Glu-Thr}}$ of the herbivores and the carnivores, again demonstrating their trophic separation.

The patterns observed using the third source amino acid, glycine (Fig. 4.7c), are generally similar to those obtained using the other two source amino acids. There are several differences, however, that again point to consumption of different plants that have distinct $\delta^{15}N$ amino acid fingerprints from each other. The mastodon has a higher $\delta^{15}N_{\text{Gly}}$ than would be expected based on the relative position of its $\delta^{15}N_{\text{Phe}}$ and $\delta^{15}N_{\text{Thr}}$ compared to the other animals. The mastodon and woolly mammoth have overlapping $\delta^{15}N_{\text{Gly}}$. It is possible that browse has a $\delta^{15}N$ amino acid fingerprint that is distinct from the graminoids and forbs that likely dominated the woolly mammoth diet, though no study of the δ^{15} N fingerprint of these plants types has been done so far.

The carnivores with the highest and lowest $\delta^{15}N_{\text{Bulk}}$ (the undated brown bear and the Holocene brown bear, respectively) also have the highest and lowest $\delta^{15}N_{\text{Gly}}$ of the carnivores, a pattern not observed for the other source amino acids. Since glycine comprises approximately a third of the amino acids in collagen, the glycine $\delta^{15}N$ may explain the $\delta^{15}N_{\text{Bulk}}$ of these carnivores. The fact that this pattern was observed in glycine but not in the other source amino acids again suggests a distinct $\delta^{15}N$ fingerprint for the plants eaten by the herbivores that the carnivores consumed. It has been suggested that $\delta^{15}N_{\text{Gly}}$ is a marker of plant decay (Calleja et al., 2013; Fogel and Tuross, 1999; Smallwood et al., 2003). On one hand, the particularly high $\delta^{5}N_{\text{Gly}}$ for the woolly mammoth, some horse samples and the undated brown bear may suggest the consumption of a large quantity of decayed plant material, which may have comprised winter or year-round fodder (Chapter 3; Schwartz-Narbonne et al., 2015; Tahmasebi, 2015). The much lower $\delta^{15}N_{\text{Gly}}$ of Holocene brown bear, on the other hand, may point to a shift in plant type or plant part being consumed following the Pleistocene.

The patterns observed for $\Delta^{15}N_{\text{Glu-Gly}}$ (Fig. 4.7f) further support the idea that some species consumed plants (or animals that consumed plants) that had different $\delta^{15}N$ fingerprints from each other. Rather the providing a clear separation between the herbivores and carnivores, a range of values is observed, with woolly mammoth $\Lambda^{15}N_{\text{Glu-Gly}}$ overlapping with some but not all of the other herbivores. Using $\Delta^{15}N_{\text{Trophic amino acid}}$ – Source amino acid to determine trophic position relies on the assumption that the same processes affect the plants at the base of the food web for all species. This approach may not be valid for all amino acids if some species consume plants with different $\delta^{15}N$ amino acid fingerprints. This possibility should be considered in future work that applies this approach when comparing the trophic level of species with potentially distinct diets.

In general, herbivores with higher $\delta^{15}N_{Bulk}$ have higher $\delta^{15}N_{The}$, $\delta^{15}N_{Thr}$ and $\delta^{15}N_{Gly}$ (Fig. 4.8). This trend suggests that similar metabolic effects occurred, and that differences in the $\delta^{15}N_{\text{Bulk}}$ arise because of differences in the $\delta^{15}N$ of the plants at the base of the food chain. Deviations from this pattern may arise because of: (i) large analytical errors, (ii) metabolic effects, and (iii) differences in the $\delta^{15}N$ amino acid fingerprint of the various plant types that different species consumed. Again, this suggests that different plant $\delta^{5}N$ fingerprints play a role in the observed patterns. Future work should focus on determining δ^{15} N fingerprints for different dietary sources.

4.4.3 Dietary patterns suggested by $\bar{\delta}^{13}$ C

LDA is an emerging technique for identifying consumer diets, and it suffers from a relatively small dataset of dietary sources and little differentiation within the groups of dietary sources (Larsen et al., 2013, 2012, 2009). Here, only four dietary groups were used: aquatic producers, bacteria, fungi, and terrestrial plants. Within the groups, there is no differentiation between the δ ¹³C fingerprints of terrestrial graminoids, forbs or browse, or between different types of bacteria (Larsen et al., 2013, 2012, 2009). This means that such dietary classifications should be treated with caution at this stage of their development. Nonetheless, there is still value in applying this technique to assess species' diets, as is considered next.

Using LDA, the majority of woolly mammoth and all horse samples are classified as having consumed primarily bacterial diets (Fig. 4.10; Table 4.4). Since these species are non-ruminants, it is unlikely that the majority of their amino acids were derived from gut microbes. In this case, the bacterial content of their diet could reflect consumption a large quantity of decayed plants and their associated bacteria and microbes (Beare et al., 1990), as may have occurred during winter or year-round (Chapter 3; Putshkov, 2003; Schwartz-Narbonne et al., 2015; Tahmasebi, 2015). Consumption of decayed plants has been hypothesized to be an explanation for the high $\delta^{15}N$ of woolly mammoth (Chapter 3; Schwartz-Narbonne et al., 2015; Tahmasebi, 2015). Some woolly mammoth samples are classified by LDA as unmodified terrestrial plants consumers, which is also consistent with interpretations of a diet consisting of graminoids and forbs (Guthrie, 2001, 1982; Haynes, 1991). Why the LDA-driven classification of dietary inputs is different among the woolly mammoth samples is unknown, especially as there is no correlation with $\delta^{15}N_{\text{Bulk}}$ (Figs. 4.10c-d), as might be expected between animals consuming unmodified terrestrial plants and decayed plants. Similarly, the LDA-driven classification of all horse samples indicated primarily bacterial inputs to diet but only some samples have high $\delta^{15}N_{\text{Bulk}}$ (Figs. 4.10c-d). These discrepancies may suggest that while consumption of decayed plants may part be of the explanation for woolly mammoth high $\delta^{15}N_{\rm Bulk}$, other aspects of dietary or habitat selection may also be involved. These discrepancies may also suggest that a larger database of plants and other dietary sources is necessary to provide a more robust classification, and that the currently available δ^{13} C fingerprints are insufficient to fully interpret megafaunal diets.

There are modern species that preferentially consume partially decayed plants. The North American pika, *Ochotona princeps*, caches plant material with high toxin levels and consumes it after decomposition has lowered the quantity of toxin in the forage (Dearing, 1997). In feeding trials, several species of freshwater herbivorous invertebrates were found to consume more decomposed plants than fresh plants, likely because of loss of toxins during decomposition, though changes in nutritional content may also have been a factor (Suren and Lake, 1989). Previous work has found that decayed plants have lower C/N ratios (Tahmasebi, 2015), and thus may be more nutritious for herbivores than

unmodified plants. Decayed plants are principally suggested as forage for herbivores in the winter, when minimal forage is not available. It is also possible that some species preferentially selected decomposing forage year-round.

The LDA-driven classification of a diet of aquatic producers for the giant beaver matches other dietary reconstructions for this species (Perkins, 2009; Stuart-Williams et al., 1997). Likewise, the mastodon was found to have consumed unmodified terrestrial plants, consistent with previous reconstructions of a browse diet (Metcalfe, 2011; Metcalfe et al., 2013). Such diets are also consistent with the hypotheses that giant beaver and mastodon lived during interglacial periods (Harington, 2011; Zazula et al., 2014) when more aquatic habitats might have been available in Old Crow. If animals ate decayed plants to survive winters during glacial periods, there may have been less need to consume decayed plants during interglacial periods.

For the most part, the LDA-driven classification suggests that carnivores consumed herbivores that had consumed bacteria. However, the $\delta^{15}N$ of carnivore source amino acids are low, which is not consistent with a diet of herbivores that ate decayed plants with high source amino acid $\delta^{5}N$. An alternative explanation is that these carnivores ate ruminant species and that the gut microbes in the ruminants' digestive tract were the source of the bacterial classification. Gut microbes have been suggested as the source of bacterial classification of diets in previous work, though they have not been studied specifically in ruminants (Arthur et al., 2014; Larsen et al., 2011). Previous work on Alaskan carnivores suggests that ruminant species may have been part of the diet for gray wolves, scimitar cats and some brown bears, and that short-faced bears and other brown bears primarily consumed caribou, a ruminant species (Fox-Dobbs et al., 2008). Using LDA, the canid is classified as a consumer of herbivores that consumed mainly unmodified terrestrial plants, which may indicate that it fed mainly on non-ruminant rather than ruminant species.

One of the undated brown bears is classified as having consumed herbivores that ate unmodified terrestrial plants, with a weak LDA classification (low posterior probabilities for this specimen's LDA classification). It is possible that this bear ate herbivores that

had eaten a mixed diet or ate a variety of herbivores with different diets; the LDA approach is not well suited to classification of mixed diets (Larsen et al., 2012).

Figure 4.10 LDA Dietary classifications versus: $\mathbf{a}. \, \delta^{13}\mathbf{C}_{\text{Bulk}}$ **for each herbivore** s pecies; \bf{b} . $\delta^{13}C_{\rm Bulk}$ for all species; \bf{c} . $\delta^{15}N_{\rm Bulk}$ for each herbivore species; \bf{d} . $\delta^{15}N_{\rm Bulk}$ **for all species. Values in parentheses in the legend indicate the number of samples analyzed.**

A Bayesian analysis could help to elucidate the exact dietary compositions of the species consumed, if a larger baseline database could be assembled (Larsen et al., 2013). It is also

possible that this bear consumed herbivores that ate a dietary input whose $\delta^{13}C$ amino acid fingerprint has yet to be characterized. For example, there is no distinction between different types of terrestrial plants currently built into the LDA groups of dietary sources.

This study found glycine to be the amino acid having the most variable δ^{13} C. This variability has been observed in earlier studies, which suggest its relationship to other portions of the diet such as lipids or carbohydrates (Jim et al., 2006). Woolly mammoth has the lowest $\delta^{13}C_{\text{Gly}}$ of any of the species analyzed here, followed by mastodon (Table 4.2). It is possible that proboscideans had a greater lipid input to the δ^{13} C of their glycine, and that this is responsible for their low $\delta^{13}C_{\text{Bulk}}$.

4.5 Conclusion

A combined interpretation of amino acid δ^{15} N and δ^{13} C provides valuable insight into the diets of Old Crow herbivores and carnivores. The majority of woolly mammoths analyzed consumed a diet with a strong bacterial amino acid isotopic signal, which may reflect significant consumption of decayed plants. The nitrogen isotopic composition of the source amino acids, particularly the high values for glycine, support the hypothesis that mammoths may have obtained a portion of their protein from bacteria associated consumption of decayed plants. Mastodon and some woolly mammoths consumed a diet of unmodified terrestrial plants. Additional investigation of carbon and nitrogen isotope plant amino acid fingerprints is needed to differentiate whether those terrestrial plants were browse for the mastodon and either graminoids or forbs, or both, for the woolly mammoth. The low $\delta^{13}C$ of glycine for woolly mammoth and mastodon may suggest derivation of a large portion of their winter diet from stored lipids. Horse consumed a diet having a strong bacterial signal, and source amino acid $\delta^{15}N$ of horse and woolly mammoth commonly overlapped, which may suggest that they both consumed decayed plants. There is less overlap, however, between horse and woolly mammoth $\delta^{5}N_{\text{Gly}}$. This amino acid has been suggested to be a strong marker for degraded plants; hence the more limited overlap may suggest that more than one factor is at play in generating the high δ^{15} N of woolly mammoth and horse. Analysis of additional horse samples for which radiocarbon dates are available may provide insight into this question; the current small

dataset makes it impossible to determine whether the differences observed in horse $\delta^{5}N$ resulted from environmental changes over time or different dietary preferences. The giant beaver consumed aquatic plants at Old Crow, consistent with previous dietary reconstructions for this animal.

All species in this study known to be either carnivores or omnivores have been classified as carnivores on the basis of the separation in $\delta^{15}N$ between their trophic and source amino acids. There are differences, however, in their amino acid isotopic compositions that suggest different diets for the two undated brown bears, and that some carnivores consumed ruminants while others consumed non-ruminants. Future work focused the isotopic compositions of all the herbivore species present at Old Crow could utilize this information, in combination with SIAR analysis of $\delta^{13}C_{\text{Bulk}}$ and $\delta^{15}N_{\text{Bulk}}$, to obtain a more accurate understanding of carnivore diet in this portion of the mammoth steppe.

The Holocene brown bear has lower $\delta^{15}N_{\text{Bulk}}$ and higher $\delta^{13}C_{\text{Bulk}}$, and a distinct pattern of δ^{15} N for its source amino acids, notwithstanding its LDA-derived amino acid signature that suggests consumption of herbivores that primarily ate diets rich in bacteria. The climatic and environmental change during the Pleistocene to Holocene transition caused significant changes in the plant species that occupied the mammoth steppe. Further work on the δ^{15} N and δ^{13} C amino acid fingerprints this entire range of plant types may allow the diet of the Holocene brown bear (and other megafauna) to be better characterized and distinguished from the diet of the Pleistocene carnivores. Overall, combined analysis of amino acid carbon and nitrogen isotopic compositions of collagen can provide a much greater amount of information about the diets of megafauna species of the mammoth steppe ecosystem than can be obtained from isotopic analysis of bulk collagen.

4.6 References

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Chapter 5

5 Insights from mathematical analysis of isotopic niche on the mammoth steppe

5.1 Introduction

5.1.1 The Pleistocene mammoth steppe

The Pleistocene mammoth steppe was a megacontinental biome, stretching from northeastern Canada (the Yukon), across Alaska and northern Asia to western Europe (Fig. 5.1; Bocherens, 2003; Guthrie, 1990, 1984, 1982). This ecosystem disappeared at the end of the Pleistocene, accompanied by the extinction or extirpation of many of the megaherbivore species that lived there (Barnosky et al., 2004; Koch and Barnosky, 2006). Stable carbon and nitrogen isotopic studies of preserved animal tissues can yield a better understanding of the species that lived there, in particular how they coexisted across this vast biome, and how they adapted to climate change during the Pleistocene. This, in turn, can inform our understanding of extant species and the adaptability of species and ecosystems to major climatic changes.

The mammoth steppe biome was defined by the occurrence of the woolly mammoth in the fossil remains and an arid, graminoid- and forb-dominated environment (Bocherens, 2003; Guthrie, 1990, 1984, 1982). This large geographic area was characterized by a diverse set of megafauna, and by a high degree of faunal homogeneity. Faunal ecosystems throughout this area were dominated by mammoth, bison and horse, andshared a number of common species among the less prevalent fauna, such as caribou. The majority of these species (e.g. saiga antelope, woolly mammoth, caballid horse, bison, etc.) migrated across the exposed Bering Strait during glacial periods, and were able to fully disperse across the mammoth steppe (Guthrie, 2001; Shapiro et al., 2004). The flora of the mammoth steppe was also relatively homogeneous, particularly during pre-Last Glacial Maximum (pre-LGM) time periods (Guthrie, 1982; Willerslev et al., 2014). Pollen, plant macrofossil and ancient DNA studies suggest that the mammoth steppe was an herb-steppe-tundra environment, dominated by grasses, sedges, forbs and

Figure 5.1 Location of sites across the mammoth steppe. 'Red' represents the mammoth steppe as defined by Guthrie (1982). 'Yellow' represents areas where woolly mammoth, horse and bison remains are present in an environment hypothesized to have had steppe elements. 'Blue' represents areas where woolly mammoth, horse and bison remains are present, but in an environment hypothesized to be primarily forested. Darker shades represent higher elevations. Sites are lettered: SP. Spain; EU. NW Europe; RP. Russian Plain; GP. Gydan Peninsula; SB. south central Siberia; TP. Taymyr Peninsula; YK. Yakutia; WI. Wrangel Island, SK. Selawik; NS. North Slope; FB. Fairbanks; HI. Herschel Island; OC. Old Crow; KD. Klondike; AB. Alberta; GL. Great Lakes Area. Artwork by Katherine Allan.

herbaceous species. There is little evidence for tree growth during glacial periods, though some studies suggest that the mammoth steppe contained forests during interglacial periods (Burns, 1991; Guthrie, 1990, 1982; Huntley et al., 2013; Iacumin et al., 2000; Mandryk, 1996; Nogués-Bravo et al., 2008; Rasic and Matheus, 2007; Willerslev et al., 2014; Zazula et al., 2011; Zimov et al., 2012).

Several other areas may have contained the same floral and faunal elements as the traditionally defined mammoth steppe (yellow in Fig. 5.1; Álvarez-Lao et al., 2009; Harington and Ashworth, 1986; Harington, 2003). For example, previous studies suggest that Alberta was cold and arid, with herb-steppe-tundra flora, and contained the same faunal elements, including the woolly mammoth, present in the traditionally defined mammoth steppe regions (Burns, 2010, 1991; Burns and Young, 1994; Jass et al., 2011; Mandryk, 1996). We suggest that these areas fit current definitions of the mammoth steppe. Still further southeast, reaching through Ontario and Quebec are sites (blue in Fig. 5.1) where woolly mammoth, horse and bison bones from the Pleistocene have been found (Harington, 2003). These remains, however, occur in contexts previously reconstructed as mesic, forested areas (Metcalfe et al., 2013; Saunders et al., 2010). In the present study, we consider these populations within the context of the other regions examined, while acknowledging this difference in floral elements from those of the traditionally defined mammoth steppe.

The coexistence of various megaherbivores in the mammoth steppe may have been facilitated by niche feeding (Graham and Lundelius, 1984; Guthrie, 1984, 1982), in which each species consumed a narrow portion of available resources, thus limiting competition. Niche feeding could have been accomplished through partitioning of habitats or forage (Britton et al., 2012; Guthrie, 1982). The exact mechanisms of niche separation are not fully understood (Bocherens, 2003; Guthrie, 2001; Schwartz-Narbonne et al., 2015). While there was a high degree of floral and faunal continuity across the mammoth steppe, it was not a uniform environment. While some species migrated across the Bering Land Bridge during glacial periods, others, such as the woolly rhinoceros and the short-faced bear, stayed in the west or the east, respectively (Guthrie, 2001). A range of environmental conditions across the mammoth steppe has also been posited (Strong and Hills, 2005; Szpak et al., 2010; Willerslev et al., 2014), along with significant ecological changes over time that affected temperature, aridity, and floral and faunal compositions (Elias, 2001, 2000; Huntley et al., 2013; Rasic and Matheus, 2007; Strong and Hills, 2005; Willerslev et al., 2014; Zazula et al., 2014).

5.1.2 Stable isotopes

5.1.2.1 Carbon isotopes in plants and collagen

There are three main plant categories of plants with distinct mechanisms of carbon fixation, and thus distinct δ^{13} C: C₃ (average –27 ‰), C₄ (average –13 ‰), and CAM (average -11 ‰; Koch, 2007; Marshall et al., 2007; O'Leary, 1988). As the high latitude environments being considered here are dominated by C_3 plants, and no C_4 vegetation has been found from glacial periods (Gaglioti et al., 2011; Wooller et al., 2007), this paper focuses on the isotopic compositions of C_3 plants. The $\delta^{13}C$ of a plant growth form or species depends on the $\delta^{13}C$ of the CO₂ accessible to the plant, the mechanism of CO₂ uptake, and the plant's access to water and thus water use efficiency. In modern tundra environments, plants have a general pattern of δ^{13} C: shrubs < forbs < graminoids < fungi < lichens (Fig. 1.2; Barnett, 1994; Ben-David et al., 2001; Drucker et al., 2010; Kristensen et al., 2011). The variation between the average $\delta^{13}C$ of any two pairs of plant groups is \geq 1.5 ‰, but the ranges overlap considerably between species (Barnett, 1994). This overlap partially results from environmental differences between habitats and microhabitats of plants, which can have a significant effect on their carbon isotopic composition. Plants in a more arid environment have higher δ^{13} C than those in a more mesic environment (de Bello et al., 2009; Diefendorf et al., 2010; Ehleringer and Cooper, 1988; Ehleringer et al., 1987; Farquhar, 1989; Kohn, 2010; Tieszen, 1991; Wooller et al., 2007). Higher elevation, higher mean annual temperature and lower latitudes also correlate with higher plant δ^{13} C, though only weakly (Kohn, 2010), and the temperature and altitude effects are disputed (Heaton, 1999; Kohn, 2011; Stevens et al., 2006). Some work suggests that temperature is a stronger control on plant δ^{13} C than aridity in Arctic environments (Iacumin et al., 2006). Also, plants underneath a dense canopy cover have lower δ^{13} C than plants growing in an open environment likely because of recycling of organic matter and/or lower light levels affecting leaf processes in forested environments (Bocherens et al., 2011; Bonafini et al., 2013).

