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Tracing Ainu and Pre-Ainu Cultural Continuity Through Cladistic Analysis of Faunal Assemblages

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TRACING AINU AND PRE-AINU CULTURAL CONTINUITY THROUGH

CLADISTIC ANALYSIS OF FAUNAL ASSEMBLAGES

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by

Christopher James Lowry

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ABSTRACT

TRACING AINU AND PRE-AINU CULTURAL CONTINUITY THROUGH
CLADISTIC ANALYSIS OF FAUNAL ASSEMBLAGES

by

Christopher James Lowry

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Cladistics (Hennig 1950, 1965, 1966), a method for establishing evolutionary relationships, is used to compare faunal assemblages from Jōmon (14,000-500 BC; 14,000–2700 cal. BP), Epi-Jōmon (3rd – 7th century; 2700-1500 cal. BP), Satsumon (7th century - 13th century AD; ca. 1500-800 cal. BP), and Ainu (13th century AD – present) period components (Habu et al. 2011; Matsumura 2006; Ōnishi 2014; Weber et al. 2013) from sites in Central Hokkaido, Japan using Generalized Frequency Coding methods (Smith & Gutberlet 2001). Associations of site components follow geographic rather than temporal trends, showing similarities in animal use across these time periods but differentiated between coastal lowland, inland lowland, and inland upland areas. Statistical analyses confirm the trends found in cladistic analysis. These findings suggest some level of cultural continuity across these time periods and important local environmental forces at work in shaping animal use.

ACKNOWLEDGEMENTS

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CHAPTER I

INTRODUCTION

Problem

Throughout the world, indigenous archaeology, or archaeology conducted

concerning and by indigenous peoples, faces issues of colonial history and perceptions of

"who has the right to control the past"(Kato 2009:47-49; Nicholas 2010; Smith & Wobst

2005). The Ainu, an indigenous people and ethnic minority in Japan and especially

Hokkaido, the island of Sakhalin, and the Kuril Islands in the north Pacific (Figure 1),

face problems inherent to indigenous archaeology (Kato 2009). In particular, the

incomplete archaeological picture and unclear origins of Ainu people and culture lead to

a cultural identity incomplete in its reach into the past (Hudson 2006:423). Aside from a

general dearth of ethnography in studies of Ainu archaeology, current Ainu cultural

concerns and insights often seem to be ignored (Kato 2010). While there are important

studies charting cultural changes between adjacent temporal components in Hokkaido,

such as Hudson's (1999) study of the Epi-Jōmon-Satsumon transition, no examinations of

cultural transitions cutting across the Jōmon (14,000-500 BC; 14,000–2700 cal. BP), Epi-

Jōmon (3rd – 7th century; 2700-1500 cal. BP), Satsumon (7th century - 13th century AD;

ca. 1500-800 cal. BP), and Ainu (13th century AD – present) periods have been

undertaken (Habu et al. 2011; Matsumura 2006; Ōnishi 2014; Weber et al. 2013).

Furthermore, none have specifically entailed tracing cultural continuity or changes using

faunal remains from across these time periods, and cultural aspects of animal use in

general has also been neglected in cladistical archaeological studies. Tracking animal use and substance changes is especially important for understanding sedentary hunter-gatherer populations with a history of animal-based religion (Batchelor 1892; Munro 1963; Ohnuki-Tierney 1976; Utagawa 1992).

Figure 1. Map showing historical range of Ainu settlement (red) and probable range (pink) based on linguistic evidence (dots) (Kwamikagami 2011).

While this incomplete understanding of the past is partially an academic concern, its cultural implications are manifested in the lack of strong Ainu identity and discrimination by the larger Japanese society (Hudson 2006; Siddle 1995). Cultural

insensitivity also appears in academic treatment of Ainu culture, exacerbating the general sense of the Ainu as being fundamentally disconnected from Japanese cultural history (Siddle 1995:89). Aside from a general dearth of ethnographic information in studies of Ainu archaeology, current Ainu cultural concerns also seem to be actively ignored (Kato 2010).

Purpose

To address these gaps in our current understanding, this thesis synthesizes archaeological evidence of animal use across temporal components and geographic locations in Central Hokkaido. I examine excavated faunal assemblage data from archaeological sites on Hokkaido including the Jōmon, Epi-Jōmon, Satsumon, and Ainu components. I use cladistic analysis to determine how similar faunal distributions are and how they change over space and time. This study shows continuity in animal use over time in Central Hokkaido, thereby adding evidence to claims of traditional animal use practices for modern Ainu.

Significance

This thesis uses a broader comparative scope than other studies in the area as well as application of methods to new areas of archaeology. A cohesive look at faunal assemblages across Central Hokkaido adds to our understanding of the area's prehistory, in ways that cannot be achieved by site-by-site reports and studies. Similarly, using a

broader temporal range can give insight into larger-scale cultural evolution. Finally, cladistics, while extensively used in evolutionary archaeology for studies of human-made objects, has yet to be used for traces of food culture, or of animal-human interface in general.

This broader perspective, including Ainu archaeology within a deeper time context, will help our overall understanding of archaeological culture in Hokkaido, and provides guidelines and points of comparison for future research in Hokkaido as new sites are discovered and new significance recognized. Finally, understanding how modern Ainu culture articulates with previous cultural traditions helps to provide a more unified historical basis and greater respect for the Ainu in modern Japanese society as a whole (Siddle 1995:73-4).

Thesis Organization

This thesis is in a journal-ready format, in which a complete article, intended to be able to stand on its own, is included within the thesis. The article contains the results, discussion, and conclusion of this study, as well as simplified versions of the introduction, background, theory, and methods sections, which precede the article in their more complete forms. No longer versions of the results, discussion, and conclusion of this study exist outside of the article.

I intend to submit the article to Arctic Anthropology, published by the University of Wisconsin Press. The citation style, reference formatting, heading and subheading

formatting, and other stylistic considerations also adhere to Arctic Anthropology

standards.

CHAPTER II

BACKGROUND

Biophysical Context

Physical Geography

While the Jōmon, Epi-Jōmon, Satsumon, and Ainu periods are present to some extent in various parts of northeast Asia (see Table 1), the focus of this study is on central Hokkaido. Hokkaido itself is split between the Japanese and North American tectonic plates running approximately northwest-southeast through eastern-central Hokkaido (Millien-Parra & Jaeger 1999). Lower sea levels during the Pleistocene meant that Hokkaido was connected to present day Sakhalin and mainland Asia (Millien-Parra & Jaeger 1999). This land-bridge is important to theories of faunal migration and differences in faunal distribution between Hokkaido and the rest of Japan (Dobson & Kawamura 1998). Topography varies across Hokkaido, from rolling hills and sloping plateaus to abrupt mountainous regions (Ohdachi & Aoi 1987). Between mountain ranges and hills, much of Hokkaido is freshwater wetland, which comprises most of the wetland in Japan (Ogawa et al. 2006). Wetlands are part of the river systems that flow down from the mountains into coastal plains (Hirayama et al. 2002). These rivers and the coasts to which they flow are important features of the Ainu landscape.

Table 1. Distributions of northeast Asian cultures by geographic area (Sato et al. 2009).

	Jōmon (14,000 BC - 1,000 BC) (Ōnishi 2014)	Epi-Jōmon (3rd century BC - 7th century AD)(Sato et al. 2009)	Satsumon (7th - 13th century AD)(Ōnishi 2014)	Ainu (13th century - present)(Ōnishi 2014)
Honshu, Japan	●	●		●
Hokkaido, Japan	●	●	●	●
Sakhalin, Russia				●
Kuril Islands, Russia				●
Kamchatka, Russia				●

Climate

The island of Hokkaido is bordered by the Okhotsk Sea to the north, Pacific Ocean to the east, and Sea of Japan to the west (Figure 1). During the Quaternary and early Holocene periods, Hokkaido was colder than it is today (Igarashi 2013). During much of this time, Hokkaido was connected to Sakhalin and the Asian mainland through land bridges, which influenced the floral and faunal development of Hokkaido (Dobson & Kawamura 1998). By 15,000 BP, these bridges had disappeared (Nakazawa et al. 2011). Variations between cool moist and cold dry climates before the Bölling-Allerød period (14,000-12,000 BP) are indicated in the pollen record (Igarashi 2011). The Bölling-Allerød period marks the beginning of significant warming with the presence of a maritime climate on the Pacific coast and a shift to a warm, moist climate throughout Hokkaido during the Pre-Boreal (ca 12,000 BP) (Igarashi 2011). More recently, the most

significant climactic change occurred from 8000 to 9000 BP, with warming indicated by a sudden increase in *Quercus* (oak) forest (Igarashi 2013). Oak forests and Erman's birch developed throughout the Holocene. The northward spread of *Fagus crenata* (Japanese beech) stopped at around 1000 BP, indicating a halt of significant further warming (Igarashi 2013). Within the study area, neither Japanese beech forests nor boreal coniferous forests are present (Figure 2), leaving the otherwise ubiquitous oak and birch forest or wetland.