The δ^{13} C of a consumer's collagen is generally higher than that of the plants consumed. For large herbivores, a difference between collagen and diet $\delta^{13}C$ ($\Delta^{13}C_{\text{Bulk-Diet}}$) of +5.1 \pm 0.3 ‰ has been measured in several systems (Drucker et al., 2008). Carbon in herbivore

collagen can be derived from the plants it eats, milk from its mother and its own fat reserves. As adult teeth and bones were selected in this study, nursing was not considered to be a factor. In high latitude environments, however, winter diets are often quite poor, and so animals are expected to rely on their fat reserves to survive. Lipids generally have low δ^{13} C, and winter reliance on lipids has been suggested to be responsible for the low δ ¹³C of Beringian mammoths (Szpak et al., 2010). It has also been suggested that ruminants should have a higher δ^{13} C than non-ruminants consuming the same diet, as the former produce more methane, and methane is depleted of ${}^{13}C$ relative to the diet (Coltrain et al., 2004).

5.1.2.2 Nitrogen isotopes in plants and collagen

In the tundra, nitrogen availability to plants is usually limited. As a result, plants take up nitrogen in several forms, from varying soil depth, and through mycorrhizal associations (Nadelhoffer et al., 1996). These variations led to a general pattern of nitrogen isotopic compositions among species in tundra ecosystems: shrubs < fungi < forbs < graminoids < lichens (Fig. 1.2; Ben-David et al., 2001; Drucker et al., 2010; Finstad and Kielland, 2011; Kristensen et al., 2011; Nadelhoffer et al., 1996). While baseline isotopic compositions may vary between environments (Richards and Hedges, 2003; Syväranta et al., 2013), the general patterns are hypothesized to be largely consistent (Fox-Dobbs et al., 2008). The $\delta^{15}N$ of an ecosystem as a whole relates to the degree of nitrogen cycling, and thus the quantity of nitrogen loss, in an ecosystem. A hotter, more arid ecosystem tends to have more nitrogen cycling and greater loss of nitrogen, predominately as 14 N. As a result, plants and soil of arid ecosystems typically have lower $\delta^{5}N$ than cooler, more mesic ecosystems (Ambrose, 1991; Amundson et al., 2003; Drucker et al., 2003a; Heaton, 1987; Stevens and Hedges, 2004; Stevens et al., 2008).

There is an increase in the $\delta^{15}N$ between an animal's collagen and the diet it consumes. Although various trophic enrichment factors have been measured, they average around +3 ‰, ranging from +2 to +5 ‰ (Gannes et al., 1998; Koch, 2007; Koch et al., 1994). Beyond the trophic enrichment, a number of physiological effects can change the $\delta^{5}N$ of animal collagen. Several authors have suggested that physiological factors cause the $\delta^{5}N$

of a consumer's tissues in arid regions to be increased beyond that expected from the increase in plant $\delta^{15}N$ (Kelly, 2000; Koch et al., 1994; Sealy et al., 1987; Sponheimer et al., 2003). As well, when animals are on below-maintenance diets, they must recycle their body protein to survive. This causes an increase in tissue $\delta^{15}N$ (Gannes et al., 1998; Hobson et al., 1993; Kelly, 2000; Koch, 2007; Polischuk et al., 2011). While suckling has the same effect on $\delta^{5}N$ as an increase in trophic level (Metcalfe et al., 2010), none of the tissues studied here are expected to be from nursing animals.

5.1.2.3 Isotopic niche

A significant body of previous work has examined the relative carbon and nitrogen isotopic compositions of several megaherbivores at single mammoth steppe sites, or of fewer species at multiple sites (e.g. Bocherens et al., 2011, 1994; Drucker et al., 2003a, b; Fizet et al., 1995; Fox-Dobbs et al., 2008; Iacumin et al., 2010; Mann et al., 2013; Metcalfe, 2011; Metcalfe et al., 2013; Raghavan et al., 2014; Stevens et al., 2009; Szpak et al., 2010), either at for single point in time or over several time periods. The present work expands that approach to a comparison of much of the available $\delta^{13}C$ and $\delta^{15}N$ data (and the associated ecological niche) across multiple species, time periods and sites for the entirety of the mammoth steppe, so far as these data have been published.

Previous work has generally focussed on the relative isotopic position in $\delta^{13}C \cdot \delta^{15}N$ space of each species, site or time period in order to determine which had a higher average δ^{13} C or δ^{15} N. This is only one of the isotopic approaches that can be used to understand ecological relationships. Also of significance is the area on a plot of $\delta^{15}N$ versus $\delta^{13}C$ encompassed by the carbon and nitrogen isotopic compositions of each group, that is, all the individuals of a species measured at a single site and time period. This area provides a representation of their 'isotopic niche'. The isotopic niche encompasses a subset of a group's ecological niche, describing the sum of the dietary, environmental and physiological factors that combine to affect the placement and size of the group's isotopic compositions (Bearhop et al., 2004; Hammerschlag-Peyer et al., 2011; Layman et al., 2012). In the present study, the isotopic niche was assessed using three metrics. First, we examined niche position using the group's average δ^{13} C and δ^{15} N. This approach

provides information about the isotopic composition of the species' main forage, which is influenced by the plant type(s) consumed and environment of plant growth (Hammerschlag-Peyer et al., 2011), and the animals' physiological state. Figure 5.2a illustrates two hypothetical groups with different isotopic niche positions. Second, we examined isotopic niche width, which describes the degree of variety in resources consumed, as illustrated in Figure 5.2b. Third, we examined isotopic niche overlap, which describes the similarity in resource use between groups, as illustrated by Figure 5.2c (Hammerschlag-Peyer et al., 2011).

Assessment of the size of the isotopic niche of an animal can be performed using several mathematical approaches. The convex hull method, otherwise known as total area (TA), describes a polygon encompassing all data points (Layman et al., 2007), as illustrated in Figure 5.3a. A larger TA suggests a dietary generalist or consumption of food from a variety of habitats. A second method uses the small-sample-size corrected standard ellipse area (SEA_c), which includes the core 40% of data (Fig. 5.3b; Jackson et al., 2011). Bayesian statistics (Markov Chain Monte Carlo) provide a third way to estimate most probable niche sizes, after taking into account sample set size (Jackson et al., 2011). In the Bayesian approach, the most probable sizes of the standard ellipse can be estimated in a statistically rigorous fashion (SEA_b) . Two sets of estimated niche sizes can be compared in a to establish the proportion of estimated niches of one set that are larger than the second set (SEA_{b-prop}) . Again, a larger sample size provides more accurate estimates.

Niche overlap between two sample groups can be assessed using either the TA or the SEA_c . The size of the overlap is calculated, and then divided by the area of the first group. This calculation provides an estimate of the degree to which two groups utilized similar forage, or habitat, or made use of similar physiological adaptations.

There are three main concerns that can decrease the power of these metrics. First, since the TA includes the total area covered within a group, adding additional samples to a group can increase the size of that group, but can never decrease it. This means that the niche for a group containing a large number of analyzed specimens has the potential to

Figure 5.2 Conceptual model of hypothetical niche differences: a. Variation in carbon and nitrogen isotopic position between the isotopic niche of two species; b. Variation in the size of two isotopic niches; c. Variation between isotopic niches with an overlap and without an overlap.

Figure 5.3 Conceptual model of isotopic niche based on hypothetical points and groupings: a. The outer edge, or convex hull, of the group of data points for each species; b. Same data as for (a), but showing a standard ellipse corrected for small sample-size. The ellipses encompass 40% of the dataset for each group.

appear larger than one containing a small number of specimens (Jackson et al., 2011). Such an outcome is a particular worry in palaeoecology, where samples sets are commonly small and of varying sizes. Second, the SEA_c and SEA_b measures of niche size assume that the data are normally distributed (Jackson et al., 2011); the results are less rigorous if the data are nonparametric. Third, these metrics should be viewed with caution when comparing groups containing fewer than 10-30 individuals each (Jackson et al., 2011; Syväranta et al., 2013). Especially for paleontological data, there are commonly severe limits on the sample sizes within a group, especially for rare species. Such cases

remain interpretable, but the test is less powerful than for ecological data meeting these conditions.

5.2 Methods

5.2.1 Sample selection

Specimens were obtained from a variety of institutions and their stable carbon and nitrogen isotopic compositions were measured. Radiocarbon dates were also obtained for a subset of these samples. These new data were integrated with other information on species proportions, radiocarbon dates, and carbon and nitrogen isotopic compositions compiled from the literature (Bellissimo, 2013; Bocherens et al., 2011, 2005, 2001, 1997, 1996, 1995, 1994; Burns, 2010, 1996; Burns and Young, 1994; Debruyne et al., 2008; Druckenmiller, 2008; Drucker and Henry-Gambier, 2005; Drucker et al., 2003a, b, 2011; Fizet et al., 1995; Fox-Dobbs et al., 2008; García-Alix et al., 2012; Guthrie, 2006, 1968; Iacumin et al., 2010, 2000; Jass et al., 2011; Jass and Beaudoin, 2014; Leonard et al., 2007; MacPhee et al., 2002; Mann et al., 2013; McAndrews and Jackson, 1988; Metcalfe, 2011; Metcalfe et al., 2013, 2010; Mol et al., 2006; Raghavan et al., 2014; Shapiro et al., 2004; Stevens and Hedges, 2004; Stevens et al., 2009; Szpak et al., 2010; Zazula et al., 2014; Zimov et al., 2012).

A compilation of the data used is provided in Appendices K-AA. Data were removed from the compilation if the collagen for which they were obtained did not meet preservation criterion (collagen yield $\geq 1\%$, C (wt %) $\geq 13\%$, N (wt %) $\geq 4.8\%$, atomic C/N ratio between 2.9-3.6 (Ambrose, 1990; DeNiro, 1985). Isotopic data for teeth from most species were not included in the compilation, except for adult mammoth teeth (Metcalfe et al., 2010) and bison third molars (Balasse et al., 1999), which are known to reflect adult diets and are devoid of nursing or weaning isotopic signals. Isotopic data for antler were also not utilized, as this tissue reflects seasonal rather than yearly signals (Chapter 2).

The database includes samples from 16 sites (Fig. 5.1): southern Alberta (Alberta), the Fairbanks area (Fairbanks), the Great Lakes area (Great Lakes), Gydan Peninsula, Herschel Island, Klondike area (Klondike), Alaskan North Slope area (North Slope),

north-western Europe (NW Europe), Old Crow area (Old Crow), Russian Plain, Selawik Wildlife Refuge and surrounding areas (Selawik), south central Siberia, Spain, Taymyr Peninsula, Wrangel Island and Yakutia. Species proportions were compiled from the literature, and assigned to the appropriate time period where possible. Stable carbon and nitrogen isotopic data were available for multiple species over multiple time periods for each site evaluated. When multiple radiocarbon dates were available for a given sample, the stable isotopic results associated with the oldest date produced for collagen that had undergone ultrafiltration was used in the mathematical analysis (Zazula et al., 2014).

5.2.2 Sample preparation and analysis

5.2.2.1 Collagen extraction

Collagen extraction was performed at the Laboratory for Stable Isotope Science, University of Western Ontario, London, Canada, following published methods with minor modifications (Metcalfe et al., 2010). Samples were extracted using a Dremel[®] cutting wheel, and the exposed surfaces cleaned. Consolidant was removed from sample surfaces using a Dremel® equipped with a burr attachment. Previous work has shown that consolidant and its removal does not significantly affect collagen carbon and nitrogen isotopic compositions (France et al., 2011). Samples were then powdered.

A subset of the samples was lipid-extracted using a modified Bligh and Dyer method (Bligh and Dyer, 1959). The powdered samples were treated with a 2:1 chloroform:methanol solution (v:v) for 15 minutes, repeated 3 times, and then dried at room temperature. A comparison of 15 samples analyzed in duplicate both with and without lipid extraction showed a standard deviation between sets for $\delta^{13}C \leq 0.1$ ‰ and for $\delta^{5}N \leq 0.2$ ‰. As this is within the expected error for method duplicates, isotopic results for untreated and lipid-extracted collagen are considered to be equivalent for the purposes of this study. All samples were treated with 0.25 M HCl at room temperature for 24 hours. This was then replaced with 0.5 M HCl at room temperature until the samples were gelatinized. After gelatinization, humic removal was performed at room temperature with a solution of 0.1 M NaOH for 20 minutes, and repeated as necessary. The samples were then rinsed with water at room temperature until NaOH was removed completely. HCl was then used to adjust the pH to less than 3, and the collagen was solubilised at 90°C.

5.2.2.2 Stable isotope analysis

A Costech elemental combustion system (ECS 4010) attached to a Thermo-Scientific Delta V or to a Thermo-Scientific Delta Plus XL stable isotope ratio mass spectrometer (IRMS) operated in continuous-flow mode was used to measure the carbon and nitrogen isotopic compositions. These data were collected over a total of 13 analytical sessions. Two-point calibrations were used to relate the measured carbon and nitrogen isotopic compositions to internationally accepted standards (VPDB for carbon, AIR for nitrogen). Values of δ^{13} C were calibrated to VPDB using NBS-22 (accepted value -30.0 ‰) and IAEA-CH-6 (accepted value *–*10.5 ‰) or USGS-40 (accepted value *–*26.4 ‰) and USGS-41 (accepted value +37.6 ‰). Values of $\delta^{5}N$ were calibrated to AIR using USGS-40 (accepted value *–*4.5 ‰) and either IAEA-N2 (accepted value +20.3 ‰) or USGS-41 (accepted value +47.6 ‰). The same standards were used to provide two-point calibration curves for sample carbon and nitrogen contents, using the following accepted values: NBS-22, C = 86.3 %; IAEA-CH-6, C = 42.1 %; USGS-40, C = 40.7%, N = 9.5 %; USGS-41, C = 40.7%, N = 9.5%; IAEA-N2, N = 21.5%.

Accuracy (and precision) was also assessed using an internal laboratory keratin standard (MP Biomedicals Inc., Catalogue No. 90211, Lot No. 9966H), which was included in all analytical sessions. For 92 measurements of this standard, $\delta^{13}C = -24.1 \pm 0.1$ % (mean \pm 1 SD) (accepted value, -24.1% ₀), $\delta^{15}N = +6.3 \pm 0.2\%$ (accepted value, $+6.4\%$), C content = 48 ± 1 wt% (accepted value, 46.8 wt%) N content = 15 ± 1 wt% (accepted value, 14.6 wt‰), and atomic C/N ratio = 3.7 ± 0.2 (accepted value, 3.7). Reproducibility of the isotopic data was evaluated for 31 samples. The difference between values varied for δ^{13} C from 0.0 - 0.5 ‰ (SD), with an average difference of 0.1 ‰, and for δ^{15} N, from 0.0 - 0.2 ‰ (SD), with an average difference of 0.1 ‰.

5.2.2.3 Radiocarbon dating

Radiocarbon dates were obtained for several samples, as listed in Appendices L, M, Q and V. Collagen extraction, combustion, graphitization and radiocarbon dating were
performed at the University of Arizona Accelerator Mass Spectrometery (AMS) Laboratory. Dates are presented as uncalibrated radiocarbon years before present (1950).

5.2.3 Mathematical treatment

The majority of the isotopic datasets were analyzed using the using SIBER (stable isotope Bayesian ellipses in R) scripts (Jackson et al., 2011) from the SIAR (stable isotope analysis in R) package (Parnell et al., 2010) in R version 3.1.1 (R Core Team, 2014) using the R Studio interface version 0.98.1083. Datasets were only included in the SIBER analysis if there were results for: (i) at least 3 specimens of a species present at a given site and time period, and (ii) at least two sets of the species, site or time, thus providing a basis for comparison. Datasets for groups that did not meet these requirements were interpreted by considering the average (mean) $\delta^{13}C$ and $\delta^{15}N$ of the group calculated in Microsoft Excel.

The data were sorted into four time bins for interpretation, pre-LGM, LGM, post-LGM and Holocene, based on their radiocarbon date, physical context (Jass et al., 2011), or prior knowledge of the species at the site (Guthrie, 2006; Zazula et al., 2014). The clear separation in $\delta^{15}N$ between pre-LGM and post-LGM samples at Alberta was used to help sort horse and caribou samples at this site (Bellissimo, 2013). Multiple definitions of the timing of the LGM are present in the literature. To test for differences that might arise in the statistical modeling from the use of different LGM timings, the data were binned twice and the results compared. The first test (binning approach A) used the timing bins applied in several previous isotopic studies (Fox-Dobbs et al., 2008; Yeakel et al., 2013): pre-LGM, > 23,000 ¹⁴C BP; LGM, 23,000-18,000 ¹⁴C BP; post-LGM, 18,000-10,000 ¹⁴C BP, and Holocene, $\lt 10,000$ ¹⁴C BP. The second test (binning approach B) used the EPILOG preferred LGM chronozone (Mix et al., 2001): pre-LGM, $> 19,500$ ¹⁴C BP; LGM, 19,500-16,100⁻¹⁴C BP; post-LGM, 16,100-10,000⁻¹⁴C, and Holocene < 10,000⁻¹⁴C BP. All dated Holocene samples used in the quantitative analysis were older than 150 years old, and therefore no corrections were made for the Suess effect.

The database was interrogated to make comparisons for three types of variation: (1) groups of species at a given site and time period; (2) groups of sites at a given time and for a given species, and (3) time periods at a given site for given species. Examples of the mathematical treatments to the data set of species in Alberta during the pre-LGM period are presented in Figure 5.4. Isotopic niche position, niche size and niche overlap of the groups was evaluated for each comparison. Niche position was determined using the mean δ^{13} C and δ^{15} N of each group. These two metrics were organized from highest to lowest within a dataset, to help discern larger ecological patterns. Niche size was determined using the TA, SEA_c and $\text{SEA}_{b\text{-prop}}$ of each group; SEA_b was calculated using 10⁶ iterations. The relative niche size rankings for two sites, species or time periods were only defined when all three metrics gave the same result. Exceptions were made when one of the three metrics produced a tie, and the other two metrics were in agreement. Niche overlap was determined by calculating the proportion of the TA or SEA_c overlap between two groups, rounded to the nearest 10%. Groups were considered to overlap if either metric showed overlap. The overlap was calculated by dividing the area of overlap by the area of one of the two groups. This created situations where an overlap was obscured because one of the two groups was much larger than the other. To prevent this, the data was processed twice. The area of overlap was divided by the size of the first group the first time, and the second group the second time.

The normality of the data was tested in R version 3.1.1 (R Core Team, 2014) using the R Studio interface version 0.98.1083 using a multivariate Shapiro-Wilk test, using the mshapiro.test function in the 'mvnormtest' package (Royston, 1982). Out of a total of 95 distinct groups of species at a specific site and time period (including all groups from age binning methods one and two), 38 (40%) are non-parametric. Virtually every site, species and time period includes groups for which the data are parametric and groups for which the data are nonparametric (Appendix HH).

5.3 Results

5.3.1 Age binning approaches

As mentioned earlier, two approaches to the age binning were tested in this work. Binning approach A followed Fox Dobbs et al. (Fox-Dobbs et al., 2008), and binning approach B followed the model presented by the EPILOG project (Mix et al., 2001),

Figure 5.4 Graphs of $\delta^{13}\text{C}$ and $\delta^{15}\text{N}$ of pre-LGM Albertan megafauna produced in **SIBER: a. Individual data; b. Small-sample-size corrected ellipses encompassing 40% of the data for each species; c. Convex hulls encompassing the total area of all data for each species; d. Density plots of the most probable sizes of the standard ellipses for each species, based on Bayesian statistical analysis. The most probable size predicted by Bayesian statistical analysis for each species is shown by a black diamond (SEAb), while the size of the small sample-size corrected ellipse (SEAc) is shown by a red square.**

which was based on a compilation of climatic evidence from a variety of proxies. When the data was subdivided using each of the approaches, and overall isotopic ecological patterns were compared, both models produced the same general results. These patterns, however, held more strongly for data that was subdivided using the Mix et al. (Mix et al., 2001) model, with fewer species, sites or time periods appearing as outliers to the general patterns. The remainder of the paper presents the results obtained solely from the second binning approach (Mix et al., 2001). Results from the first binning approach are listed in Appendices BB, DD and GG.