Figure 2. Map of Hokkaido compiled from Igarashi (2013), Maphill (2011), and the World Wildlife Fund (2017b). 1 – Boreal coniferous forest; 2 – *Fagus crenata* forest and Nihonkai montane deciduous forest ecoregion (PA0428)(World Wildlife Fund 2017c); 3 – Hokkaido montane coniferous forest ecoregion (PA0510)(World Wildlife Fund 2017a). The remaining land makes up the Temperate Broadleaf and Mixed Forest of Hokkaido (PA0423)(Yumiko 2017).

Hokkaido today is noted for its cold, snowy winters and mild summers. Ocean currents and monsoon winds are responsible for the temperature and precipitation patterns in Hokkaido, with the Tsushima and Soya Warm Currents affecting the west and north sides and the Oyashio Cold Current affecting the east (Igarashi 2013). The Okhotsk High system cools the summer, and monsoon winds from the Siberian High system brings snow in the winter (Aoyama 2012; Igarashi 2013). All of this cooling and warming action results in average monthly temperatures ranging from -6.2 °C in January to 17.8°C in July (Millien-Parra and Jaeger 1999).

Flora

Much of Hokkaido is forest or wetland, with many species of trees (Ogawa et al.2006). The forest is divided between boreal and cool-temperate (Igarashi 2013)(Figure 2; Table 2). Aside from the southwest peninsula of Hokkaido, where Japanese beech (*Fagus crenata*) is the primary forest cover, and a small pocket of Erman's birch (*Betula ermanii*) forest covering part of the eastern Pacific coast, the difference between boreal forest and cool-temperate forest seems to be one of elevation, with the former dominating higher elevations (Igarashi 2013). This elevation-based gradient also corresponds with a deciduous-coniferous gradient (Okitsu 2003).

Table 2. Main tree species in Hokkaido forests (Igarashi 2013; Ogawa et al. 2006).

	Scientific name	Common name
Southwest Hokkaido		
	Fagus crenata	Japanese beech
Boreal		
	Picea jezoensis	Yezo Spruce
	Picea glehnii	Glehn's spruce
	Abies sachalinensis	Sakhalin fir
Cool-temperate		
	Quercus crispula	Mongolian oak
	Quercus mongolica var, *grosseserata*	Mongolian oak
	Acer mono	Painted maple
	Tilia japonica	Japanese lime
	Fraxinus mandshuria var. *japonica*	Japanese Manchurian ash
	Phellodendron amurense	Amur cork-tree
	Sasa kurilensis	Chishima dwarf bamboo
	Alnus spp.	Alder shrubs
Pacific coast		
	Betula ermanii	Erman's birch

Lowland deciduous forests mainly include Mongolian oak (*Quercus mongolica*), as well as elm (*Ulmus davidiana*), ash (*Fraxinus mandshurica*), and basswoods (*Tilia japonica*), with an understory of dwarf bamboo (*Sasa* sp.) and wildflowers (Ohara 2009). Wetlands contain grasses, sedges, alder shrubs (*Alnus* sp.), and even ash, willow, spruce, and dwarf bamboo (Ogawa et al. 2006). The study area for this thesis falls mostly within this lowland deciduous regime, with some cool-temperate mixed forest at one upland site (Kamihoronaimoi). The mixed forest regime contains both deciduous vegetation from the lowlands and coniferous vegetation of the boreal regime (Ohara 2009). Boreal coniferous forest is dominated by Ezo spruce (*Picea jezoensis*) and Sakhalin fir (*Abis sachalinensis*),

as well as Glehn's spruce (*P. glehnii*) (Okitsu 2003; Qian 2003). Ezo Spruce (*Picea jezoensis*), haskap (*Lonicera caerulea*), and Siberian onion (*Allium ochotense*) are well-known Hokkaido plants.

Fauna

The land bridge between Hokkaido and mainland Siberia during glacial periods has affected the mammalian fauna there, distinguishing it as boreal Eurasian fauna as opposed to the more Indo-Malayan fauna in the rest of Japan (Dobson 1994:91). While some species were extinct by about 10,000 BP, such as moose (*Alces alces*), steppe bison (*Bison priscus*), and aurochs (*Bos primigenius*), the fauna of Hokkaido maintains its distinctive Siberian-style regimes (Dobson & Kawamura 1998). The most famous animals on Hokkaido include the Hokkaido Brown Bear (*Ursus arctos yesoensis*), foxes (*Vulpes* spp.), owls (Strigiformes), red-crowned cranes (*Grus japonensis*), and, until the 19th century, wolves (*Canis lupus hattai*). Deer (*Cervus nippon*), salmon (Salmonidae), and seals (Pinnipedia) have also been notable in Ainu diet and trade hunting (Aoyama 2012; Hudson 1999). Through the work of Dobson and Kawamura (1998) on ancient and extant fauna of Hokkaido and work of Ohdachi and Aoi (1987) on the diet of Hokkaido brown bears, we see a variety of species living in Hokkaido. A sample of extant fauna is listed in Table 3.

Table 3. Animal species noted by the World Wildlife Fund as found in the Temperate Broadleaf and Mixed Forest of Hokkaido (PA0423) and Temperate Coniferous Forest of Hokkaido (PA0510) ecoregions (Yumiko 2017; World Wildlife Fund 2017) with select Hokkaido Fauna as determined by Dobson & Kawamura (1998) and Ohdachi & Aoi (1987) denoted by *. Species reported in all references are denoted by **.

Temperate Broadleaf and Mixed Forest (PA0423) and Temperate Coniferous Forest (PA0510)	
Common Name	**Scientific Name**
Birds	
Stellar's Sea eagle	*Haliaeetus pelagicus*
Common merganser	*Mergus merganser*
Tufted Puffin	*Lunda cirrhata*
Hazel grouse	*Tetrastes bonasia*
Three-toed woodpecker	*Picoides tridactylus*
Willow tit	*Parus palustris*
Japanese crane	*Grus japonensis*
Blakiston's fish owl	*Keputa blakistoni*
Microbats	
Rodents	
Dsinezumi shrew	*Crocidura dsinezumi* *
Laxmann's shrew	*Sorex caecutiens* *
Slender shrew	*Sorex gracillimus* *
Long-clawed shrew	*Sorex unguiculatus* *
Red squirrel	*Sciurus vulgaris* *
Siberian chipmunk	*Tamias sibiricus* *
Siberian flying squirrel	*Pteromys volans* *
Grey red-backed vole	*Clethrionomys rufocanus* *
Northern red-backed vole	*Clethrionomys rutilus* *
Rabbits/Hare (Lagomorphs)	
Mountain hare	*Lepus timidus* *
(Small Mustelids)	
Mammals	
Red fox	*Vulpes vulpes*
Sika deer	*Cervus nippon yesoensis*

TABLE 3 (CONTINUED)

Temperate Broadleaf and Mixed Forest (PA0423) and Temperate Coniferous Forest (PA0510)	
Common Name	**Scientific Name**
Hokkaido brown bear	*Ursus arctos yesoensis* **
Temperate Coniferous Forest (PA0510)	
Common Name	**Scientific Name**
Pika (Northern Pika)	*Ochotona hyperborea yesoensis* **
Sable	*Martes zibellina brachyuran* **