5.3.2 Species proportions at each site

Data on species proportions were available for: (1) two Russian sites, Taymyr Peninsula and Koluma River Lowland, Siberia (Mol et al., 2006; Zimov et al., 2012); (2) three Alaskan sites, Fairbanks, the North Slope and Selawik (Druckenmiller, 2008; Guthrie, 1968; Mann et al., 2013), and one Canadian site, Alberta (Appendix K; Jass et al., 2011). These analyses were conducted by counting the number of individual specimens, and generally were not corrected for differences in the number of skeletal elements in different species, or other collection biases, such as the risk of over-representing species with more robust material (Guthrie, 1968; Mann et al., 2013; Zimov et al., 2012). Neither of the two Russian sites has strong associated dating. The Yakutia site is known to contain specimens spanning the range from the pre-LGM to the post-LGM time periods (Zimov et al., 2012). Some samples from Taymyr Peninsula are dated, and the majority of these are from the pre-LGM time period (MacPhee et al., 2002; Mol et al., 2006). Four sites from Fairbanks (Guthrie, 1968) were first considered separately. As the general patterns obtained were similar for each site, an average set of proportions was then calculated; all samples from Guthrie's study are undated. Dates for the North Slope site (Mann et al., 2013) were combined with information from Groves (2015, personal communication) to obtain time-dependent species proportions. Radiocarbon dates were obtained for several Selawik samples in this study and in previous work (Druckenmiller, 2008), the majority of which were pre-LGM. Species abundances and radiocarbon dating are available at the Alberta site (Jass et al., 2011) for both the pre-LGM and post-LGM time periods.

Individual sites across the entire mammoth steppe, or even just within eastern Beringia, show a large difference in relative species abundances, even between sites that are geographically close (Fig. 5.5; Appendix K). For example, Fairbanks is bison-dominated, the North Slope is horse-dominated and the Selawik is mammoth-dominated, despite these all being Alaskan sites. Some weak patterns can be discerned from these data, although out of the six sites, no pattern holds for more than four sites. Generally, horse is most prevalent at a site, followed by bison and then mammoth or muskox, and caribou is less prevalent than mammoth, bison or horse.

The two sites for which the strongest temporal control is available show different patterns in their response to the LGM (Fig. 5.6). Alberta shifts from a horse-dominated assemblage with bison as the secondary species to a bison-dominated assemblage with horse as the secondary species after the LGM. The North Slope remained horsedominated during the entire late Pleistocene, and there was an increase in the proportion of horse at the site over time. The secondary species at the North Slope shifted from bison during the pre-LGM, to caribou during the LGM, and then back to bison during the post-LGM time period. The modern North Slope is composed almost entirely of caribou.

5.3.3 Variation between species at a given site and time period

The isotopic niche characteristics for each species at a given site and time period are detailed in Appendix CC. Figure 5.7 displays SEA_c for species at two sites (Alberta, North Slope) for two time periods (pre-LGM, post-LGM).

5.3.3.1 Typical pre-LGM patterns and exceptions

The pattern of species' average δ^{13} C and δ^{15} N is relatively consistent among the 7 measured mammoth steppe sites for the pre-LGM time period (Fig. 5.8), though there were deviations from typical species δ^{13} C and δ^{15} N patterns at one site. Average δ^{13} C of horse \lt mastodon at Fairbanks, and average δ^5 N of mastodon $>$ caribou and horse at Fairbanks (Fig. 5.9). At the majority of sites (Klondike, NW Europe, North Slope, Fairbanks and Yakutia), mammoth and mastodon isotopic niches were smaller than those

Figure 5.5 Herbivore species proportions at sites across the mammoth steppe. Sites lettered as in Figure 5.1. Proportions are shown for sites known to represent pre-LGM species abundances (Alberta and North Slope), sites that are primarily composed of pre-LGM samples (Selawik and Taymry Peninsula), and sites for which there is no dating control (Fairbanks and Yakutia). Higher altitudes are represented by darker shades of grey. Artwork by Katherine Allan.

Figure 5.6 Changes in herbivore species proportions over time at Alberta and the North Slope. Sites lettered as in Figure 5.1. Higher altitudes are represented by darker shades of grey. Artwork by Katherine Allan.

Figure 5.7 Small-sample size corrected ellipses (SEAc) of species at two periods at two sites: a. Alberta species during the pre-LGM period; b. Alberta species during the post-LGM period; c. North Slope species during the pre-LGM period; d. North Slope species during the post-LGM period.

for muskox, horse and caribou. Only at Alberta and Taymyr was the mammoth isotopic niche larger than caribou, horse or muskox. The typically smaller isotopic niche of pre-LGM mammoths and mastodons than muskox, horse and caribou can be seen in Figure 5.7c. The larger isotopic niche of mammoth at Alberta is displayed in Figure 5.7a.

Figure 5.8 Typical carbon and nitrogen isotopic ranking of species at pre-LGM sites. From lowest to highest, average $\delta^{13}C$ tended to follow the order: mammoth $<$ **mastodon = horse < bison < muskox < caribou. From lowest to highest, the average** *δ* **¹⁵N tended to follow the order: mastodon < caribou < bison < horse < muskox < mammoth. Artwork by Katherine Allan. Mammoth drawing from Chapter 3 and Schwartz-Narbonne et al. (2015). Mastodon drawing from Chapter 4.**

Species are considered to overlap when there is at least 10% overlap using one of the two metrics. There are five species pairings showing isotopic niche overlap at multiple sites: bison-horse, bison-caribou, bison-muskox, horse-mammoth, and horse-mastodon. These five overlaps are considered 'typical' niche overlaps. Figures 5.7a and 5.7c display the horse-mammoth overlap at Alberta and the North Slope and the bison-muskox overlap at the North Slope. The TA isotopic niches overlapped for the bison-horse at Alberta and the North Slope (e.g. Fig. 5.4c), and for bison-caribou at the North Slope, but these overlaps are not visible in the graphs illustrating SEA_c.

Figure 5.9 continues on next page.

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Figure 5.9 continues on next page.

Figure 5.9 Average and nitrogen isotopic rankings of species from at all pre-LGM site having sufficient data for qualitative analysis. Sites lettered as in Figure 5.1. Higher altitudes are represented by darker shades of grey: a. Pre-LGM isotopic rankings; b. LGM isotopic rankings; c. Post-LGM isotopic rankings; d. Holocene isotopic rankings. Artwork by Katherine Allan. Mammoth drawing from Schwartz-Narbonne et al. (2015). Mastodon drawing from Chapter 4.

There are exceptions to the 'typical' niche overlaps. Situations where these niche overlaps are missing are mostly related to species occurring in smaller abundances than typical, or niche sizes that are small relative to other species at the site. For example, horse and mammoth did not overlap at Fairbanks or Selawik. At Fairbanks, horse abundance is lower than bison, which is atypical for the mammoth steppe. At Selawik, mammoth abundance is higher than horse. Likewise, bison and caribou did not overlap at Alberta. There, caribou has the smallest isotopic niche and caribou abundance is low compared to other species at this site.

There are also a number of isotopic niche overlaps that occur only at one site, and which can be related to species with the largest niches at that site. Bison and mammoth overlapped at Alberta, where they had the largest niches but abundances lower than horse (Figs. 5.4c; 5.5). Muskox-mastodon and mastodon-mammoth overlap at Klondike, a pattern driven by the large niches of mastodon and muskox. Caribou-horse overlap in NW Europe, where they have the largest niche, as is also the case for the North Slope for muskox-caribou. There is also overlap between horse-muskox at the North Slope.

5.3.3.2 Typical LGM patterns and exceptions

Three sites had sufficient dated samples for analysis of the species patterns for caribou and horse during the LGM (Fairbanks, North Slope and NW Europe). The $\delta^{13}C$ patterns were the same as for the pre-LGM, but the average $\delta^{15}N$ of horse was lower than caribou at all three sites (Fig. 5.9b). This shift corresponded to an increase in the relative proportion of caribou at the North Slope (Fig. 5.6). This site shifted from horse- and bison-dominated to horse-dominated, with caribou being the second most prevalent species. There was no overlap between caribou and horse at these three sites, which corresponds to expected pre-LGM conditions.

5.3.3.3 Typical post-LGM patterns and exceptions

Only four sites had sufficient samples for δ^{13} C and δ^{15} N patterns to be assigned to species (Alberta, NW Europe, North Slope and Taymyr Peninsula; see Fig. 5.9c). Horse, bison, caribou, mammoth and muskox all had the same and expected patterns for average

species δ^{13} C observed for the pre-LGM and LGM. There was too much variation among sites to ascribe patterns to the average $\delta^{5}N$ of the species. The Taymyr Peninsula retained the expected relative $\delta^{15}N$ rankings of mammoth and muskox from the pre-LGM. No consistent patterns were observed in horse, bison and caribou $\delta^{15}N$ rankings at Alberta, NW Europe or North Slope. The three sites did not consistently follow patterns expected based on pre-LGM $\delta^{15}N$ or the post-LGM $\delta^{15}N$. This variation can be seen in Figures 5.7a-d. In Alberta, the average $\delta^{15}N$ of pre-LGM horse are higher than bison for the pre-LGM, but lower for the post-LGM (Figs. 5.7a, b). In contrast, in the North Slope, the horse consistently has higher average $\delta^{15}N$ than bison for both pre-LGM and post-LGM (Figs. 5.7c, d). Alberta shifted from horse-dominated during the pre-LGM to bisondominated during the post-LGM (Fig. 5.6). In contrast the North Slope remained horsedominated throughout the late Pleistocene. At both Alberta and the North Slope, the bison isotopic niche was larger than the horse niche during the pre-LGM, and was smaller during the post-LGM (Fig. 5.7). At both sites, there was a shift from pre-LGM overlap between the species to no overlap during the post-LGM. NW Europe was distinct in its complete overlap among the four species measured at the site (bison, elk, caribou and horse). A shift also occurs in the position of caribou, which moves from generally having the lowest $\delta^{5}N$ during the pre-LGM to commonly having the same or higher average higher $\delta^{15}N$ than bison and horse at North Slope and NW Europe (Fig. 5.9c). This change in position comes without a change in caribou relative abundance at the North Slope, where it is remains less abundant than horse or bison (Fig. 5.6). During the post-LGM, the caribou overlaps with horse and bison at NW Europe but not at the North Slope, and caribou has a smaller isotopic niche than horse at both sites.

5.3.3.4 Typical Holocene patterns and exceptions

Holocene samples were only measured for the North Slope and NW Europe (Fig. 5.9d). There were no common species between the two sites. Both sites contained species that were present at those sites during earlier time periods. In NW Europe, elk and horse were both present and exhibited niche overlap during the post-LGM time period and the Holocene. The average $\delta^{13}C$ and $\delta^{15}N$ rankings, however, changed between these time periods. During the post-LGM period, horse had lower average $\delta^{13}C$ and $\delta^{15}N$ than elk,

while in the Holocene horse and elk had the same average δ^{13} C and horse had higher average $\delta^{5}N$ than elk. The horse and elk isotopic niches overlapped.

Muskox and caribou were both present at the North Slope during the pre-LGM and the Holocene. The $\delta^{13}C$ and $\delta^{15}N$ rankings remained consistent between these species, but niche overlap disappeared in the Holocene. The species proportions of muskox also decreased considerably, and caribou became dominant species at the North Slope in the Holocene.

5.3.3.5 Qualitative interpretations

In some cases where there are insufficient numbers of dated specimens to make quantitative comparisons of the isotopic data, there remains value in comparing the average δ^{13} C and δ^{15} N of a species to their expected patterns in isotopic space. The ranking of δ^{13} C for mastodon and horse was not well-established in the quantitative results, since these two species only coexisted in time at two sites, and one of those sites was Fairbanks which did not follow typical isotopic patterns for the majority of species at the site. For this reason, the "typical" pattern of mastodon and horse having the same average δ^{13} C is not observed in the qualitative analysis of other sites. At Alberta, the Klondike and Old Crow, the δ^{13} C pattern was horse < mastodon. This was consistent with the pattern observed at Fairbanks.

When considering patterns other than the mastodon versus the horse, of the ten sites where qualitative observations were available, six sites for $\delta^{13}C$ and three sites for $\delta^{15}N$ did not match the expected pattern for at least one species. At Fairbanks, the bison average $\delta^{5}N$ fits the expected pre-LGM pattern for the most part; mastodon, however, is not in its typical place in the pattern, as was previously observed when comparing other species at this site to mastodon. At Yakutia, the pre-LGM material follows the expected patterns, whereas undated material does not. This may suggest that the majority of the undated material is not from the pre-LGM, and that the pattern of average $\delta^{15}N$ of species at the site changed over time. Post-LGM elk and caribou in south central Siberia do not match the pattern observed in NW Europe. Similarly, Holocene moose and caribou at Selawik do not match the North Slope pattern when only dated caribou specimens are

considered, though they match when both dated and undated material are included in comparisons. Pre-LGM bison, caribou, horse and muskox do not follow the expected patterns at Selawik; horse and bison do not follow expected patterns in later time periods at this site.

There were three species for which the isotopic data could only be examined qualitatively: sheep, woolly rhinoceros, and muskox. At Fairbanks, the muskox species *Symbos cavifrons* (helmeted muskox) was sampled rather than *Ovibos* sp. *S. cavifrons* had the same pattern of average δ^{13} C as the other species of muskox, but had the lowest δ^{15} N of any species at the site for any time period. Data for woolly rhinoceros was available in NW Europe for both pre- and post-LGM time periods. In both cases, it had the second highest $\delta^{15}N$, following mammoth. Its $\delta^{13}C$ ranking varied between time periods, but was generally similar to bison. Data for Dall sheep were examined both for Fairbanks and Klondike, though for different time periods. Their average $\delta^{13}C$ tended to be high, similar to caribou and higher than muskox. The average $\delta^{15}N$ of Dall sheep were always lower than woolly mammoth. At Fairbanks, Dall sheep had a higher average $\delta^{15}N$ than horse, and at Klondike average $\delta^{15}N$ was lower than muskox.

5.3.4 Variation between sites for a given species and time period

The isotopic niche characteristics of a species at a given time period between varied sites are detailed in Appendix EE. The SEA_c for two species (bison and horse) during two time periods (pre-LGM and post-LGM) are illuststrated in Figure 5.10. The overall patterns based on the quantitative results are displayed in Figure 5.11, and the patterns based on both quantitative and qualitative results are displayed in Figure 5.12.

5.3.4.1 Typical pre-LGM patterns and exceptions

General patterns of site differentiation are displayed in Figures 5.11a and b, where sites are listed from west to east. As seen in Figure 5.11a, δ^{13} C tended to be lowest for animals from sites between Taymyr Peninsula and Fairbanks, with higher average $\delta^{13}C$ associated with animals of the same species that lived to the west in NW Europe and to the east in Klondike or Alberta. A similar pattern is visible in the average $\delta^{15}N$ of sites (Fig. 5.11b).

Figure 5.10 Small-sample size corrected ellipses (SEAc) of sites at two periods for two species: a. Bison during the pre-LGM period; b. Bison during the post-LGM period; c. Horse during the pre-LGM period; d. Horse during the post-LGM period.

Species who lived in the west (NW Europe and Yakutia) or east (Alberta) had higher average $\delta^{5}N$ than species who lived in the middle region from Selawik to Klondike.

In several cases, unambiguous distinction between sites was not possible using the available data, in which case those sites were assigned the same relative position in δ^{13} C- δ^{15} N isotopic space. Sites were not ranked if data were available for only one species or if data were available for only two species and gave conflicting rankings. Nonetheless,

using the ranking associated with each bin, the same sites – Fairbanks or North Slope – always fell outside of expected patterns. These deviations can be seen in four cases: (i) the average δ^{13} C of Fairbanks was higher than NW Europe or North Slope for mammoth, (ii) the average δ^{13} C of Alberta was higher than North Slope for caribou, (iii) the average δ^{15} N of North Slope was higher than NW Europe for horse (see Fig. 5.10c), and (iv) average $\delta^{5}N$ of North Slope was lower than Fairbanks and Klondike for mastodon. In all other cases, the species fit the expected patterns (see Figs. 5.10a, c)

No consistent pattern of niche size ranking could be discerned among sites for the pre-LGM samples. The isotopic niches for the majority of sites (~two-thirds) overlapped for the species analyzed (e.g. Figs. 5.10a, c). Three sets of sites, however, did not show isotopic niche overlap for multiple species: (i) Alberta-Fairbanks for caribou or horse (Fig. 5.10c) (though there was overlap for mammoth); (ii) Alberta-Selawik for horse or mammoth (Fig. 5.10c); and (iii) Fairbanks-Old Crow for mammoth or mastodon. The isotopic niches for ~one-third of the sites did not overlap for mammoth and mastodon. These were the only two species that showed no isotopic niche overlap for multiple site pairs where those site pairs had overlap for other species.

5.3.4.2 Typical LGM patterns and exceptions

The δ^{13} C pattern of Fairbanks, NW Europe and North Slope for horse and caribou are similar to the pre-LGM (Figs. 5.11a, c). The only difference is that the average $\delta^{13}C$ of species at the North Slope is higher than those in NW Europe during the LGM (Fig. 5.11c). The $\delta^{15}N$ pattern of the pre-LGM is not retained in the LGM for horse or caribou. As well, unlike the pre-LGM, Fairbanks-North Slope and North Slope-NW Europe isotopic niches no longer overlap, though Fairbanks-NW Europe isotopic niches continue to overlap.

5.3.4.3 Typical post-LGM patterns and exceptions

The general site patterns for the post-LGM time period based on δ^{13} C are similar to the pre-LGM (Figs. 5.11a, e). In contrast, the patterns based on $\delta^{15}N$ are largely reversed compared to the pre-LGM, though they are somewhat similar to the LGM (Figs. 5.11b, d, f). A clear pattern of isotopic niches sizes for species at individual sites is difficult to discern, as there were too few species that were found at multiple sites. Similarly to the LGM, there were a greater proportion of sites without isotopic niche overlap than there was during the pre-LGM. Approximately two-thirds of sites did not have isotopic overlap during the post-LGM period. This greater degree of separation between sites is illustrated in Figure 5.10, where the isotopic niches of horse and bison from different sites are shown to be less likely to overlap during the post-LGM period than the pre-LGM period.

Figure 5.11 continues on next page.

Figure 5.11 continues on next page.

Figure 5.11 Typical isotopic ranking of sites across the mammoth steppe based on the *δ***-values of multiple species, incorporating results from quantitative analysis. Sites are presented from west to east; note x-axis spacing is not proportional to geographic separation: a. Average pre-LGM** *δ* **¹³C: Fairbanks = Yakutia = Selawik = Taymyr Peninsula (Taymyr) < NW Europe = North Slope < Alberta = Klondike; b. Average pre-LGM** *δ* **¹⁵N: Fairbanks = Klondike = Selawik < North Slope < NW** \bold{E} urope < Yakutia = Alberta; **c.** Average post-LGM δ^{13} C: North Slope = NW Europe **< Alberta. d. Average post-LGM** *δ* **¹⁵N: Alberta < NW Europe < North Slope.**

Figure 5.12 continues on next page.

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Figure 5.12 continues on next page.

Caption on facing page.

Figure 5.12 Typical isotopic ranking of sites across the mammoth steppe based on the *δ***-values of multiple species, incorporating results from both qualitative and quantitative analysis. Sites are presented from west to east; note x-axis spacing is not proportional to geographic separation: a. Average pre-LGM** *δ* **¹³C: Fairbanks = Yakutia = Selawik = Taymyr Peninsula (Taymyr) < NW Europe = North Slope < Spain < Alberta = Klondike < Russian Plain = south central Siberia (SC Siberia); b. Average LGM** *δ* **¹³C: Yakutia < Fairbanks < NW Europe < SC Siberia = Selawik = North Slope = Old Crow < Klondike; c. Average post-LGM** *δ* **¹³C: Yakutia < Old Crow < Selawik = Fairbanks = North Slope = NW Europe = Gydan Peninsula (Gydan) < SC Siberia < Klondike < Russian Plain = Great Lakes = Alberta; d. Average Holocene** *δ* **¹³C: Yakutia < Taymyr = Selawik < North Slope = Klondike =** Fairbanks; **e. Average pre-LGM** δ^{15} **N: Fairbanks = Klondike = Selawik < North Slope < SC Siberia = NW Europe < Yakutia = Alberta < Russian Plain < Spain; f. Average LGM ¹⁵N: SC Siberia = Selawik = NW Europe = Fairbanks < Yakutia <** North Slope < Old Crow; g. Average post-LGM $\delta^{15}N$: Alberta = SC Siberia = **Klondike < Russian Plain < NW Europe = Fairbanks < Great Lakes = Selawik < Yakutia = North Slope = Old Crow = Taymyr = Gydan; h. Average Holocene** δ^{15} **N: Fairbanks < North Slope < Klondike = Taymyr = Yakutia.**

5.3.4.4 Typical Holocene patterns and exceptions

There are only two Holocene species, muskox and caribou, where samples were analyzed from more than one site. Since the two species were not found at the same two sites, analysis of 'typical' Holocene patterns is not possible. The rankings of the two species can be compared to the typical patterns during the pre-LGM, as presented in Figures 5.11a, b. The δ^{13} C pattern for Taymyr Peninsula and North Slope based on the muskox average δ^{13} C is the same as the typical pattern during the pre-LGM, but this pattern is reversed from the typical pre-LGM pattern for $\delta^{15}N$. For caribou, the $\delta^{13}C$ and $\delta^{15}N$ pattern for Klondike and North Slope are not the same as the typical patterns during the pre-LGM.