Terrestrial Hokkaido fauna types are split between alpine and forest or wetland regimes, with the alpine containing small mammals, such as pika (*Ochotona hyperborea yesoensis*) and sable (*Martes zibellina brachyura*) that otherwise are absent from the non-alpine zones (Yumiko 2017; World Wildlife Fund 2017) (Table 3). Within these regimes, only two species are noted as exclusive to the alpine ecoregion (PA0510) in Hokkaido, and the rest cover both ecoregions of Hokkaido (PA0510 and PA0423)(Figure 2; Table 3). Since study area is in the Temperate Broadleaf and Mixed Forest ecoregion of Hokkaido (PA0423), it only includes fauna from this regime (Figure 2,3). Non-terrestrial fauna, such as fish and aquatic mammals, can be divided into marine and freshwater, as well as species that exist in both. Fauna present in assemblages of study sites are listed in Table 4, and a list of fauna from select sites of the Ainu and Satsumon periods comprises Table 5 (Nishimoto 1985). Remains from all Hokkaido fauna categories are found in Hokkaido archaeological sites (Table 5). From the study sites, one faunal type (Cyprinidae) is found in freshwater, one (Marine mammal (M-L size class)) is marine, and four (Salmonidae, Tribolodon, *Hucho perryi*, and *Clupea pallasii*) are found in both (Table 4).
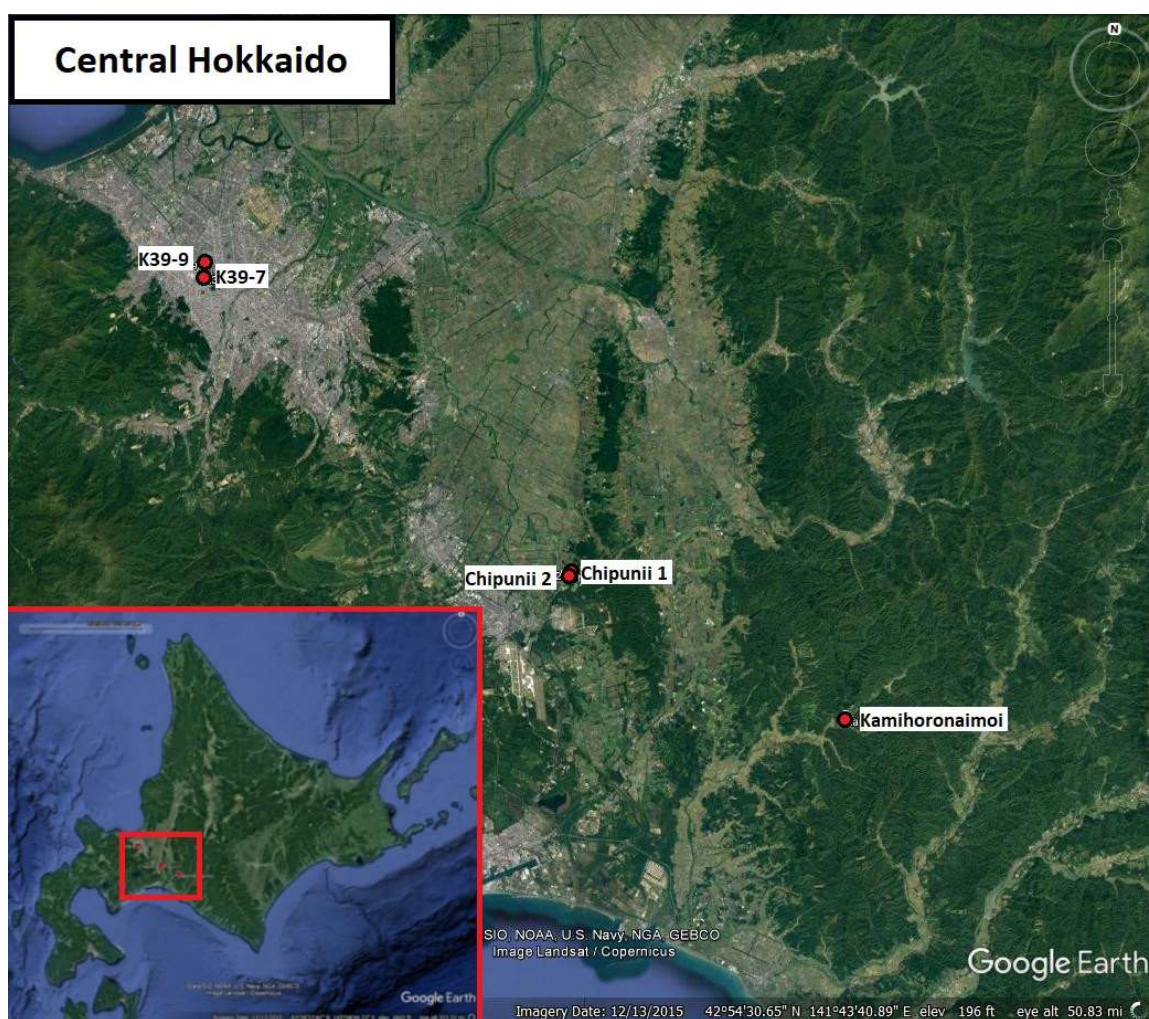
Figure 3. Map of the study area and sites included in the study in Central Hokkaido.

Table 4. Faunal remains by component present in study sites.