5.3.4.5 Qualitative interpretations

Based on the qualitative observations, additional sites were added to the quantitative patterns, as depicted in Figures 5.12a-h. Generally, similar trends were observed from east to west as were observed using the quantitative analysis. During the pre-LGM, the lowest average *δ* ¹³C was generally observed for species living between Taymyr Peninsula and Fairbanks (Fig. 5.12a). This general trend of the highest average $\delta^{13}C$ occurring in species that lived in the east or west regions of the mammoth steppe held throughout the Pleistocene and Holocene, though there was considerable variability between specific sites (Figs. 5.12b-d). Similarly, the quantitative pre-LGM $\delta^{15}N$ patterns were also present in the qualitative results, with species living in sites between Selawik and Klondike having lower average $\delta^{5}N$ than those to the east and to the west (Fig. 5.12e). This pattern shifted over time such that sites on the east and west of the mammoth steppe tended to have the lowest, rather than the highest, average $\delta^{15}N$ for the species that lived there during the LGM, post-LGM and Holocene (Figs. 5.12 f-h). Again, this matched the changes in the $\delta^{15}N$ pattern over time detected using the quantitative approach (Figs. 5.11b, d, f).

5.3.5 Variation between time periods for a given species and site

The isotopic niche characteristics of a species at a site over varying time periods are detailed in Appendix GG. The SEA_c for two species (bison and horse) for two sites (Alberta and North Slope) are illustrated in Figure 5.13. The overall patterns are shown in Figure 5.14.

5.3.5.1 Typical patterns and exceptions

The typical δ^{13} C and δ^{15} N patterns for the time periods (Fig. 5.14a) are highly generalized. While a comparison of any two time periods for either isotope retained these patterns in most cases, results for almost half of the species analyzed at specific sites do not match the general pattern for at least one isotope during at least one time period. For example, bison and horse from Alberta and North Slope follow the expected pattern for average $\delta^{15}N$ but Alberta bison and North Slope horse do not follow the expected pattern

Figure 5.13 Small-sample size corrected ellipses (SEAc) of multiple time periods for two species at two sites: a. Bison in Alberta; b. Horse in Alberta; c. Bison in the North Slope; d. Horse in the North Slope.

for average δ^{13} C (Figs. 5.13a, d). As well, the extent of the isotopic shift over time varies between species at a site. For example, the change of $\delta^{15}N$ for bison in Alberta from the pre-LGM to the post-LGM is less than the change observed for horse (Figs. 5.13a, b).

The relative sizes of isotopic niche for species at a specific site changed between time periods. At most sites, the largest number of species have the smallest isotopic niches during the LGM, larger niches during the post-LGM, and the largest niches during the

Figure 5.14 Typical isotopic ranking of time periods in the mammoth steppe: a. Rankings based on quantitative observations. Average $\delta^{13}\text{C}$ **: Holocene < post-LGM < pre-LGM; average** *δ* **¹⁵N: post-LGM < pre-LGM = Holocene; b. Rankings based** both on qualitative and quantitative observations. Average $\delta^{13}\mathrm{C}\text{: Holocene} <$ post-**LGM < pre-LGM < LGM. Average** *δ* **¹⁵N: post-LGM < Holocene = pre-LGM = LGM.**

pre-LGM. A comparison of the size of the isotopic niches for bison and horse from Alberta and North Slope provides a good example (Fig. 5.13). For bison at both site, and for Albertan horse, the niches were larger for pre-LGM than they were for post-LGM. At the North Slope, horse and bison had overlapping isotopic niches between time periods (Figs. 13c, d). This pattern of overlap was observed for most species at most sites. Bison

and horse in Alberta were some of the exceptions to the general pattern, as their isotopic niches did not overlap between the pre-LGM and post-LGM periods (Figs. 5.13a, b).

5.3.5.2 Qualitative results

Patterns observed for groups of individuals of the same species at the same site, but having only limited numbers of radiocarbon dates, are similar to those arising from the datasets for which quantitative analysis was possible. The isotopic characteristics of the various time periods are better resolved when information from the qualitative inspection of the dataset is combined with that of the quantitative analysis and the isotopic ranking of the LGM can be added to the general patterns. As seen in Figure 5.14b, when the qualitative data is added to the quantitative data, the δ^{13} C and δ^{15} N isotopic ranking of the LGM can be added to the observed patterns.

5.4 Discussion

5.4.1 Pre-LGM mammoth steppe

5.4.1.1 Species

The statistical and qualitative examinations of the isotopic data suggest that the mammoth steppe was a relatively homogeneous ecosystem during the pre-LGM. There is remarkable consistency in the patterns of average carbon and nitrogen isotopic compositions among species at various sites (Fig. 5.8). This consistency suggests that the herbivores' main dietary and environmental niches were conserved across the mammoth steppe. This general pre-LGM pattern has been suggested previously (Bocherens, 2015) and its causes are discussed below.

Horses, bison and mammoth were the grazers of the mammoth steppe (Bocherens, 2015, 2003; Guthrie, 2001, 1990). While all three species primarily ate grasses, there is some isotopic evidence that horse and bison diets included sedges and herbaceous plant species (Fox-Dobbs et al., 2008), and some authors have suggested that bison diets included a minor browse component (Rivals et al., 2007). Other forms of plant or habitat differentiation have also been suggested among grazers. Modern European horses are known to consume shorter herbaceous forage (monocots) than ruminants such as bison,

which tend to consume more dicots (Britton et al., 2012). These factors could have contributed to the generally lower δ^{13} C and δ^{15} N of bison than horse. Mammoths have been shown to consume an isotopically distinct food source with higher $\delta^{5}N$, likely because they ate in arid regions, fertilized plants with dung, selected specific plants or plant parts and/or ate decayed plants (Chapter 3, 4; Schwartz-Narbonne et al., 2015; Tahmasebi, 2015).

Mixed-feeding or browse dietary niches have been suggested for mastodon, caribou and muskox. The browse component of mastodon diet could be responsible for their low $\delta^{15}N$ (Coltrain et al., 2004; Koch et al., 1998; Metcalfe et al., 2013; Zazula et al., 2014). Evidence from plant material preserved in caribou teeth suggests winter feeding on lichens, and an otherwise mixed-feeding diet (Guthrie, 2001), potentially containing a large quantity of moss and fungi. Such a diet has been hypothesized to be responsible for the generally low $\delta^{15}N$ and generally high $\delta^{13}C$ of Pleistocene caribou (Bocherens, 2015, 2003; Bocherens et al., 1996; Fizet et al., 1995; Fox-Dobbs et al., 2008; Iacumin et al., 2000). Reconstructed diets of Pleistocene muskox have included varying proportions of graze (graminoids, forbs, sedges) and browse (Guthrie, 2001; Mann et al., 2013; Raghavan et al., 2014), and/or large quantities of lichen (Fox-Dobbs et al., 2008). The fact that muskox generally had higher $\delta^{15}N$ than the grazing horse and bison, and much higher $\delta^{15}N$ than the browsing mastodon suggests that it did not consume much browse in the mammoth steppe. Perhaps it was a grazer that ate from more arid environments than horse or bison. More studies are necessary to further characterize the isotopic compositions of plant families (e.g. graminoids, forbs and shrubs) and plant parts at high latitude environments, including amino-acid-specific stable isotopic studies, which might help to better understand plant isotopic responses to environmental stressors.

Some of the isotopic differences among species have been attributed to physiological differences, rather than environmental or dietary origins. The non-ruminant species (mammoth, mastodon and horse) have lower average δ^{13} C than the ruminant species (caribou, bison, muskox), perhaps because the latter release a larger quantity of methane, which has low δ^{13} C, than the former (France et al., 2007). While this physiological explanation may be part of the answer, it does not explain the variation in average $\delta^{13}C$

within ruminant and non-ruminant species, or the fact that the differences in average $\delta^{13}C$ are not consistent between sites, which might be expected if the cause was purely physiological (Britton et al., 2012).

Animals living in high latitude environments rely on their fat reserves for nourishment in winter; this fat is depleted of 13 C relative to the whole body, which likely contributes to a lower δ^{13} C in all species than would otherwise occur (Szpak et al., 2010). The impact, however, was likely larger for some species than others. For example, mastodons are suggested to have lived on the mammoth steppe only during interglacial periods (Zazula et al., 2014), which would have had milder winters than during glacial periods. By comparison, mammoths, whose fossils include individuals present during interglacial and glacial periods, would have been present during harsher winters and relied more on their fat reserves, thus leading to their lower δ^{13} C than mastodons. This is consistent with mastodons generally having higher δ^{13} C than horses, which were also present during glacial and interglacial periods (Fig. 5.4). More detailed feeding studies of megaherbivores are necessary to better discriminate among the physiological, habitat and dietary components contributing to the δ^{13} C of herbivore collagen.

Some studies have suggested that the $\delta^{15}N$ of ruminant and non-ruminant species is also affected by gut physiology and digestive capacity (Britton et al., 2012; Coltrain et al., 2004; Fizet et al., 1995). However, there is no clear separation in the $\delta^{5}N$ of ruminant versus non-ruminant species considered in this study, or in previous work (Britton et al., 2012).

Mammoth and mastodon isotopic niches were generally smaller than muskox, horse and caribou niches, suggesting that mammoth and mastodon were more specialized to their distinct niche. This conclusion supports previous hypothesis regarding the woolly mammoth (Chapter 3; Schwartz-Narbonne et al., 2015) and mastodon (Zazula et al., 2014). In the present study, mammoth and mastodon were two of the species that occasionally did not fit the typical pattern of species isotopic compositions. This outcome may relate to their tracking a specialized diet or habitat niche that did not shift in isotopic tandem with the rest of the forage. For example, an increase in aridity could have caused

higher δ^{13} C and δ^{15} N for the majority of the plants in an ecosystem. However, it is possible that the browse species preferred by the mastodon were unable to grow in more arid environments. If so, the mastodon would have eaten from more mesic microhabitats or only lived in the region during more mesic time periods, and its forage – and thus its collagen isotopic composition – would not have shown the same increase in δ^{13} C and δ^{15} N as the rest of the plants and animals in the ecosystem.

Horse typically overlapped their isotopic niche with bison, mammoth and mastodon, suggesting that it consumed a mix of food from different niches, rather than eating from a separate, distinct niche. As well, when the relative isotopic ranking of two species changed from the expected pattern, horse was commonly one of the two species whose ranking changed. This supports the hypothesis that horse ate from a mix of niches rather than being confined to one specific niche. Bison also typically overlapped their isotopic niche with three herbivore species: caribou, muskox and horse. Again, this suggests that bison were more generalized foragers. It has been suggested that horse and bison had flexible feeding niches during the Pleistocene and Holocene (Britton et al., 2012). This more generalist strategy seems to correspond to a higher relative abundance of horse or bison than mammoth, muskox or caribou at a majority of sites. Interestingly, species identified as generalists (horse and bison) typically had smaller isotopic niches than the species with which they were sharing an isotopic niche (bison and mammoth for horse; muskox and caribou for bison). This may indicate that, by their very numbers, horse and bison monopolized the most favourable forage or habitat at these sites, forcing other species to expand beyond their ideal isotopic and ecological niche.

Situations where an atypical overlap between two isotopic niches was present, or a typical overlap between two isotopic niches was absent, corresponded to larger or smaller niches sizes for one of the two species involved. Commonly, this increase or decrease in isotopic niche size can be correlated to smaller relative abundances of that species at the site. Niche contraction may arise from an external cause, such as predation, which causes a species' relative abundance to decline while a large quantity of ideal forage remained, or it may indicate a species that was not able to adapt to changing conditions such as the loss of habitat or forage. Predation is known to play a role in determining the ecological

niche width, with species that are under less predation pressure able to expand their niches (Hammerschlag-Peyer et al., 2011).

Only qualitative assessments were possible for three species. The extinct muskox species *Symbos cavifrons*, the helmeted muskox, was examined at Fairbanks, while every other site contained *Ovibos* sp. *S. cavifrons* had unusually low $\delta^{15}N$ and did not fit the expected δ^{15} N pattern for muskox, suggesting that it had an entirely distinct diet, possibly containing a larger browse element. The woolly rhinocerous had a high average $\delta^{5}N$, second only to the woolly mammoth, and a similar average δ^{13} C to bison, consistent with its currently accepted status as a grazer (Bocherens, 2003). Based on the $\delta^{13}C$ and $\delta^{15}N$ of Dall sheep they seem to have occupied a similar isotopic niche to muskox (*Ovibos* sp.). The Dall sheep and the muskox (*Ovibos* sp.) both escaped terminal Pleistocene extinction. Dall sheep currently occupy alpine habitats (Guthrie, 1982), while the muskox inhabit in some North American sites (Koch and Barnosky, 2006). If the extinctions occurred because species experienced a loss of their habitat or dietary niche (Barnosky et al., 2004; Koch and Barnosky, 2006; Shapiro et al., 2004), it appears that these sheep and muskox were able to find places where their niche persisted, and to live in these habitats.

5.4.1.2 Sites

This study examines isotopic differences in megafauna collagen that occur in tandem for multiple species at each site. These differences result from environmental shifts that either caused (i) changes in the isotopic compositions of the plants at the base of the food web, or (ii) physiological responses that provoked the same isotopic changes in all the species. Since the observed changes affect multiple species at the same time, despite the varied diets of these species, it is unlikely to have resulted from a dietary shift. As shown by Figure 5.11a, the lowest pre-LGM δ^{13} C for the majority of the species occur in Yakutia. Values of $\delta^{13}C$ increase moving both eastward through North America, and, to a lesser extent, westward through Europe. The qualitative data (Fig. 5.12a.) support these patterns, with increasing average δ^{13} C observed moving south and westward into Europe. These isotopic patterns generally correspond to those observed using only data for woolly mammoth (Iacumin et al., 2000; Szpak et al., 2010). These results were interpreted as

reflecting an increase in fat use, resulting from colder conditions and harsher winters (Szpak et al., 2010).

As seen in Figure 5.11b, the highest pre-LGM $\delta^{5}N$ for the majority of species occurred in Yakutia. The values generally decrease to the east and west, opposite to that observed for δ^{13} C. There are exceptions; for example, the lowest δ^{13} C occurs in North America, while the average $\delta^{5}N$ is higher in NW Europe than in North America (Fig. 5.6e). Average $\delta^{15}N$ is similar in Yakutia and in Alberta, which follows the general pattern observed in previous work (Bocherens et al., 1994; Szpak et al., 2010). Greater aridity in Eurasia than much of North America is the most likely explanation for the higher $\delta^{15}N$. The results, however, also suggest that Alberta was atypically arid relative to the other North America sites, perhaps because it was located within the rain shadow of the Rocky Mountains. Other explanations are possible. For example, if colder winters led to increased nutritional stress as well as increased fat use, it would explain the inverse correlation between $\delta^{13}C$ and $\delta^{15}N$. However, that would not explain why Alberta was an exceptions to these patterns. Amino acid analyses would allow the baseline shifts in the plants' δ^{15} N arising from aridity to be distinguished from increases in animal protein recycling, and is recommended for future work (Chapter 3; Schwartz-Narbonne et al., 2015; Styring et al., 2010).

The overlap among sites in isotopic niches occupied by each species suggests a level of similarity that surpasses differences in foodweb baseline isotopic compositions among sites. Mammoth and mastodon are the most likely not to show overlap, which likely relates to their generally smaller isotopic niches (i.e., specialist status) than other species. Fairbanks and Alberta are the only sites that did not show isotopic overlap with multiple sites for multiple species. Alberta's climate seems to have been strongly influenced by local topography of the Rocky Mountains. Fairbanks provides an exception to many of the typical isotopic patterns across the mammoth steppe, being bison-dominated, and having multiple species showing atypical patterns of average $\delta^{13}C$ or $\delta^{15}N$ (Fig. 9a). Based on species proportions and qualitative inspection of species isotopic ranking, Selawik also may be an exception to many of the typical mammoth steppe isotopic
patterns. More dating and stable isotopic analyses are needed to determine whether and why these sites differ from the majority of other sites examined.

The average isotopic niche pattern of species and sites, and species proportions, are relatively consistent for the pre-LGM mammoth steppe, but exceptions exist for virtually every pattern. This suggests that generalized observations for the entire landscape are not sufficient to describe and understand variability across the mammoth steppe. Smaller scale, site-specific environmental or vegetation differences likely play a significant role. This is consistent with earlier reconstructions of the mammoth steppe that describe it a mosaic of smaller floral units (Guthrie, 1982). It is also clear, however, that the pre-LGM had a strong level of connectivity and similarity across the entirety of the biome.

5.4.2 Response of the mammoth steppe to environmental changes over time

The response of the mammoth steppe as a whole to the climatic change that occurred from the pre-LGM to the Holocene can be examined using the shifts in typical $\delta^{13}C, \delta^{15}N$ and niche size of each species at each site with time (Fig. 5.14a). In general, pre-LGM groups have higher $\delta^{13}C$ and $\delta^{15}N$ than post-LGM groups, and larger isotopic niche sizes.

Several previous studies have observed decreases in the δ^{13} C of plant and animal specimens over the Pleistocene and into the pre-industrial Holocene, although it has not been observed in every study, and the cause of this shift is disputed. Changes in the atmospheric $pCO₂$ during these time periods could have affected the isotopic composition of the plants, and thus the animals that consumed them (Bocherens, 2003; Richards and Hedges, 2003; Schubert and Jahren, 2015; Stevens and Hedges, 2004). The decrease in δ ¹³C at some sites has also be attributed to changes in degree of canopy cover (Drucker et al., 2008; Iacumin et al., 1997). Previous work did not identify temporal changes in the δ ¹³C of herbivores at Fairbanks, and suggested that such changes were either site-specific and local, or affected plants or habitats not used by most of the herbivores (Fox-Dobbs et al., 2008). The δ^{13} C shift is not observed in all species at all sites examined in this study, suggesting that it is a weaker trend that can be overprinted by other site- or speciesspecific variables, such as local changes in aridity or canopy cover. The trend to lower

 δ^{15} N in the post-LGM relative to the pre-LGM has been observed at multiple sites, though its timing and magnitude varied among sites and species (Bocherens et al., 2011; Drucker et al., 2003a; Fox-Dobbs et al., 2008; Mann et al., 2013; Stevens and Hedges, 2004; Stevens et al., 2008). The lowering of $\delta^{15}N$ in the post-LGM has been attributed to increased moisture from permafrost melting and to shifts in the floral species (Stevens and Hedges, 2004; Stevens et al., 2008). The large variability in isotopic patterns of time periods for varying species at varying sites may relate to differences in the extent to which a species' diet or microhabitat was affected by climate change, or other factors, such as distance from the ice front (Drucker et al., 2003b).

Many of the species at many of the sites here do not follow the general pattern of $\delta^{13}C$ or δ^{15} N rankings of time periods shown in Figure 5.14a. When they do follow a pattern, the extent of changes of δ^{13} C and δ^{15} N varies between species within a site, and between sites. This outcome suggests that the interplay of global factors and site- or speciesspecific factors is more complex than previously documented. The addition of qualitative data to the quantitative data set gave better resolution in the isotopic patterns of different time periods (Fig. 5.14b), suggesting more isotopic data may help to resolve the isotopic changes over time. As well, more detailed mathematical tools could be used. Principal component analysis of these plus additional data may be invaluable. Similarly, time series analysis of each species at each could fully elucidate the shifts in patterns over time, though this method will require much better dating control than is currently available.

Isotopic niche size changes substantially between time bins, with LGM and post-LGM species generally having smaller niches than pre-LGM species (e.g. Fig. 5.13). The LGM was a disruption to the ecological equilibrium that characterized pre-LGM time, and after the change, almost every species measured at every site had a more specialized isotopic niche (Alberta bison, North Slope bison, North Slope caribou, south central Siberia caribou, NW Europe caribou, Alberta horse, NW Europe horse and Hershel Island muskox). This may have been caused by reduced availability of different floral species after the LGM (Willerslev et al., 2014).

These changing niches can also be explored by comparing the shifts in the $\delta^{13}C$ and $\delta^{15}N$ patterns of species at a site over the different time periods (Fig. 5.9). The average δ^{13} C patterns of species are relatively constant through time when only the quantitative results are considered, suggesting that this was heavily controlled by a species' physiology. There are some differences in the δ^{13} C patterns of species using the qualitative results, which admittedly have weaker temporal control. This suggests that the changes in the δ ¹³C of a species at a site over time may make ranking the species without strong temporal control impossible, as the isotopic differences between species are overprinted by the isotopic differences over time. The average $\delta^{5}N$ patterns of species at a site are not constant over time in either the quantitative or qualitative results. Similarly, there are differences in which species had overlap, and some expected overlaps, such as between the horse and the bison, were not seen post-LGM (e.g. Fig. 5.7). These differences suggest that some species were not able to return to their previously occupied niche in post-LGM time; instead they were forced to specialize in different dietary or habitat niches, where they may have had reduced fitness, as was previously noted for European bison (Bocherens et al., 2015). In Alberta, between the pre-LGM and post-LGM, the relative niche ranking of horse and bison became reversed, as was their relative isotopic niche sizes and relative abundances. This site was glaciated and repopulated post-LGM (Burns, 2010; Jass et al., 2011). There appears to have been a complete shift in the ecosystem resulting from this change. Even at sites that were not glaciated during the LGM, (e.g. North Slope), the ecosystem clearly changed over time. Species proportions, isotopic patterns of species, species isotopic niche size, and isotopic niche overlaps among species all changed at the North Slope after the pre-LGM (Figs. 5.6; 5.7; 5.9; 5.13).

The δ^{13} C patterns of sites are relatively stable, but there are changes in δ^{15} N patterns of the sites during the LGM, post-LGM and Holocene (Figs. 5.11, 5.12). This likely reflects a fundamental shift in the ecosystems of the mammoth steppe over time. The pre-LGM pattern has been interpreted as suggesting that sites in the east (Alberta) and west (Yakutia and NW Europe) were more arid. However, during and after the LGM, the reverse situation may have occurred. There is a large increase in the number of species

where their isotopic niches at different sites that do not overlap post-LGM, likely because of the general decrease in isotopic niche sizes that occurred post-LGM.

It is intriguing that there is no return to pre-LGM isotopic niche sizes, niche patterns or niche overlaps of species at any site after the LGM (Fig. 5.9). The ranking of post-LGM average $\delta^{15}N$ of sites is also distinct from the pre-LGM (Fig. 5.11). Clearly, the mammoth steppe did not return to its previous state of equilibrium after the LGM, and instead became a more heterogeneous, and likely more fragmented ecosystem. This pattern echoes the floral pattern observed in the Arctic, where post-LGM flora had more geographic diversity than pre-LGM flora, and different plant species were present post-LGM (Willerslev et al., 2014), and the general patterns observed in the Americas that Pleistocene ecosystems were more sensitive to perturbations than Holocene ecosystems (Pires et al., 2015). Ecological changes during the LGM may have permanently destabilized the mammoth steppe. Changes in the physical geography may also have played a role, such as the opening and closing of the Bering land bridge over time. It is possible that the ecosystem shifted during each previous glaciation event (Stevens and Hedges, 2004), or that the LGM was a particularly severe glaciation event. It is also possible, however, that restoration of mammoth steppe equilibrium required more than the few thousand years before the Holocene climate changes and/or human impacts perturbed the system to the point that there was a major state change that led to the loss of the entire biome.

5.5 Conclusion

By the start of the Holocene, a permanent change had affected the mammoth steppe ecosystem, including extinction or extirpation of many of its megafauna species. It has been suggested that megafaunal herbivores had previously maintained this ecosystem through mechanisms such as trampling and selective consumption of flora (Willerslev et al., 2014). The isotopic changes in the ecosystem over time, however, even at sites having the typical mammoth steppe herbivore species, suggest that this was not necessarily the case. The Great Lakes area during the post-LGM period particularly demonstrates that mammoth steppe herbivores were not always able to maintain their

ideal forage and habitat. Yet, the species examined at this site retained the expected isotopic pattern, notwithstanding that the habitat was primarily forested rather than steppe-like (Metcalfe et al., 2013; Saunders et al., 2010). Rather than the loss of the species contributing to the changing of the ecosystem, the reverse may have occurred. The fragmentation of the mammoth steppe into heterogeneous ecosystems may have contributed to some extirpations, as this loss of connectivity may have prevented species from locating ideal habitat and forage. As such, these species may have been restricted to narrow ranges with reduced migration range or sub-ideal habitat and forage. In short, although many megafaunal species survived the climate changes of the LGM, significant changes to the overall ecosystem impacted their ability to survive into the Holocene.

5.6 References

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Chapter 6

6 Conclusions

This thesis explores the ecology of megaherbivore species across the mammoth steppe. The use of several techniques that had not been previously applied to the mammoth steppe research has allowed a deeper understanding of the diets and habitat preferences of these animals. This chapter summarizes those techniques, the conclusions drawn from them regarding the ecology of mammoth steppe megafauna, and the implications for mammoth steppe ecology and extinction as a whole.

6.1 Summary of the thesis

To fully understand mammoth steppe ecology, a better understanding of the diet and habitats of individual mammoth steppe species was necessary. In Chapter 2, the seasonal diets of species with antlers (moose, elk and caribou) were investigated through isotopic analysis of serially sampled antler collagen, and comparison of the isotopic composition of antler to that of bone collagen. Moose consumed aquatic plants in the summer, and browse during the rest of the year. Elk consumed graminoids and forbs during the fall and winter, and browse during the spring and summer. Caribou consumed primarily lichen in the winter. Caribou ate some ground shrubs during the late spring, and concentrated their diet on graminoids and forbs during the rest of the year. In Chapters 3 and 4, the diet and habitat preferences of a number of non-ruminant herbivores (woolly mammoth, mastodon, beaver, horse) were assessed through carbon and nitrogen isotopic analysis of bone, tooth and tusk collagen amino acids and comparisons with carnivore bone collagen and plant tissue amino acid isotopic compositions. Woolly mammoth consumed a distinct diet or food from a distinct habitat. This could reflect forage from extremely arid areas, plants fertilized by dung, and/or selection for specific plants. I suggest that woolly mammoths selected for decayed plants, primarily during the winter. Horse also ate decayed plants, though they consumed plants with a wider variety of isotopic compositions than woolly mammoths; this additional forage likely included fresh

graminoids and forbs. Mastodon focused their diet on terrestrial plants, mostly browse. Giant beaver consumed primarily aquatic plants.

The review in Chapter 5 of the carbon and nitrogen isotopic patterns exhibited by megaherbivores at 16 sites across the mammoth steppe provided context for these dietary patterns. The isotopic patterns exhibited by a variety of species from the mammoth steppe during various time slices of the Pleistocene and Holocene were considered using the mathematical tool SIBER in R (Jackson et al., 2011; Parnell et al., 2010; R Core Team, 2014). The general isotopic pattern (relative position of δ^{13} C and δ^{15} N in isotopic space) of species during the pre-LGM (Last Glacial Maximum) was found to be consistent among most sites, which suggests that the dietary and habitat patterns reported in Chapters 2-4 were typical of each species during this time period across the entirety of the mammoth steppe. Figure 6.1 presents the typical carbon and nitrogen isotopic pattern of pre-LGM mammoth steppe species, as well as the diets suggested by the carbon and nitrogen isotopic analyses of antler and bone collagen and amino acids from bone, tooth and tusk collagen. It also details which species had larger isotopic niches (larger standard ellipses or convex hulls in carbon and nitrogen isotopic space as measured in per mil), suggesting that they were generalists (caribou and horse) and which had smaller isotopic niches, suggesting that they were specialists (mammoth and mastodon).

The changes in species' carbon and nitrogen isotopic patterns and in species' relative niche that occurred in the mammoth steppe during the Pleistocene and Holocene are also described in Chapter 5. The size of a species' isotopic niche tended to be smaller in the post-LGM than the pre-LGM. The relative positions of species isotopic niches in nitrogen-carbon isotopic space (e.g., Fig. 6.1) also changed from the LGM to the post-LGM to the Holocene. These changes suggest that the ecological equilibrium that allowed megaherbivores to coexist during the pre-LGM period was not re-established in later times.

6.2 Mammoth steppe ecology and extinction

It is important to consider both how the mammoth steppe biome was maintained as well as the causes for its disappearance. Guthrie (2001, 1982) suggested that mammoth steppe

Figure 6.1 Typical carbon and nitrogen isotopic pattern observed for collagen of pre-LGM mammoth steppe megaherivores, as well as the hypothesized diets of these animals. Megaherbivores images drawn by Kate Allan. Spruce from https://en.wikipedia.org/wiki/Spruce. Lichen from https://en.wikipedia.org/wiki/Lichen. Grass from https://en.wikipedia.org/wiki/Grass. Decayed plants from http://biogrounds.org/category/life-in-soils/.

herbivores coexisted by minimizing competition through ecological niche partitioning. The consistency of the isotopic niches (Fig. 6.1), as described in Chapter 5 and in previous work (Bocherens, 2015, 2003) supports this hypothesis for the pre-LGM mammoth steppe. However, the isotopic niches of several species invariably overlap (bison-horse, bison-caribou, bison-muskox, horse-mammoth, and horse-mastodon). These species may have used other mechanisms to avoid competition that are not visible isotopically, or there may have been some ecological overlap, particularly among species with more generalist feeding strategies.

At the end of the Pleistocene, several mammoth steppe species were extirpated or went extinct, and the ecological relationships characteristic of the ecosystem were lost. This thesis demonstrates that the mammoth steppe underwent ecological shifts in response to the climatic changes of the LGM. An evaluation of the North American Pleistocene megafaunal networks by Pires et al. (2015) found that they were more vulnerable to perturbations than the megafaunal networks of Africa (Pires et al., 2015). This thesis suggests that the LGM caused a major ecological perturbation that resulted in changed species associations. This change might have been sufficient to destabilize the biome. It is also possible, however, that the ecosystem would have returned to its previous equilibrium, or developed a new one, given time, and that it was the combination of ecosystem instability caused by climatic changes and hunting pressure from anatomically modern humans that caused the extinctions to occur.

6.3 Future work

There are a number of additional groundwork-level isotopic studies that could aid the interpretation of the data presented in this thesis, and are recommended for future studies. In Chapter 2, serial sampling of antler was performed at 10 cm intervals. Antlers, however, do not grow at a constant rate (Chapman, 1975), and so the distance between measurements did not represent a constant interval of time. Future work should determine a generalized sampling strategy for antlers through a histological analysis of the antler tissue, including thin sectioning and observations of antler cross-sections. As well, more isotopic analysis of bone and antler from populations with known or controlled diets is

needed to establish if there are any physiological differences between the two tissues, or if differences in their isotopic compositions are based purely on dietary and habitat differences.

More groundwork is necessary to more firmly establish and distinguish the carbon and nitrogen amino acid isotopic compositions of dietary sources (plants, fungi and bacteria). Previous work has established that several forage types (terrestrial plants, aquatic plants, fungi and bacteria) have a δ^{13} C fingerprint that is distinct to that dietary source (Arthur et al., 2014; Larsen et al., 2013, 2012, 2009). Previous investigations of the amino acid isotopic compositions of plants suggests that there might be distinct patterns visible in both the $\delta^{13}C$ and $\delta^{15}N$ of different plant types, different plant parts, plants grown in different environments, and decayed plants (Bol et al., 2002; Calleja et al., 2013; Chikaraishi et al., 2010; Fogel and Tuross, 2003, 1999; Larsen et al., 2013, 2012, 2011, 2009; Lynch et al., 2011; Smallwood et al., 2003; Styring et al., 2014). Elucidating these patterns would allow a more comprehensive analysis of the amino acid isotopic compositions of the mammoth steppe fauna that consumed them.

There are a number of further analyses that could be performed on the samples and data presented in Chapter 5. This thesis performed amino acid analysis solely on species from Old Crow, Yukon Territory, and the majority of the samples were dated to the pre-LGM. Amino acid analyses of species from different time periods and sites could provide insights into the sources of variability. As well, more comprehensive mathematical modeling of the bulk collagen isotopic compositions would be valuable in helping to explain why certain species and sites were outliers from the general observed patterns. Time-series analysis, for example, would allow species isotopic compositions to be compared without the potential bias introduced by selection of one particular method for binning samples into time periods. A substantial investiment in the dating of many more samples, however, would be prerequisite to such an effort.

6.4 Concluding remarks

Understanding the ecology of mammoth steppe megaherbivores is necessary to understand how this biome was maintained during the Pleistocene, and what factors may have been involved in its disappearance. This study has provided an in-depth analysis of the diet and habitat preferences of several species, as well as providing insight into their interactions. It also considered how those interactions shifted over time, which was likely a response to climatic changes and possibly also anthropogenic influences. In short, the results of this thesis improve our understanding of the Pleistocene ecology of the mammoth steppe, and of how its species and ecosystems responded to environmental changes.

6.5 References

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Appendices

Appendix A: Sample information for specimens whose isotopic compositions were included in this study. Previously reported radiocarbon dates are taken from literature sources (Druckenmiller, 2008; Mann et al., 2013; Meiri et al., 2014, Zazula, pers. comm., 2015).

RAM = Royal Alberta Museum

UAMES = University of Alaska Museum Earth Sciences

YG = Yukon Government

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Appendix B: Carbon and nitrogen isotopic compositions of serially sampled antlers, as well as information about sample size and antler beam completeness.

Max. -18.4 4.5

Samples analyzed multiple times in this work are in bold and the average value is given.

Specimens are classified by how complete they are along the beam that was sampled. They range from fully complete, to a small section broken off, to a large portion of the antler missing.

Appendix C: Carbon and nitrogen isotopic data for collagen from specimens described in this study.

SD₁

 0.4 1.1

Samples analyzed multiple times in Chapter 2 are in bold and the average value is given.

Single refers to specimens where a single sample was taken.

Serial refers to specimens which were serially sampled, and the average value is given.

A = Antler

B = Bone

References:

- Druckenmiller, P.S., 2008. Survey of Pleistocene (Ice Age) vertebrates from the Selawik and Kobuk River areas of Northwestern Alaska. Intern. Rep. U.S. Fish Wildl. Serv. 1–56.
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Lab ID Pre-collagen extraction treatment d13C d15N %C %N C/N Ratio Yield YT101B None -20.01 2.95 40.15 15.42 3.02 23.8 YT101B Lipids extracted -20.02 2.96 39.65 15.11 3.04 13.0 Mean -20.0 3.0 39.9 15.3 3.0 18.4 SD 0.01 0.00 0.35 0.22 0.02 7.64 YT87 None -19.87 1.58 39.02 14.64 3.09 9.6 YT87 None -19.82 1.65 39.08 14.77 3.06 YT87 Lipids extracted -19.83 1.62 37.81 14.31 3.06 9.4 Mean -19.8 1.6 38.6 14.6 3.1 9.5 SD 0.03 0.04 0.72 0.24 0.01 0.08 YT85 None -19.04 2.38 38.22 14.44 3.07 16.3 YT85 Lipids extracted -18.96 2.43 37.26 14.02 3.08 11.5 Mean -19.0 2.4 37.7 14.2 3.1 13.9 SD 0.06 0.03 0.67 0.30 0.01 3.39 YT108 None -20.89 3.31 37.24 13.66 3.18 11.7 YT108 Lipids extracted -21.06 3.12 42.00 15.89 3.08 17.7 Mean -21.0 3.2 39.6 14.8 3.1 14.7 SD 0.12 0.14 3.37 1.58 0.07 4.28 YT95 None -20.20 0.99 38.88 14.78 3.05 12.7 YT95 Lipids extracted -20.27 0.93 39.90 15.04 3.10 15.3 Mean -20.2 1.0 39.4 14.9 3.1 14.0 SD 0.05 0.04 0.72 0.19 0.04 1.83 UAK10 None -19.42 2.84 42.32 14.94 3.30 15.37 UAK10 None -19.41 2.81 42.29 14.82 3.33 UAK10 Lipids extracted -19.37 2.86 40.08 14.02 3.33 13.79 Mean 19.4 2.8 41.6 14.6 3.3 14.6 Std. Dev. 0.03 0.02 1.29 0.50 0.02 1.12 AB16 None -18.34 5.00 41.74 15.87 3.07 22.99 AB16 None -18.35 4.89 40.62 15.44 3.07 AB16 Lipids extracted -18.31 4.87 41.72 15.87 3.07 23.37 Mean 18.3 4.9 41.4 15.7 3.1 23.2 SD 0.02 0.07 0.64 0.25 0.00 0.27 Maximum SD 0.1 0.1 3.4 1.6 0.1 7.6

Mean SD 0.0 0.0 1.1 0.5 0.0 2.7

Appendix D: Comparison of the δ^{13} C and δ^{15} N of lipid-extracted versus unextracted

tissues.

Appendix E Sample Information for Old Crow megafauna analyzed in Chapter 3.

YG = Yukon Government

AMNH = American Museum of Natural History. Radiocarbon dates shown in bold were measured as part of this study. *Radiocarbon date previously reported (Metcalfe et al., 2010). † Date previously reported (Metcalfe, 2011).

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Lab ID	Source	Species	$\delta^{15}\!N_{\rm Bulk}$	% Yield	$\%C$	%N	C/N	$\delta^{15}N_{\rm Phe}$	$\delta^{15} \rm N_{Glu}$	$\varDelta^{15}N_{Glu\text{-}Phe}$
YT1RD	YG	Mammoth*	$+8.7$	14.4	41.6	15.6	3.1	$+11.6 \pm 0.7$	$+7.2 \pm 0.1$	-4.4 ± 0.9
YT2RD	YG	Mammoth*	$+8.4$	11.0	39.2	14.6	3.1	$+16.1 \pm 0.9$	$+11.9 \pm 0.5$	-4.2 ± 1.4
YT3D	YG	Mammoth*	$+9.7$	>6.7	44.0	16.4	3.1	$+15.3 \pm 0.7$	$+11.5 \pm 0.3$	-3.8 ± 1.0
YT4B	YG	Mammoth*	$+9.5$	13.1	41.1	15.2	3.1	$+14.0 \pm 0.7$	$+10.8 \pm 0.2$	-3.2 ± 0.9
YT5RD	YG	Mammoth*	$+9.8$	11.2	42.9	15.5	3.2	$+13.2 \pm 0.9$	$+10.6 \pm 0.4$	-2.6 ± 1.4
YT ₆ C	YG	Mammoth*	$+7.7$	10.1	42.5	15.2	3.3	$+13.8 \pm 1.4$	$+9.6 \pm 1.5$	-4.2 ± 2.9
YT7B	YG	Mammoth*	$+7.6$	15.7	42.3	15.8	3.1	$+11.7 \pm 0.3$	$+9.5 \pm 0.7$	-2.2 ± 1.0
YT9C	YG	Mammoth*	$+8.2$	7.1	41.4	15.0	3.2	$+11.6 \pm 0.8$	$+9.4 \pm 0.5$	-2.2 ± 1.4
YT10RD	YG	Mammoth*	$+9.8$	11.4	38.9	14.4	$3.2\,$	$+11.2 \pm 0.2$	$+10.6 \pm 0.8$	-0.6 ± 0.9
YT11C	YG	Mammoth*	$+8.3$	18.2	44.1	15.9	3.2	$+10.4 \pm 0.5$	$+11.6 \pm 0.3$	$+1.2 \pm 0.7$
YT11RD	YG	Mammoth ⁺	$+9.5$	14.3	47.2	17.6	3.1	$+14.1 \pm 1.3$	$+8.8 \pm 3.9$	-5.3 ± 5.2
YT51T	YG	Mammoth*	$+11.3$	18.6	37.9	13.9	3.2	$+12.9 \pm 1.3$	$+12.4 \pm 1.0$	-0.5 ± 2.2
YT68	YG	Brown Bear	$+8.4$	9.7	45.4	16.8	3.1	$+9.3 \pm 0.7$	$+13.7 \pm 0.6$	$+4.4 \pm 1.3$
YT81	YG	Short-Faced Bear	$+9.1$	7.6	45.0	16.7	3.2	$+10.1 \pm 0.4$	$+16.6 \pm 0.4$	$+6.5 \pm 0.7$
YT82	YG	Scimitar Cat	$+9.9$	$\ \, 8.0$	46.0	17.2	3.1	$+9.7 \pm 0.8$	$+14.3\pm0.6$	$+4.6 \pm 1.4$
YT84	YG	Brown Bear	$+11.5$	6.2	43.6	16.1	3.2	$+10.7 \pm 0.3$	$+13.3 \pm 0.8$	$+2.6 \pm 1.1$
AMNH ₃	AMNH	Canid	$+8.5$	8.5	42.0	15.1	3.2	$+8.7 \pm 0.9$	$+11.8 \pm 0.7$	$+3.1 \pm 1.6$
YT129	YG	Horse	$+7.0$	10.2	39.7	15.5	3.3	$+11.2 \pm 0.5$	$+8.6 \pm 0.8$	-2.6 ± 1.3
YT130	YG	Horse	$+8.1$	11.2	40.3	15.6	3.2	$+10.6 \pm 0.7$	$+11.1 \pm 0.7$	$+0.5 \pm 1.3$
YT131	YG	Horse	$+9.9$	5.4	36.1	14.0	3.4	$+12.0 \pm 0.0$	$+11.2 \pm 0.7$	-0.8 ± 0.7
YT132	YG	Horse	$+4.2$	8.2	38.5	14.8	3.1	$+7.8 \pm 0.7$	$+6.7 \pm 0.8$	-1.1 ± 1.6

Appendix F Nitrogen isotopic data and preservation information.