Component	Faunal Remains Present
Ainu	**Mammal**
	Cervus nippon (Sika deer)
	Fish
	Cyprinidae (minnow and carp); Tribolodon (redfin dace)

TABLE 4 (CONTINUED)

Ainu	**Fish**
	Salmonidae (Salmonids); *Hucho perryi* (Sakhalin taimen)
	Mollusc
	Ezohelix gainesi gainesi (terrestrial mollusc)
	Clausliidae (door snail); Snail
Satsumon	**Mammal**
	Cervus nippon (Sika deer)
	Cetacea (whale, dolphin, porpoise family)
	Fish
	Cyprinidae (minnow and carp); Tribolodon (redfin dace)
	Salmonidae (Salmonids); *Hucho perryi* (Sakhalin taimen)
	Clupeinae (*Clupea pallasii*) (Pacific herring)
	Mollusc
	Snail; Clausliidae (door snail)
Epi-Jōmon	**Mammal**
	Cervus nippon (Sika deer)
	Marine mammal (M-L size class)
	Fish
	Cyprinidae (minnow and carp); Tribolodon (redfin dace)
	Salmonidae (Salmonids); *Hucho perryi* (Sakhalin taimen)
	Crustacean
	Arthropoda (Crustacean)
Jōmon	**Mammal**
	Cervus nippon (Sika deer)
	Sus scrofa leucomystax (Japanese boar)
	Fish
	Salmonidae (Salmonids)

Table 5. Species present in select Hokkaido sites divided by component, from Nishimoto (1985).

Component	Scientific name (Common name), *Marine, **Brackish-water, †Freshwater, ‡Both Marine & Freshwater
Satsumon & Ainu	Mammal: *Ursus arctos yesoensis* (Hokkaido brown bear), *Canis lupus familiaris* (Dog), *Canis lupus hattai* (Hokkaido wolf), *Vulpes vulpes schrenki* (Ezo red fox), Felis (Cats), Equus (Horses), *Cervus nippon yesoensis* (Yezo sika deer), *Nyctereutes procyonides albus* (Ezo tanuki/raccoon dog), *Lepus timidus ainu* (Ezo mountain hare), *Martes zibellina brachyura* (Japanese sable), Cetacea (Whales, dolphins, porpoises)*, Dolphins*, *Eumetopias jubatus* (Steller sea lion)*, Phocidae (Earless seal)*, *Zalophus japonicus* (Japanese sea lion)*, Arctocephalinae (Fur seal)*
	Bird: Laridae (Gulls & Terns), Diomedeidae (Albatross), *Gavia arctica/pacifica* (Arctic or Pacific loon), Phalacrocoracidae (Cormorant), Uria (Murres)
	Fish: *Gadus macrocephalus* (Pacific cod)*, *Paralichthys olivaceus* (Olive flounder)*, Thunnus (Tuna)*, *Xiphias gladius* (Swordfish)*, Pleuronectiformes (Flatfish)‡, Tribolodon (Dace)‡, Salmonidae (Salmonids)‡, Scorpaeniformes (Scorpionfish, rockfish, sculpins, etc.)‡
	Reptile: Chelonioidea (Sea turtle)*
	Mollusc: *Margaritifera laevis* (Freshwater pearl mussel)†, *Mercenaria stimpsoni* (species of venus clam)*, *Saxidomus purpurata* (Purple butter clam)*, *Spisula sachalinensis* (species of surf clam)*, *Haliotis discus discus* (Black abalone)*, *Patinopecten yesoensis* (species of scallop)*, *Barbitonia arthritica* (a sea snail)*
	Echinoidea: Echinoidea (Sea urchin)*
Satsumon	Mammal: Felis (Cats),

TABLE 5 (CONTINUED)