Tissue: RD = root dentin, D = crown dentin, T = tusk dentin, B = bone, C = cementum, E = enamel.

The average results of duplicate measurements for bulk collagen are shown in bold-faced font.

***Data for bulk collagen previously reported (Metcalfe et al., 2010).**

†Data for bulk collagen previously reported (Metcalfe, 2011).

Amino acid $\delta^{15}N$ values represent the average $(\pm 1 \text{ SD})$ of triplicate analyses.

References:

- Metcalfe, J.Z., 2011. Late Pleistocene climate and proboscidean paleoecology in North America: insights from stable isotope compositions of skeletal remains. University of Western Ontario.
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Ala = alanine, Val = valine, Gly = glycine, Leu = leucine, Thr = threonine, Pro = proline, Asp = aspartate, Ser = serine, Glu = glutamate, Phe = phenylalanine and Hyp = hydroxyproline.

The top scan is the ratio of mass 29/28, and the bottom scan is the amplitude of mass 28.

Lab ID	Common Name	Species Name	Sample Number	${}^{14}C$ Date	Latitude	Longitude	Collection Site	Tissue	Tissue Type	${}^{14}C$ Lab No.	Source	$\%$ Yield	% C	%N	C/N
YT83 AMNH ₂	Brown Bear Giant Beaver	Ursus arctos Castoroides ohioensis	236.157 F:AM 65187	$5,941\pm 66$ >41,100	68.0	-139.6	CRH 67 Old Crow River Old Crow River	Bone Bone	Right femur	AA103837 AA97952	YG AMNH	9.2 0.3	44.1 18.0	16.5 5.5	- 3.1 3.8

Appendix H Sample information for additional specimens used in this study.

YG = Yukon Government, AMNH = American Museum of Natural History. Results shown in bold-faced font are the average of replicate measurements.

Appendix I Gas chromatogram arising from compound-specific carbon isotopic measurements of amino acids from collagen extracted from sample YT51T following derivatization to their N-acetyl-methyl ester.

Ala = alanine, Val = valine, Gly = glycine, Leu = leucine, Thr = threonine, Pro = proline, Glu = glutamate, Phe = phenylalanine, Hyp = hydroxyproline and Ref = reference gas.

The scans show different masses.

The upper graph shows the ratio of CO² mass 45/44 peak for each amino acid on the y-axis and the retention time of that compound on the x-axis.

The lower graph shows the relative amplitude of the CO² mass 46 peak for each amino acid on the y-axis and the retention time of that compound on the x-axis.

Lab ID	Sample Type	Treatment	Ala	Arg	Asp	Cys	Glu	Gly	His	Hyp	Ile	Leu	Lys	Met	Phe	Pro	Ser	Thr	Tyr	Val
YT7B	Mammoth Bone	Collagen Extrated	12.3	5.1	4.5	0.0	7.0	33.3	0.5	9.3	1.0	2.6	2.4	0.6	1.5	12.4	3.1	1.6	0.3	2.4
YT11C	Mammoth Cementum	Collagen Extrated	12.4	5.1	4.6	0.0	7.1	32.4	0.5	9.7	1.1	2.7	2.7	0.6	1.5	12.0	3.2	1.6	0.5	2.5
YT11RD	Mammoth Root Dentin	Collagen Extrated	12.5	5.1	4.8	0.0	7.2	32.3	0.5	9.6	1.0	2.6	2.5	0.6	1.5	12.2	3.2	1.6	0.4	2.4
YT12RD	Juvenile Mammoth Root Dentin	Collagen Extrated	12.6	5.1	4.5	0.0	7.0	33.5	0.4	10.0	1.0	2.5	2.6	0.5	1.4	11.7	3.0	1.6	0.2	2.4
YT51T	Mammoth Tusk	Collagen Extrated	12.9	4.9	4.7	0.0	6.9	33.5	0.4	10.0	1.0	2.4	2.2	0.5	1.1	12.3	3.1	1.6	0.1	2.4
YT8D	Mastodon Crown Dentin	Collagen Extrated	12.6	5.0	4.6	0.0	7.1	32.6	0.4	10.1	1.1	2.6	2.7	0.5	1.5	11.8	3.2	1.6	0.4	2.4
YT8D	Mastodon Crown Dentin	Whole	13.9	5.7	1.0	0.0	3.4	32.6	0.5	11.4	1.3	3.2	3.2	0.5	1.8	13.4	2.9	1.7	0.5	2.8
REG97	Archeological Human Rib Bone	Collagen Extrated	12.2	5.0	4.4	0.0	6.9	33.1	0.6	9.8	1.1	2.6	2.9	0.6	1.4	12.2	2.7	1.5	0.4	2.6
REG97	Archeological Human Rib Bone	Whole	13.4	5.6	1.3	0.0	3.7	33.3	0.6	11.4	1.3	3.1	2.8	0.6	1.7	13.7	2.3	1.5	0.5	3.2
KFC	Modern Cow Femur Bone	Collagen Extrated Collagen	12.4	5.6	4.7	0.0	7.6	31.6	0.6	9.5	1.2	2.7	2.7	0.6	1.4	12.0	2.9	1.6	0.5	2.4
KFC	Modern Cow Femur Bone	Extrated and Hydrolyzed	11.4	5.3	4.5	0.0	7.5	32.9	0.5	10.4	1.1	2.7	2.3	0.4	1.4	12.1	3.5	1.6	0.4	1.9
KFC	Modern Cow Femur Bone	Whole	13.5	6.0	1.0	0.0	3.7	31.1	0.7	11.5	1.6	3.5	3.2	0.7	1.9	13.7	2.6	1.7	0.8	2.9

Appendix J Amino acid profiles of collagenous tissues determined in this study and previous work.

Ala = alanine, Val = valine, Gly = glycine, Leu = leucine, Thr = threonine, Pro = proline, Glu = glutamate, Phe = phenylalanine and Hyp = hydroxyproline. Amino acid profiles are presented as the percentage of the tissue comprising each amino acid.

The amino acid profile for REG97 has been presented previously by Olsen et al. (2010).

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Olsen, K., White, C., Longstaffe, F., von Heyking, K., McGlynn, G., 2010. Bulk and compound-specific isotope analysis of pathological bone collagen: preliminary results, in: 4th International Symposium on Biomolecular Archaeology. Copenhagen, Denmark.

Appendix K Relative abundances of megafaunal herbivores from various sites across the mammoth steppe.

Modern Reference: Mann et al., 2013

Species (Scientific Name) Percent abundance Bison priscus 97 Alces alces <1 Muskox *Ovibos moschatus* <1

Predator+~ 3

References:

information from Groves (2015)

Druckenmiller, P.S., 2008. Survey of Pleistocene (Ice Age) vertebrates from the Selawik and Kobuk River areas of Northwestern Alaska. Intern. Rep. U.S. Fish Wildl. Serv. 1–56.

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Appendix L Sample information for megafaunal herbivores from Alberta.

Appendix L continues below.

Samples analyzed multiple times (duplicate/triplicate) in Chapter 5 are in bold Dates obtained in Chapter 5 are in bold

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Average of repeat measurements on different tissues from the same specimen are underlined
RAM = Royal Alberta Museum
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Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

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Appendix M Sample information for megafaunal herbivores from Fairbanks.

Appendix M continues below

 -19.8 2.9
 -20.5 5.2

 -20.5

 AMNH

B AMNH

 Upp

261

Samples analyzed multiple times (duplicate/triplicate) in Chapter 5 are in bold

Dates obtained in Chapter 5 are in bold

AMNH = American Museum of Natural History; UAMES = University of Alaska Museum Earth Science

Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

References:

- Bocherens, H., Fizet, M., Mariotti, A., Gangloff, R., Burns, J., 1994. Contribution of isotopic biogeochemistry (¹³C, ¹⁵N, ¹⁸O) to the paleoecology of mammoths (*Mammuthus primigenius*). Hist. Biol. 7, 187–202.
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Appendix N Sample information for megafaunal herbivores from the Great Lakes Area.

Appendix N continues below.

Average of repeat measurements on different tissues from the same specimen are underlined

^a Yield may be artifically low

b This radiocarbon date may correspond to a different individual

Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

References:

McAndrews, J., Jackson, L., 1988. Age and environment of late Pleistocene mastodont and mammoth in southern Ontario. Bull. Buffalo Soc. Nat. Sci. 33, 161–172.

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^c Range for the Hiscock mastodon bone collagen which had been radiocarbon dated (Laub, 2010, 2003).

Appendix O Sample information for megafaunal herbivores from the Gydan Peninsula.

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Appendix P Sample information for megafaunal herbivores from Herschel Island.

Appendix P continues below.

YG = Yukon Government Paleontology Program Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

References:

- Metcalfe, J.Z., 2011. Late Pleistocene climate and proboscidean paleoecology in North America: insights from stable isotope compositions of skeletal remains. Doctoral Thesis. University of Western Ontario.
- Raghavan, M., Espregueira Themudo, G., Smith, C.I., Zazula, G., Campos, P.F., 2014. Musk ox (Ovibos moschatus) of the mammoth steppe: tracing palaeodietary and palaeoenvironmental changes over the last 50,000 years using carbon and nitrogen isotopic analysis. Quat. Sci. Rev. 102, 192–201. doi:10.1016/j.quascirev.2014.08.001
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Appendix Q Sample information for megafaunal herbivores from the Klondike area.

Appendix Q continues below.

Samples analyzed multiple times (duplicate/triplicate) in Chapter 5 are in bold

Dates obtained in Chapter 5 are in bold

YG = Yukon Government Paleontology Program; CMN = Canadian Museum of Nature; AMNH = American Museum of Natural History Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

References:

Debruyne, R., Chu, G., King, C.E., Bos, K., Kuch, M., Schwarz, C., Szpak, P., Gröcke, D.R., Matheus, P., Zazula, G., Guthrie, D., Froese, D., Buigues, B., de Marliave, C., Flemming, C., Poinar, D., Fisher, D., Southon, J., Tikhonov, A.N., MacPhee, R.D.E., Poinar, H.N., 2008. Out of America: ancient DNA evidence for a new world origin of late Quaternary woolly mammoths. Curr. Biol. 18, 1320–6. doi:10.1016/j.cub.2008.07.061

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Zazula, G., Personal communication (e-mail), 2015

Lab ID/Fie ld ID	Common Name	Scientific Name	Sample Number	Stable Isotope Reference	${}^{14}C$ Date	Date Lab $\#$	Date reference	Site	Tissue	Tissue Type	Source	$\delta^{13}\!C_{\text{Bulk}}$	$\delta^{15}\!N_{\rm Bulk}$
IK98- 0343	Bison	Bison priscus	UAMES 9079	Mann et al., 2013	10,510 ±50	CAMS- 53767	Mann et al., 2013	Ikpikpuk R.	B	humerus	UAMES	-20.6	2.8
IK98- 1114	Bison	Bison priscus	UAMES 9896	Mann et al., 2013	10,990 ±50	CAMS- 53891	Mann et al., 2013	Ikpikpuk R.	$\, {\bf B}$	astragalus	UAMES	-20.1	2.7
IK98- 0027	Bison	Bison priscus	UAMES 8847	Mann et al., 2013	11,810 ±50	CAMS- 53756	Mann et al., 2013	Ikpikpuk R.	$\, {\bf B}$	astragalus	UAMES	-20.7	2.6
IK98- 0528	Bison	Bison priscus	UAMES 9577	Mann et al., 2013	12,270 ±50	CAMS- 53774	Mann et al., 2013	Ikpikpuk R.	$\, {\bf B}$	humerus	UAMES	-20.2	4.1
IK98- 0303	Bison	Bison priscus		Mann et al., 2013	12,320 ± 60	CAMS- 58091	Mann et al., 2013	Ikpikpuk R.	B	vertebra	UAMES	-20.2	3.7
IK98- 0142	Bison	Bison priscus	UAMES 8801	Mann et al., 2013	12,410 ±50	CAMS- 53760	Mann et al., 2013	Ikpikpuk R.	B	metatarsal	UAMES	-20.0	2.7
IK01- 428	Bison	Bison priscus	UAMES 11664	Mann et al., 2013	12,560 ±130	AA- 48281	Mann et al., 2013	Ikpikpuk R.	$\, {\bf B}$	astragalus	UAMES	-20.0	2.7
IK98- 0661	Bison	Bison priscus	UAMES 9464	Mann et al., 2013	17,160 ±80	CAMS- 53777	Mann et al., 2013	Ikpikpuk R.	$\, {\bf B}$	metapodial	UAMES	-20.2	2.8
IK98- 0504	Bison	Bison priscus	UAMES 9238	Mann et al., 2013	19,420 ± 100	CAMS- 53772	Mann et al., 2013	Ikpikpuk R.	B	femur	UAMES	-20.0	3.8
IK98- 1090	Bison	Bison priscus	UAMES 9804	Mann et al., 2013	21,040 ±120	CAMS- 53890	Mann et al., 2013	Ikpikpuk R.	B	astragalus	UAMES	-20.0	6.5
IK98- 0401	Bison	Bison priscus	UAMES 8842	Mann et al., 2013	21,530 ±130	CAMS- 53770	Mann et al., 2013	Ikpikpuk R.	$\, {\bf B}$	metatarsal	UAMES	-20.4	4.4
IK98- 1254	Bison	Bison priscus	UAMES 9967	Mann et al., 2013	23,680 ±170	CAMS- 53901	Mann et al., 2013	Ikpikpuk R.	B	humerus	UAMES	-19.9	5.5
IK98- 0302	Bison	Bison priscus	UAMES 8998	Mann et al., 2013	24,500 ±180	CAMS- 53764	Mann et al., 2013	Ikpikpuk R.	$\, {\bf B}$	metatarsal	UAMES	-20.2	4.3
IK98- 1184	Bison	Bison priscus	UAMES 10031	Mann et al., 2013	25,980 ±230	CAMS- 53899	Mann et al., 2013	Ikpikpuk R.	$\, {\bf B}$	horn core	UAMES	-19.7	4.2
IK98- 1043	Bison	Bison priscus	UAMES 10043	Mann et al., 2013	26,550 ± 230	CAMS- 53888	Mann et al., 2013	Ikpikpuk R.	$\, {\bf B}$	astragalus	UAMES	-19.5	5.7

Appendix R Sample information for megafaunal herbivores from the North Slope.

Appendix R continues below. A limited number of specimens had additional information (i.e. % yield, %C, %N and C/N).

UAMES = University of Alaska Museum Earth Sciences Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

References:

- Mann, D.H., Groves, P., Kunz, M.L., Reanier, R.E., Gaglioti, B. V., 2013. Ice-age megafauna in Arctic Alaska: extinction, invasion, survival. Quat. Sci. Rev. 70, 91–108. doi:10.1016/j.quascirev.2013.03.015
- Zazula, G.D., MacPhee, R.D., Metcalfe, J.Z., Reyes, A. V., Brock, F., Druckenmiller, P.S., Groves, P., Harington, R., Hodgins, G.W.L., Kunz, M.L., Longstaffe, F.J., Mann, D.H., McDonald, H.G., Nalawade-Chavan, S., Southon, J.R., 2014. American mastodon extirpation in the Arctic and Subarctic predates human colonization and terminal Pleistocene climate change. Proc. Natl. Acad. Sci. 111, 18460–18465.
| Lab ID | Common
Name | Scientific
Name | Sample
Number | Stable Isotope Reference | ${}^{14}C$ Date | Date Lab # | Calibrated
Date | Date reference |
|----------------|----------------|----------------------|--------------------|--------------------------------------------------------------------|-----------------|------------|--------------------|------------------------|
| $KSL-10$ | Bison | <i>Bison</i> sp. | M001:144 | Bocherens et al., 2011 | $~14 - 12,000$ | | | Bocherens et al., 2011 |
| $KSL-11$ | Bison | <i>Bison</i> sp. | M001:152 | Bocherens et al., 2011 | $~14 - 12,000$ | | | Bocherens et al., 2011 |
| $KSL-12$ | Bison | <i>Bison</i> sp. | HE30:8 | Bocherens et al., 2011 | $~14 - 12,000$ | | | Bocherens et al., 2011 |
| Goyet-A3-13 | Bison | Bison priscus | 2230-1 | Bocherens et al., 2011 | $~24 - 40,000$ | | | Bocherens et al., 2011 |
| Goyet-A3-14 | Bison | Bison priscus | 2230-2 | Bocherens et al., 2011 | $~24 - 40,000$ | | | Bocherens et al., 2011 |
| Goyet-B4-5 | Bison | Bison priscus | 2737-1 | Bocherens et al., 2011 | $~24 - 40,000$ | | | Bocherens et al., 2011 |
| Goyet-B4-7 | Bison | Bison priscus | 2737-3 | Bocherens et al., 2011 | $~24 - 40,000$ | | | Bocherens et al., 2011 |
| SC29000 | Bison | Bison priscus | SC91 213
H30(4) | Bocherens et al., 2011 | $~24 - 40,000$ | | | Bocherens et al., 2011 |
| LBR100 | Bison | Bison priscus | | Bocherens et al., 2005 | | | ~235,000 | Bocherens et al., 2005 |
| LBR200 | Bison | Bison priscus | | Bocherens et al., 2005 | | | ~235,000 | Bocherens et al., 2005 |
| LBR300 | Bison | Bison priscus | | Bocherens et al., 2005 | | | ~25,000 | Bocherens et al., 2005 |
| LBR400 | Bison | Bison priscus | | Bocherens et al., 2005 | | | ~25,000 | Bocherens et al., 2005 |
| LBR500 | Bison | Bison priscus | | Bocherens et al., 2005 | | | ~25,000 | Bocherens et al., 2005 |
| LBR600 | Bison | Bison priscus | | Bocherens et al., 2005 | | | ~25,000 | Bocherens et al., 2005 |
| LBR700 | Bison | Bison priscus | | Bocherens et al., 2005 | | | ~235,000 | Bocherens et al., 2005 |
| LBR3100 | Bison | Bison priscus | | Bocherens et al., 2005 | | | ~235,000 | Bocherens et al., 2005 |
| | Bison | Bison priscus | | Fizet et al., 1995 | | | $~140-$
45,000 | Fizet et al., 1995 |
| | Bison | Bison priscus | | Fizet et al., 1995 | | | $-40-$
45,000 | Fizet et al., 1995 |
| | Bison | Bison priscus | | Fizet et al., 1995 | | | $-40-$
45,000 | Fizet et al., 1995 |
| | Bison | Bison priscus | | Fizet et al., 1995 | | | $-40-$
45,000 | Fizet et al., 1995 |
| | Bison | Bison priscus | | Fizet et al., 1995 | | | $-40-$
45,000 | Fizet et al., 1995 |
| RA-KSL-
620 | Caribou* | Rangifer
tarandus | | Drucker et al., 2011 as
referenced in Bocherens et
al., 2011 | $~14 - 12,000$ | | | Bocherens et al., 2011 |

Appendix S Sample information for megafaunal herbivores from NW Europe.

Appendix S continues below.

Goyet-A3

Goyet-A3

Goyet-A3

***In Western Beringia, this would have been a reindeer, rather than a caribou. However, consistent naming of species is used in the thesis. **In Western Beringia, this would have been a red deer or a wapiti rather than an elk. However, consistent naming of species is used in the thesis. Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin**

- Bocherens, H., Billiou, D., Patou-Mathis, M., Bonjean, D., Otte, M., Mariotti, A., 1997. Paleobiological implications of the isotopic Signatures $(^{13}C,^{15}N)$ of fossil mammal collagen in Scladina Cave (Sclayn, Belgium). Quat. Res. 48, 370–380. doi:10.1006/qres.1997.1927
- Bocherens, H., Billiou, D., Mariotti, A., Toussaint, M., Patou-Mathis, M., Bonjean, D., Otte, M., 2001. New isotopic evidence for dietary habits of Neandertals from Belgium. J. Hum. Evol. 40, 497–505. doi:10.1006/jhev.2000.0452
- Bocherens, H., Drucker, D.G., Billiou, D., Patou-Mathis, M., Vandermeersch, B., 2005. Isotopic evidence for diet and subsistence pattern of the Saint-Césaire I Neanderthal: review and use of a multi-source mixing model. J. Hum. Evol. 49, 71–87. doi:10.1016/j.jhevol.2005.03.003
- Bocherens, H., Drucker, D.G., Bonjean, D., Bridault, A., Conard, N.J., Cupillard, C., Germonpré, M., Höneisen, M., Münzel, S.C., Napierala, H., Patou-Mathis, M., Stephan, E., Uerpmann, H.-P., Ziegler, R., 2011. Isotopic evidence for dietary ecology of cave lion (*Panthera spelaea*) in North-Western Europe: prey choice, competition and implications for extinction. Quat. Int. 245, 249–

261. doi:10.1016/j.quaint.2011.02.023

- Drucker, D.G., Bocherens, H., Bridault, A., Billiou, D., 2003a. Carbon and nitrogen isotopic composition of red deer (*Cervus elaphus*) collagen as a tool for tracking palaeoenvironmental change during the Late-Glacial and Early Holocene in the northern Jura (France). Palaeogeogr. Palaeoclimatol. Palaeoecol. 195, 375–388. doi:10.1016/S0031-0182(03)00366-3
- Drucker, D.G., Bocherens, H., Billiou, D., 2003b. Evidence for shifting environmental conditions in Southwestern France from 33 000 to 15 000 years ago derived from carbon-13 and nitrogen-15 natural abundances in collagen of large herbivores. Earth Planet. Sci. Lett. 216, 163–173. doi:10.1016/S0012-821X(03)00514-4
- Drucker, D.G., Bridault, A., Cupillard, C., Hujic, A., Bocherens, H., 2011. Evolution of habitat and environment of red deer (*Cervus elaphus*) during the Late-glacial and early Holocene in eastern France (French Jura and the western Alps) using multi-isotope analysis ($\delta^{13}C$, $\delta^{15}N$, $\delta^{18}O$, $\delta^{34}S$) of archaeological remains. Quat. Int. 245, 268–278. doi:10.1016/j.quaint.2011.07.019
- Fizet, M., Mariotti, A., Bocherens, H., Lange-Badré, B., Vandermeersch, B., Borel, J.P., Bellon, G., 1995. Effect of diet, physiology and climate on carbon and nitrogen stable isotopes of collagen in a Late Pleistocene anthropic palaeoecosystem: Marillac, Charente, France. J. Archaeol. Sci. 22, 67–79.
- Stevens, R.E., Germonpré, M., Petrie, C.A., O'Connell, T.C., 2009. Palaeoenvironmental and chronological investigations of the Magdalenian sites of Goyet Cave and Trou de Chaleux (Belgium), via stable isotope and radiocarbon analyses of horse skeletal remains. J. Archaeol. Sci. 36, 653–662. doi:10.1016/j.jas.2008.10.008
- Stevens, R.E., Hedges, R.E.., 2004. Carbon and nitrogen stable isotope analysis of northwest European horse bone and tooth collagen, 40,000 BP – present: palaeoclimatic interpretations. Quat. Sci. Rev. 23, 977–991. doi:10.1016/j.quascirev.2003.06.024

Lab ID	Common Name	Scientific Name	Sample Number	Stable Isotope Reference	${}^{14}C$ Date	Date Lab #	Date reference	Source
YT129	Horse	<i>Equus</i> sp.	178.9	Chapter 3; Schwartz-Narbonne et al., 2015	$27,189 \pm 420$	AA103890	Schwartz-Narbonne et al., 2015	YG
YT130	Horse	Equus sp.	179.14	Chapter 3; Schwartz-Narbonne et al., 2015				YG
YT131	Horse	<i>Equus</i> sp.	236.235	Chapter 3; Schwartz-Narbonne et al., 2015	18,370 ±260	AA103835	Schwartz-Narbonne et al., 2015	YG
YT132	Horse	<i>Equus</i> sp.	295.2	Chapter 2; Schwartz-Narbonne et al., 2015	>41,100	AA103836	Schwartz-Narbonne et al., 2015	YG
YT133	Horse	<i>Equus</i> sp.	315.1	Chapter 2; Schwartz-Narbonne et al., 2015				YG
YT1RD	Mammoth	Mammuthus	291.1	Metcalfe et al., 2010	>41,100	AA84987	Metcalfe et al., 2010	YG
YT2RD	Mammoth	Mammuthus	122.2	Metcalfe et al., 2010	>41,100	AA84992	Metcalfe et al., 2010	YG
YT3D	Mammoth	Mammuthus	173.5	Metcalfe et al., 2010				YG
YT4B	Mammoth	Mammuthus	285.1	Metcalfe et al., 2010	>39,100	AA85002	Metcalfe et al., 2010	YG
YT5RD	Mammoth	Mammuthus	60.2	Metcalfe et al., 2010				YG
YT6C	Mammoth	Mammuthus	57.1	Metcalfe et al., 2010				YG
YT7B	Mammoth	Mammuthus	325.22	Metcalfe et al., 2010	>40,100	AA84984	Metcalfe et al., 2010	YG
YT9C	Mammoth	Mammuthus	284.4	Metcalfe et al., 2010				YG
YT10RD	Mammoth	Mammuthus	252.2	Metcalfe et al., 2010	>40,000	AA85001	Metcalfe et al., 2010	YG
YT11C	Mammoth	Mammuthus	173.1	Metcalfe et al., 2010				YG
YT11RD	Mammoth	Mammuthus	173.1	Metcalfe et al., 2010				YG
YT51T	Mammoth	Mammuthus	317.51	Metcalfe et al., 2010	MIS5, ~140,000		Metcalfe (2011)	YG
YT8D	Mastodon	Mammut	357.1	Metcalfe (2011)	>41,100	AA84995	Metcalfe (2011)	YG
K-15352	Mastodon	Mammut	CMN 15352	Zazula et al., 2014	$45700 \pm$ 2500	UCIAMS78695	Zazula et al., 2014	
K-31898	Mastodon	Mammut	CMN 31898	Zazula et al., 2014	50300±3500	UCIAMS78696	Zazula et al., 2014	
K-33066	Mastodon	Mammut	CMN 33066	Zazula et al., 2014	>49900	UCIAMS78697	Zazula et al., 2014	

Appendix T Sample information for megafaunal herbivores from Old Crow.

Appendix T continues below.

Dates obtained in Chapter 5 are in bold

Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

References:

Metcalfe, J.Z., Longstaffe, F.J., Zazula, G.D., 2010. Nursing, weaning, and tooth development in woolly mammoths from Old Crow, Yukon, Canada: implications for Pleistocene extinctions. Palaeogeogr. Palaeoclimatol. Palaeoecol. 298, 257–270.

doi:10.1016/j.palaeo.2010.09.032

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- Zazula, G.D., MacPhee, R.D., Metcalfe, J.Z., Reyes, A. V., Brock, F., Druckenmiller, P.S., Groves, P., Harington, R., Hodgins, G.W.L., Kunz, M.L., Longstaffe, F.J., Mann, D.H., McDonald, H.G., Nalawade-Chavan, S., Southon, J.R., 2014. American mastodon extirpation in the Arctic and Subarctic predates human colonization and terminal Pleistocene climate change. Proc. Natl. Acad. Sci. 111, 18460–18465.

Appendix U Sample information for megafaunal herbivores from the Russian Plain.

Appendix U continues below.

Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

- Bocherens, H., Fizet, M., Mariotti, A., Gangloff, R., Burns, J., 1994. Contribution of isotopic biogeochemistry (¹³C, ¹⁵N, ¹⁸O) to the paleoecology of mammoths (*Mammuthus primigenius*). Hist. Biol. 7, 187–202.
- Iacumin, P., Nikolaev, V., Ramigni, M., 2000. C and N stable isotope measurements on Eurasian fossil mammals, 40 000 to 10 000 years BP: herbivore physiologies and palaeoenvironmental reconstruction. Palaeogeogr. Palaeoclimatol. Palaeoecol. 163, 33–47.

Lab ID	Common Name	Sample Number	Stable Isotope Reference	^{14}C Date	Date Lab #	Date reference
UAK38	Bison	UAMES 2206	Chapter 5	$16,220\pm 190$	AA103839	Chapter 5
UAK31	Bison	UAMES 1106	Chapter 5	37,700±2,600	AA103838	Chapter 5
UAK25	Bison	UAMES 991	Chapter 5			
UAK26	Bison	UAMES 1014	Chapter 5			
UAK27	Bison	UAMES 1088	Chapter 5			
UAK28	Bison	UAMES 1095	Chapter 5	>40,300	AA103884	
UAK29	Bison	UAMES 1096	Chapter 5			
UAK30	Bison	UAMES 1097	Chapter 5			
UAK32	Bison	UAMES 1107	Chapter 5			
UAK33	Bison	UAMES 1119	Chapter 5			
UAK34	Bison	UAMES 1121	Chapter 5			
UAK35	Bison	UAMES 1125	Chapter 5			
UAK36	Bison	UAMES 1172	Chapter 5			
UAK37	Bison	UAMES 2096	Chapter 5			
UAK ₆	Caribou	UAMES 1122	Chapter 2	26,360±650	AA103840	Chapter 2
UAK12	Caribou	UAMES 2214	Chapter 2	$29,020\pm910$	AA103841	Chapter 2
UAK8	Caribou	UAMES 1151	Chapter 2			
UAK9	Caribou	UAMES 1180	Chapter 2			
UAK7	Caribou	UAMES 1123	Chapter 2			
UAK11	Caribou	UAMES 2114	Chapter 2			
UAK1	Caribou	UAMES1033	Chapter 2	201 ± 33	AA103881	Chapter 2
UAK ₂	Caribou	UAMES1035	Chapter 2			
UAK3	Caribou	UAMES 1036	Chapter 2			
UAK14	Horse	UAMES 1024	Chapter 5			
UAK15	Horse	UAMES 1063	Chapter 5			
UAK16	Horse	UAMES 1152	Chapter 5			
UAK17	Horse	UAMES 1153	Chapter 5			
UAK18	Horse	UAMES 1154	Chapter 5			
UAK19	Horse	UAMES 1155	Chapter 5	>40,300	AA103882	Chapter 5
UAK20	Horse	UAMES 1156	Chapter 5			
UAK21	Horse	UAMES 1159	Chapter 5	$14,790 \pm 100$	AA103883	Chapter 5
UAK22	Horse	UAMES 1178	Chapter 5			
UAK ₂₃	Horse	UAMES 1179	Chapter 5	$30,400 \pm 1,100$	AA103829	Chapter 5
UAK24	Horse	UAMES 2170	Chapter 5			
	Horse	UAMES	Drukenmiller,	$27,980\pm180$		Drukenmiller,
		29664	2008			2008
	Horse	UAMES 1064	Drukenmiller, 2008	$17,130\pm80$		Drukenmiller, 2008
UAK41	Mammoth	UAMES 2073	Chapter 5	>41,100	AA103828	Chapter 5
UAK42	Mammoth	UAMES 2100	Chapter 5			
UAK43	Mammoth	UAMES 2115	Chapter 5			
UAK44	Mammoth	UAMES 2117	Chapter 5			
UAK45	Mammoth	UAMES 2129	Chapter 5	$26,230\pm380$	AA103885	Chapter 5
UAK46	Mammoth	UAMES 2153	Chapter 5			
UAK47	Mammoth	UAMES 2156	Chapter 5			
UAK48	Mammoth	UAMES 2160	Chapter 5	$25,070\pm570$	AA103827	Chapter 5
UAK49	Mammoth	UAMES 2180	Chapter 5			
UAK50	Mammoth	UAMES 2209	Chapter 5			
UAK51	Mammoth	UAMES 2217	Chapter 5			

Appendix V Sample information for megafaunal herbivores from the Selawik area.

Appendix V continues below.

Samples analyzed multiple times (duplicate/triplicate) in Chapter 5 are in bold Dates obtained in Chapter 5 are in bold UAMES = University of Alaska Museum Earth Science

Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

- Bocherens, H., Fizet, M., Mariotti, A., Gangloff, R., Burns, J., 1994. Contribution of isotopic biogeochemistry (${}^{13}C, {}^{15}N, {}^{18}O$) to the paleoecology of mammoths (*Mammuthus primigenius*). Hist. Biol. 7, 187–202.
- Druckenmiller, P.S., 2008. Survey of Pleistocene (Ice Age) vertebrates from the Selawik and Kobuk River areas of Northwestern Alaska. Intern. Rep. U.S. Fish Wildl. Serv. 1–56.

Sample Number	Stable Isotope Reference	${}^{14}C$ Date	Date Lab #	Date reference
11/1	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)
11/2	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)
11/5	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)
11/8	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)
11/12	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)
11/13	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)
11/17	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)
11/19	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)
11/22	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)
11/23	Iacumin et al. (2000)	~14,000	dating based on cultural layer	Iacumin et al. (2000)
11/27	Iacumin et al. (2000)	~14,000	dating based on cultural layer	Iacumin et al. (2000)
11/29	Iacumin et al. (2000)	~14,000	dating based on cultural layer	Iacumin et al. (2000)
11/31	Iacumin et al. (2000)	~14,000	dating based on cultural layer	Iacumin et al. (2000)
11/34	Iacumin et al. (2000)	~15,000	dating based on cultural layer	Iacumin et al. (2000)
14/1	Iacumin et al. (2000)	~13,500 to ~20,000	dating based on cultural layer	Iacumin et al. (2000)
15/1	Iacumin et al. (2000)	21000		Iacumin et al. (2000)
15/2	Iacumin et al. (2000)	21000		Iacumin et al. (2000)
15/3	Iacumin et al. (2000)	21000		Iacumin et al. (2000)
15/4	Iacumin et al. (2000)	21000		Iacumin et al. (2000)
15/5	Iacumin et al. (2000)	21000		Iacumin et al. (2000)
15/7	Iacumin et al. (2000)	21000		Iacumin et al. (2000)
15/9	Iacumin et al. (2000)	21000		Iacumin et al. (2000)
12/1	Iacumin et al. (2000)			
12/2	Iacumin et al. (2000)			
12/3	Iacumin et al. (2000)			
11/18	Iacumin et al. (2000)	~13,000	dating based on cultural layer	Iacumin et al. (2000)

Appendix W Sample information for megafaunal herbivores from south central Siberia.

Appendix W continues below.

***In Western Beringia, this would have been a reindeer, rather than a caribou. However, consistent naming of species is used in the thesis.**

****In Western Beringia, this would have been a red deer or a wapiti rather than an elk. However, consistent naming of species is used in the thesis.**

Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

References:

Iacumin, P., Nikolaev, V., Ramigni, M., 2000. C and N stable isotope measurements on Eurasian fossil mammals, 40 000 to 10 000 years BP: herbivore physiologies and palaeoenvironmental reconstruction. Palaeogeogr. Palaeoclimatol. Palaeoecol. 163, 33–47.

Appendix X Sample information for megafaunal herbivores from Spain.

Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

- Álvarez-Lao, D.J., Kahlke, R.-D., García, N., Mol, D., 2009. The Padul mammoth finds On the southernmost record of *Mammuthus primigenius* in Europe and its southern spread during the Late Pleistocene. Palaeogeogr. Palaeoclimatol. Palaeoecol. 278, 57–70. doi:10.1016/j.palaeo.2009.04.011
- García-Alix, a., Delgado Huertas, a., Martín Suárez, E., 2012. Unravelling the Late Pleistocene habitat of the southernmost woolly mammoths in Europe. Quat. Sci. Rev. 32, 75–85. doi:10.1016/j.quascirev.2011.11.00

Common Name	Scientific Name	Sample Number	Stable Isotope Reference	${}^{14}C$ Date	Date reference	Tissue
Mammoth	Mammuthus primigenius	20/411	Iacumin et al., 2000	$11,140\pm180$	Iacumin et al., 2000	$\mathbf B$
Mammoth	Mammuthus primigenius	20/407	Iacumin et al., 2000	39,800±600	Iacumin et al., 2000	B
Mammoth	Mammuthus primigenius	20/412	Iacumin et al., 2000	$39,800\pm500$	Iacumin et al., 2000	$\, {\bf B}$
Mammoth	Mammuthus primigenius	$20/A-50$	Iacumin et al., 2000			$\, {\bf B}$
Mammoth	Mammuthus primigenius	20/415	Iacumin et al., 2000	$40,800\pm200$	Iacumin et al., 2000	$\, {\bf B}$
Mammoth	Mammuthus primigenius	20/408	Iacumin et al., 2000			$\, {\bf B}$
Mammoth	Mammuthus primigenius	20/8833	Iacumin et al., 2000			$\mathbf B$
Mammoth	Mammuthus primigenius	2000/173	Szpak et al., 2010	$11,900\pm40$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2000/174	Szpak et al., 2010	$28,210\pm210$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2000/183	Szpak et al., 2010	$28,260\pm170$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2000/198	Szpak et al., 2010	$15,390\pm50$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2001/412	Szpak et al., 2010	>44,400	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2002/472	Szpak et al., 2010	>48,800	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2002/473	Szpak et al., 2010	$46,700\pm2,800$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2002/594	Szpak et al., 2010			
Mammoth	Mammuthus primigenius	2005/897	Szpak et al., 2010	$40,150\pm990$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2005/900	Szpak et al., 2010	$28,700\pm310$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2005/901	Szpak et al., 2010	$17,300\pm 60$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2005/907	Szpak et al., 2010	$41,000\pm1,400$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2005/915	Szpak et al., 2010	$27,740\pm220$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2005/916	Szpak et al., 2010			
Mammoth	Mammuthus primigenius	2005/917	Szpak et al., 2010	$35,380 \pm 550$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2005/928	Szpak et al., 2010			
Mammoth	Mammuthus primigenius	2005/945	Szpak et al., 2010	$28,260\pm170$	Debruyne et al., 2008	
Mammoth	Mammuthus primigenius	2005/988	Szpak et al., 2010			
Mammoth	Mammuthus primigenius	2005/999	Szpak et al., 2010	>49,900	Debruyne et al., 2008	
Muskox	Ovibos	KIC 2002/537	Raghavan et al., 2014	2756 ± 27	Raghavan et al., 2014	B
Muskox	<i>Ovibos</i>	KIC 2003/756	Raghavan et al., 2014	2918 ± 28	Raghavan et al., 2014	$\, {\bf B}$
Muskox	Ovibos	KIC 2003/757	Raghavan et al., 2014	3372 ± 43	Raghavan et al., 2014	$\, {\bf B}$
Muskox	Ovibos	KIC 2003/764	Raghavan et al., 2014	4082 ± 30	Raghavan et al., 2014	$\, {\bf B}$
Muskox	Ovibos	KIC 2003/763	Raghavan et al., 2014	5364 ± 49	Raghavan et al., 2014	B
Muskox	Ovibos	PIN 3913-13	Raghavan et al., 2014	12830 ± 80	Raghavan et al., 2014	$\mathbf B$

Appendix Y Sample information for megafaunal herbivores from the Taymyr Peninsula.

Appendix Y continues below.

KIC 2005/926	Taymyr	-20.5	6.2	4.4	44.4	16.3	3.2
KIC 2003/767	Taymyr	-20.8	5.4	17.7	47.3		3.1
KIC 2001/434	Taymyr	-20.3	6.4	7.2	42.8	15.9	3.1
KIC 2003/768	Taymyr	-21.1	5.4	11.8	44.2	16.5	3.2
KIC 2002/505	Taymyr	-21.0	5.9	6.6	43.0	15.9	3.2
KIC 2003/766	Taymyr	-20.3	4.8	3.9	42.9	15.9	3.2
KIC 2001/433	Taymyr	-20.0	5.6	2.9	42.0	15.5	3.2
KIC 2003/759	Taymyr	-20.5	6.4	6.7	44.8	16.5	3.2
KIC 2003/606	Taymyr	-21.1	6.1	8.1	43.9	16.2	3.2
KIC 2003/603	Taymyr	-21.0	4.7	6.4	44.2	16.4	3.2
KIC 2000/57	Taymyr	-20.7	7.6	5.4	44.2	16.4	3.1
KIC 2003/649	Taymyr	-20.9	6.3	5.6	44.8	16.6	3.2
KIC 2000/66	Taymyr	-21.1	5.6	3.7	42.6	15.5	3.2
KIC 2000/103	Taymyr	-21.1	5.4	5.7	44.1	16.4	3.1
KIC 2003/667	Taymyr	-20.6	4.7	10.4	42.7		3.2
KIC 2002/511	Taymyr	-20.8	5.2	5.1	47.4	17.7	3.2
PIN 3913-55	Taymyr	-20.0	4.9	10.1	44.0		3.1
KIC 2003/668	Taymyr	-20.7	3.0	4.2	43.3	16.0	3.2
PIN 3913-65	Taymyr	-20.6	5.1	7.6	44.6	16.4	3.2
PIN 3913-60	Taymyr	-21.0	5.9	5.2	43.7	16.0	3.2
\mathbf{D}_{out} dentise $C = C$ encontrary $\mathbf{D} = C$ excess dentise $\mathbf{T} = T$ such dentise							

Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

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Appendix Z Sample information for megafaunal herbivores from Wrangel Island.