Satsumon	Fish: Thunnus (Tuna)
Ainu	Mammal: *Lutra lutra nippon* (Japanese river otter)
	Bird: Accipitriformes (Eagles and hawks), Anatidae (Ducks, swans, and geese), Corvidae (Crows, ravens, jays, magpies)
	Fish: Elasmobranchii (Sharks, skates, rays, sawfish)*, *Pagrus major* (Red seabream)*, *Pleurogrammus azonus* (Okhotsk atka mackerel)*, *Seriola quinqueradiata* (Japanese amberjack)*, *Eleginus gracilis* (Saffron cod)‡, *Clupea pallasii* (Pacific herring)‡, *Hucho perryi* (Sakhalin taimen)‡, Acipenseridae (Sturgeon)‡, Cottus (Freshwater sculpins)†
	Mollusc: *Glycymeris albolineata* (species of bittersweet clam)*, Mytilus (Mytilus (certain mussels)*, *Gomphina melanegis* (species of venus clam)*, *Crassostrea gigas* (Pacific oyster)*, *Mytilus galloprovincialis* (Mediterranean mussel)*, *Meretrix lusoria* (Hamaguri / Common Orient clam)*, *Corbicula japonica* (Japanese basket clam)**
	Crustacean: Brachyura (Crabs)‡

Cultural Context

Archaeological studies in Hokkaido distinguish between the Jōmon, Epi-Jōmon, Satsumon, and Ainu time periods (*Atsuma-cho Kyouiku Iinkai* 2009; *Hokkaido Maizou Bunkazai Sentaa* 2002, 2004; *Sapporo-shi Maizou Bunkazai Sentaa* 2001, 2002) broadly based on changes in material culture. It must be noted that the time periods here are assigned modern categories, rather than a set of distinctions made by the peoples living in the time periods themselves. While the transition between Jōmon and Epi-Jōmon seems to be one of small-scale change marked mostly by the lack of replacement by Yayoi cultural features, the transitions from Epi-Jōmon to Satsumon and from Satsumon to Ainu are more clear-cut (Hudson 1999; Kodansha 1983; Okada 1998; Utagawa 1992). Features used to define these time periods, such as house types, level of plant cultivation, pottery, and tools, will be discussed further in this section.

Populations associated with each cultural period addressed in this thesis are assumed to be related (Sato et al. 2009). It is generally accepted that the Epi-Jōmon and subsequent Satsumon populations descended from the Jōmon, though Satsumon human remains are rare (Adachi et al. 2009; Matsumura et al. 2006; Sato et al. 2009). Genetic studies, however, have been used to determine connections between the Ainu and Jōmon. Using mtDNA haplogrouping, comparisons of Ainu mtDNA with that of Jōmon and other human remains show that the Ainu have close genetic similarities with the Jōmon, including N9, D1, and G1 haplogroups (Sato et al. 2009). However, there is a clear influx of genetic material from the

Okhotsk, a cultural group found in Hokkaido from the 5th to 13th centuries AD and assumed to have come from the Amur River region in mainland northeast Asia north of present day Hokkaido (Amano 2003; Sato et al. 2007, 2009). Also, the Ainu share Y-haplogroup D with other groups thought to have descended from the Jōmon, such as the modern Japanese (Tajima et al. 2004). Some differences between modern Japanese and Ainu Y-haplogroups have been traced to outside of the Japanese archipelago (such as O-M122 from China), suggesting that later imported genetics altered in modern Japanese what they once shared with the Ainu, which suggests Jōmon ancestry (Tajima et al. 2004). Overall, while there remain questions as to the exact descent and genetic contributions, the Ainu are strongly theorized to have descended from the Jōmon people.

While the genetic connections reveal some evidence of biological ancestry (Adachi et al. 2009; Sato et al. 2009; Tajima et a. 2004), it is also clear that certain cultural similarities exist between the Jōmon, Epi-Jōmon, Satsumon, and Ainu traditions. In this section, I briefly describe the current understanding of these archaeological and historical traditions.

Jōmon (14,000-500 BC; 14,000–2700 cal. BP)

The Jōmon period began in about 14,000 BC and lasted until the first millenium BC transition to the Epi-Jōmon (Ōnishi 2014:282). These dates are somewhat inconsistent in the literature, with some citing the transition at 100 BC (Hudson 2007:14) and others citing the 3rd century BC (Ōnishi 2014) or 500 BC (Habu et al. 2011). The start of this period is also in question, ranging from 14,000 BC (ca. 16,000 BP)(Habu et al. 2011) to 14,000 cal. BP (ca.

12,000 BC)(Weber et al. 2013). The Jōmon period followed Japan's Paleolithic past, and existed in various forms throughout the archipelago, from the Ryukyu islands in the south to Hokkaido in the north (Hudson 2007:13-14). At around 300 or 400 BC, the Yayoi culture was introduced in southern Japan, and spread northward throughout the archipelago, though never reaching Hokkaido or the Ryukyu islands (Akazawa 1999:223; Hudson 2007:13-14). Unlike the rest of Japan, Hokkaido instead transitioned to the Epi-Jōmon (Hudson 2007:13; Ōnishi 2014).