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Appendix AA Sample information for megafaunal herbivores from Yakutia.

Appendix AA continues below.

***In Western Beringia, this would have been a reindeer, rather than a caribou. However, consistent naming of species is used in the thesis. **These are approximate dates based on the cultural layer.**

Average of repeat measurements on different tissues from the same specimen are underlined

Tissue: B = Bone; RD = Root dentin; C = Cementum; D = Crown dentin; T= Tusk dentin

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Appendix BB Results of the mathematical analysis on groups for each site and time period, with the time periods defined using binning approach A.

North Slope LGM													
Bison	1.0	2.0	0.5	-20.1	4.9	3	Bison	Horse	0.0	0.0	0.2	0.1	0.1
Horse	0.6	0.7	1.3	-20.6	5.8	12							
North Slope Post-													
LGM													
Bison	0.5	0.5	0.5	-20.3	3.0	8	Bison	Caribou	1.0	0.0	0.0	0.0	0.0
Caribou	2.1	2.7	2.2	-19.0	5.1	5	Bison	Horse	0.9	0.0	0.0	0.0	0.0
Horse	1.4	1.4	4.4	-20.8	5.9	19	Caribou	Horse	0.0	0.0	0.0	0.0	0.0
North Slope													
Holocene													
Caribou	2.2	2.4	5.6	-18.5	2.2	13	Caribou	Moose	1.0	0.0	0.0	0.0	0.0
Moose	3.9	4.6	6.9	-20.5	1.8	8	Caribou	Muskox	0.7	0.0	0.0	0.0	0.0
Muskox	2.6	3.5	2.6	-19.6	4.9	5	Moose	Muskox	0.2	0.0	0.0	0.0	0.0
Old Crow Pre-LGM													
Mammoth	1.2	1.5	1.5	-21.4	9.5	6	Mammoth	Mastodon	0.4	0.0	0.0	0.0	0.0
Mastodon	1.1	1.6	0.8	-20.1	3.1	$\overline{4}$							
Selawik Pre-LGM													
Horse	0.3	0.5	0.1	-21.1	3.5	3	Horse	Mammoth	0.3	0.0	0.0	0.0	0.0
Mammoth	1.0	2.0	0.6	-21.8	7.4	3							
Taymyr Peninsula													
Pre-LGM													
Mammoth	1.5	1.6	3.2	-21.7	9.1	15	Mammoth	Muskox	0.3	0.0	0.0	0.0	0.0
Muskox	1.2	1.3	2.9	-20.7	5.5	14							
Taymyr Peninsula													
Post-LGM													
Mammoth	1.2	1.8	0.9	-21.7	9.6	$\overline{4}$	Mammoth	Muskox	0.3	0.0	0.0	0.0	0.0
Muskox	2.0	2.2	5.3	-20.2	5.5	15							
Yakutia Pre-LGM													
Bison	3.2	6.3	1.7	-20.9	6.2	3	Bison	Mammoth	0.0	0.0	0.0	0.0	0.0
Mammoth	1.2	1.2	4.4	-22.2	9.2	23	Bison	Muskox	0.4	0.4	1.0	2.2	0.4
Muskox	2.9	3.0	9.4	-20.7	6.7	30	Mammoth	Muskox	1.0	0.0	0.0	0.0	0.0

Legend
SEA Standard ellipse area SEA_c **Standard ellipse area corrected for small sample size**

	SEA	SEA_c	TA	$\delta^{13}C$	$\delta^{15}N$	No.	First	Second	SEA _{bron}	SEA_c overlan(1.2)	TA overla $p_{(1,2)}$	SEA _c overlap(2.1	TA overla $p_{(2,1)}$
Alberta Pre-LGM													
Bison	1.9	2.2	3.3	-19.5	6.7	10	Bison	Caribou	0.0	0.0	0.0	0.0	0.0
Caribou	0.1	0.2	0.2	-18.7	4.8	τ	Bison	Horse	0.2	0.0	0.2	0.0	0.3
Horse	1.0	1.1	2.4	-20.3	7.6	17	Bison	Mammoth	0.9	0.0	0.1	0.0	0.1
Mammoth	3.2	4.0	4.2	-20.7	8.1	6	Caribou	Horse	0.9	0.0	0.0	0.0	0.0
							Caribou	Mammoth	1.0	0.0	0.0	0.0	0.0
							Horse	Mammoth	1.0	0.8	0.6	0.2	0.4
Alberta Post-LGM													
Bison	0.5	0.6	0.9	-19.5	2.0	9	Bison	Horse	0.6	0.0	0.0	0.0	0.0
Horse	0.7	0.9	1.3	-20.5	0.7	9							
Fairbanks Pre-LGM													
Caribou	1.0	1.3	1.2	-19.5	3.2	6	Caribou	Horse	0.2	0.0	0.0	0.0	0.0
Horse	1.1	1.2	3.4	-21.2	3.5	22	Caribou	Mammoth	0.8	0.0	0.0	0.0	0.0
Mammoth	0.9	1.3	1.1	-20.8	6.7	5	Caribou	Mastodon	0.2	0.0	0.0	0.0	0.0
Mastodon	0.1	0.1	0.1	-21.0	4.4	5	Horse	Mammoth	1.0	0.0	0.0	0.0	0.0
							Horse	Mastodon	0.4	0.1	0.0	0.7	1.0
							Mammoth	Mastodon	0.1	0.0	0.0	0.0	0.0
Fairbanks LGM													
Caribou	2.1	4.3	1.2	-19.5	3.5	3	Caribou	Horse	0.2	0.0	0.0	0.0	0.0
Horse	0.2	0.4	0.1	-21.1	3.0	3							
Klondike Pre-LGM													
Mammoth	0.7	0.7	2.5	-20.7	7.3	24	Mammoth	Mastodon	1.0	0.0	0.1	0.0	0.1
Mastodon	1.6	1.8	3.7	-20.6	4.4	12	Mammoth	Muskox	1.0	0.0	0.0	0.0	0.0
Muskox	2.1	2.4	4.2	-19.6	5.8	9	Mastodon	Muskox	0.8	0.0	0.1	0.0	0.1
Northwest Europe Pre- LGM													
Bison	0.9	1.0	2.5	-20.2	5.6	18	Bison	Caribou	0.8	0.0	0.2	0.0	0.1
Caribou	1.8	1.8	8.8	-19.2	4.3	50	Bison	Horse	1.0	0.8	1.0	0.2	0.1
Horse	3.4	3.4	17.5	-20.7	5.7	85	Bison	Mammoth	0.5	0.0	0.0	0.0	0.0

Appendix CC Results of the mathematical analysis on groups for each site and time period, with the time periods defined using binning approach B.

	SEA	SEA_c	TA	$\delta^{13}C$	$\delta^{15}N$	No.	First	Second	SEA_{bprop}	SEA_c overlap(1.2)	TA overla $p_{(1,2)}$	SEA _c overlan(2.1)	TA overla $p_{(2,1)}$
Bison Pre-													
LGM Alberta	1.9	2.2	3.3	-19.5	6.7	10	Alberta	North Slope	0.4	0.0	0.3	0.0	0.1
North Slope	2.0	2.0	11.2	-20.1	4.6	58	Alberta	Northwest Europe	0.1	0.0	0.2	0.1	0.3
Northwest													
Europe	0.9	1.0	2.5	-20.2	5.6	18	Alberta	Yakutia	0.8	0.2	0.0	0.1	0.0
Yakutia	3.2	6.3	1.7	-20.9	6.2	3	North Slope	Northwest Europe	0.1	0.2	0.2	0.5	0.9
							North Slope	Yakutia	0.8	0.4	0.1	0.1	0.3
							Northwest Europe	Yakutia	1.0	1.0	0.1	0.2	0.2
Caribou Pre-LGM													
Alberta	0.1	0.2	0.2	-18.7	4.8	7	Alberta	Fairbanks	0.9	0.0	0.0	0.0	0.0
Fairbanks	0.6	0.8	0.6	-19.4	3.1	5	Alberta	North Slope	1.0	1.0	1.0	0.0	0.0
North Slope	3.6	3.7	14.0	-18.3	3.3	35	Alberta	Northwest Europe	1.0	0.0	1.0	0.0	0.0
Northwest Europe	1.9	2.0	8.8	-19.2	4.2	44	Fairbanks	North Slope	0.8	0.0	0.9	0.0	0.0
							Fairbanks	Northwest Europe	0.4	0.5	1.0	0.2	0.1
							North Slope	Northwest Europe	0.0	0.1	0.5	0.2	0.8
Horse Pre- LGM													
Alberta	1.0	1.1	2.4	-20.3	7.6	17	Alberta	Fairbanks	0.7	0.0	0.0	0.0	0.0
Fairbanks	1.2	1.3	2.1	-21.2	2.7	10	Alberta	North Slope	0.8	0.0	0.5	0.0	0.1
North Slope	1.9	1.9	10.1	-21.0	6.1	52	Alberta	Northwest Europe	1.0	0.3	1.0	0.1	0.1
Northwest Europe	3.2	3.3	16.0	-20.7	5.7	84	Alberta	Selawik	1.0	0.0	0.0	0.0	0.0
Selawik	0.3	0.5	0.1	-21.1	3.5	3	Fairbanks	North Slope	0.5	0.0	0.4	0.0	0.1
							Fairbanks	Northwest Europe	0.9	0.0	0.5	0.0	0.1
							Fairbanks	Selawik	0.9	0.2	0.0	0.4	0.6
							North Slope	Northwest Europe	1.0	0.8	0.9	0.4	0.6
							North Slope	Selawik	0.9	0.1	0.0	0.3	0.8
							Northwest Europe	Selawik	0.7	0.0	0.0	0.3	0.8

Appendix DD Results of the mathematical analysis on groups for each species and time period, with the time periods defined using binning approach A.

	SEA	SEA_c	TA	$\delta^{13}C$	$\delta^{15}N$	No.	First Second		SEA_{bprop}	SEA _c overlap(1.2)	TA overlap _{$(1, 2)$}	SEA _c overlap (2.1)	TA overlap (2.1)
Bison Pre-LGM													
Alberta	1.9	2.2	3.3	-19.5	6.7	10	Alberta North Slope		0.4	0.0	0.3	0.0	0.1
North Slope	2.0	2.0	11.2	-20.1	4.6	60	Alberta Northwest Europe		0.1	0.0	0.2	0.1	0.3
Northwest Europe	0.9	1.0	2.5	-20.2	5.6	18	Alberta Yakutia		0.8	0.2	0.0	0.1	0.0
Yakutia	3.2	6.3	1.7	-20.9	6.2	3	North Slope Northwest Europe		0.1	0.3	0.2	0.5	0.9
							North Slope	Yakutia	0.9	0.4	0.1	0.1	0.3
							Northwest Europe	Yakutia	1.0	1.0	0.1	0.2	0.2
Caribou Pre-LGM													
Alberta	0.1	0.2	0.2	-18.7	4.8	$\overline{7}$	Alberta	Fairbanks	0.9	0.0	0.0	0.0	0.0
Fairbanks	1.0	1.3	1.2	-19.5	3.2	6	Alberta	North Slope	1.0	1.0	1.0	0.0	0.0
North Slope	3.7	3.8	14.0	-18.3	3.4	36	Alberta	Northwest Europe	0.9	0.0	1.0	0.0	0.0
Northwest Europe	1.8	1.8	8.8	-19.2	4.3	50	Alberta	South Central Siberia	0.7	0.0	0.0	0.0	0.0
South Central Siberia	0.5	0.6	0.7	-18.3	3.8	7	Fairbanks	North Slope	0.9	0.0	0.6	0.0	0.1
							Fairbanks	Northwest Europe	0.4	0.2	1.0	0.2	0.1
							Fairbanks	South Central Siberia	0.1	0.0	0.0	0.0	0.0
							North Slope	Northwest Europe	0.0	0.1	0.5	0.2	0.8
							North Slope	South Central Siberia	0.0	0.1	0.1	1.0	1.0
							Northwest Europe	South Central Siberia	$0.2\,$	0.0	0.0	0.1	0.5
Horse Pre-LGM													
Alberta	1.0	1.1	2.4	-20.3	7.6	17	Alberta	Fairbanks	0.5	0.0	0.0	0.0	0.0
Fairbanks	1.1	1.2	3.4	-21.2	3.5	22	Alberta	North Slope	0.7	0.1	0.5	0.0	0.0
North Slope	1.8	1.8	10.1	-20.9	6.0	64	Alberta	Northwest Europe	1.0	0.3	1.0	0.0	0.0
Northwest Europe	3.4	3.4	17.5	-20.7	5.7	85	Alberta	Selawik	1.0	0.0	0.0	0.0	0.0
Selawik	0.3	0.5	0.1	-21.1	3.5	3	Fairbanks	North Slope	0.8	0.0	0.4	0.0	0.3
							Fairbanks	Northwest Europe	1.0	0.1	0.8	0.0	0.2
							Fairbanks	Selawik	1.0	0.2	0.0	0.1	0.0

Appendix EE Results of the mathematical analysis on groups for each species and time period, with the time periods defined using binning approach B.

Klondike Russian Plain 0.7 0.0 0.0 0.0 0.0 Klondike Selawik 0.9 0.0 0.0 0.0 0.0 Klondike Taymyr 1.0 0.0 0.1 0.0 0.1 Klondike Yakutia 0.8 0.0 0.0 0.0 0.0 North Slope Northwest Europe 0.4 0.6 0.2 0.9 1.0 North Slope 01d Crow 0.8 0.2 0.1 0.2 0.7 North Slope Russian Plain 0.4 0.0 0.0 0.0 0.0 North Slope Selawik 0.8 0.5 0.1 0.4 1.0 North Slope Taymyr 0.8 0.3 0.3 0.3 0.8 North Slope Yakutia 0.2 0.0 0.4 0.0 0.6

Appendix FF Results of the mathematical analysis on groups for each species and site, with the time periods defined using binning approach A.

	SEA	SEA_c	TA	$\delta^{13}C$	$\delta^{15}N$	No.	First	Second	SEA_{bprop}	SEA _c overlan(1.2)	TA overla $p_{(1,2)}$	SEA_c overlap $(2,1)$	TA overla $p_{(2,1)}$
Bison Alberta													
Pre-LGM	1.9	2.2	3.3	-19.5	6.7	10	Pre-LGM	Post-LGM	0.1	0.0	0.0	0.0	0.0
Post-LGM	0.5	0.6	0.9	-19.5	2.0	9							
Bison North Slope													
Pre-LGM	2.0	2.0	11.2	-20.1	4.6	60	Pre-LGM	Post-LGM	0.1	0.1	0.0	0.3	1.0
Post-LGM	0.5	0.6	0.5	-20.3	3.0	7							
Bison Northwest Europe													
Pre-LGM	0.9	1.0	2.5	-20.2	5.6	18	Pre-LGM	Post-LGM	0.7	0.0	0.0	0.0	0.0
Post-LGM	0.1	0.1	0.0	-20.0	2.3	3							
Caribou Fairbanks													
Pre-LGM	1.0	1.3	1.2	-19.5	3.2	6	Pre-LGM	LGM	0.8	1.0	0.6	0.3	0.6
LGM	2.1	4.3	1.2	-19.5	3.5	3							
Caribou North Slope													
Pre-LGM	3.7	3.8	14.0	-18.3	3.4	36	Pre-LGM	LGM	0.5	0.0	0.0	0.0	0.6
LGM	0.9	1.8	0.5	-19.0	7.6	3	Pre-LGM	Post-LGM	0.1	0.0	0.0	0.1	1.0
Post-LGM	0.1	0.2	0.1	-19.0	3.0	3	Pre-LGM	Holocene	0.1	0.3	0.2	0.5	0.5
Holocene	2.2	2.4	5.6	-18.5	2.2	13	LGM	Post-LGM	0.2	0.0	0.0	0.0	0.0
							LGM	Holocene	0.2	0.0	0.0	0.0	0.0
							Post-						
Caribou South Central							LGM	Holocene	0.7	0.2	1.0	0.0	0.0
Siberia													
Pre-LGM	0.5	0.6	0.7	-18.3	3.8	τ	Pre-LGM	Post-LGM	0.1	0.0	0.0	0.0	0.0
Post-LGM	0.3	0.3	0.6	-18.6	1.8	14							
Caribou Northwest Europe													
Pre-LGM	1.8	1.8	8.8	-19.2	4.3	50	Pre-LGM	LGM	0.0	0.3	0.3	0.7	1.0
LGM	0.8	0.8	3.0	-19.3	3.6	27	Pre-LGM	Post-LGM	0.0	0.0	0.3	0.0	0.6
$\operatorname{\textsf{Post-LGM}}$	0.8	0.9	4.2	-19.6	2.6	80	LGM	Post-LGM	0.4	0.2	0.6	0.2	0.5
Elk Northwest Europe													
Post-LGM	1.5	1.6	5.7	-20.4	2.7	32	Post-	Holocene	1.0	0.0	0.2	0.0	0.2

Appendix GG Results of the mathematical analysis on groups for each species and site, with the time periods defined using binning approach B.

Site	Species	Time Bin	p -value (Bin A)	p -value (Bin B)
Alberta	Bison	Pre-LGM	0.79	0.79
		Post-		
		LGM	0.00	0.00
	Caribou	Pre-LGM	0.23	0.23
	Horse	Pre-LGM	0.40	0.40
		Post-		
		LGM	0.52	0.52
	Mammoth	Pre-LGM	0.15	0.15
Fairbanks	Caribou	Pre-LGM	0.01	0.04
		LGM Post-		0.00
		LGM	0.02	
	Horse	Pre-LGM	0.66	0.08
		LGM	0.32	0.00
		Post-		
		LGM	0.09	0.13
	Mammoth	Pre-LGM	0.53	0.53
	Mastodon	Pre-LGM	0.01	0.01
Herschel Island	Muskox	Pre-LGM	0.18	0.16
		Post-		
		LGM	0.36	0.00
Klondike	Elk	Post- LGM	0.00	0.00
	Mammoth	Pre-LGM	0.40	0.12
	Mastodon	Pre-LGM	0.07	0.07
	Moose	Holocene	0.27	0.27
	Muskox	Pre-LGM	0.12	0.12
		Post-		
North Slope	Bison	LGM	0.00	0.01
		LGM	0.00	
		Pre-LGM	0.00	0.00
	Caribou	Holocene	0.00	0.00
		Post-		
		LGM	0.90	0.00
		LGM		0.00
		Pre-LGM	0.07	0.08
		Post-		
	Horse	LGM	0.12	0.25
		LGM	0.01	0.27
		Pre-LGM	0.33	0.48
	Mammoth Mastodon	Pre-LGM Pre-LGM	0.05 0.77	0.03 0.77
	Moose	Holocene	$0.00\,$	0.00
	Muskox	Holocene	0.03	0.03
		Pre-LGM		
		Post-	0.11	0.10
Northwest Europe	Bison	LGM	0.00	0.00
		Pre-LGM	0.53	0.53
		Post-		
	Caribou	LGM	0.08	0.29
		LGM	0.46	0.74
		Pre-LGM	0.04	0.02

Appendix HH Results of the normality tests on all groups of data.

Appendix II Copyright release

Chapter 3 was published in Scientific Reports. The following is an except from the Scientific Reports website, accessed December 6, 2015:

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Signed,

Katherine Allan

Curriculum Vitae

2011-2013

Publications:

- **Schwartz-Narbonne, R.,** Longstaffe, F.J., Metcalfe, J.Z., and Zazula, G. Solving the woolly mammoth conundrum: amino acid ¹⁵N-enrichment suggests a distinct forage or habitat, *Scientific Reports*, 5, 9791 (2015)
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- + five presentations and accompanying abstracts at one national and four international conferences since 2011 and two contributions to the LSIS Technical Memoranda series