The Jōmon period is characterized in part by hunting-fishing-gathering subsistence (Akazawa 1999). In Hokkaido, there was a heavy emphasis on marine resources, as seen in isotopic analyses of human remains (Akazawa 1999:228). These findings are corroborated by the presence of numerous fishing and marine-harvesting tools, especially toggle-headed harpoons, in large numbers unique to Hokkaido and north Japan (Habu 2004:77). While Jōmon shell middens are abundant throughout Japan, there is a notably high density of middens in Southern Hokkaido (Takahashi et al. 1998:55). There is evidence for a year-round hunting-fishing-gathering schedule of different natural seasonal resources, though there is no evidence necessarily of corresponding seasonal mobility (Habu 2004:62-63). The clear evidence of fishing and marine mammal-hunting, collection of nuts and other plant foods, land mammal hunting, and shellfish gathering has been interpreted as following a seasonal round during optimal seasons for each activity (Habu 2004:62). For example, nut collection would have had to take place in the autumn, when nuts were ready for harvest (Habu 2004:62). The other seasons proposed include winter for land mammal-hunting, summer for fishing and marine mammal-hunting, and spring for shellfish gathering (Habu

2004:62). While there are similar indications of the "best" seasons for the other activities

mentioned, there is little evidence as yet to show their exclusivity to particular seasons (Habu

2004:62). Shell middens provide evidence of some shellfish exploitation limited to the spring

and early summer, when other food sources are scarce (Habu 2000; 2002; 2004:73; Koike

1981). Carbon and nitrogen isotope analysis show that Jōmon people in Hokkaido relied

more heavily on marine resources than those in Honshu, particularly on marine mammal

hunting (Habu 2004; Minagawa & Akazawa 1992). Also, as noted with Honshu Jōmon

populations, whether a site was coastal or inland would affect how much reliance on marine

resources was possible (Habu 2004). This is important because the sole Jōmon site included

in this study is inland (Figure 3).

 While hunting and marine resources were important, there was also at least a low-

degree dependence on plant husbandry (Crawford et al. 1976:147, 152). Plants cultivated

include buckwheat (Fagopyrum), rice (*Oryza sativa*), barley (*Hordeum vulgare*), burdock

(*Arctium lappa*), shiso (*Perilla frutescens* var. *crispa*), millet (Echinochloa), and bean

(Leguminosae), among others (Habu 2004:59).

 Jōmon people were largely sedentary, and lived in pithouses (Hudson 2007:18). This

sedentism of hunter-gatherers as seen in the Jōmon period may indicate high levels of

resources or a collector strategy, in which unevenly distributed resources are exploited from a

strategically-located settlement (Binford 1980; 1982; Habu 2004). Jōmon settlements in

Hokkaido were usually on "riverside wetlands and on river terraces," with additional sites

found on river terraces and wetland sites showing food-processing activities but no house pits

(Ōnishi 2014:284-285; see also Crawford et al. 1976:145). Storage pits were utilized,

including wet pits for nut storage in western Japan and dry pits for unknown purposes in eastern Japan (Habu 2004:64-68). Also present in the Jōmon period is "some of the oldest pottery in Asia" (Adachi et al. 2009:256) dating to 15,300 cal BP (Yoshida et al. 2013). Residue from terrestrial and marine plant and animal sources indicate use of ceramic pots for cooking (Yoshida et al. 2013).

Despite the common view of hunter-gatherers as egalitarian, differentiation of grave goods (especially for children), exotic items, and house types and facilities have been interpreted as showing some level of social stratification within Jōmon societies (Nakamura 1999; Pearson 2004).

Epi-Jōmon (3rd – 7th century; 2700-1500 cal. BP)

After the Jōmon period, Hokkaido's cultural history split from that of the rest of Japan, with the advent of the Yayoi culture in the south of Japan and the transition to the Epi-Jōmon in Hokkaido (Moriya 2015). The Epi-Jōmon lasted from the 3rd century BC to the 7th century AD, after which the population in Hokkaido shifted to the Satsumon cultural tradition (Ōnishi 2014).

In terms of settlement patterns, the Epi-Jōmon may be split into two periods: the first period, where people lived in pit-houses on river terraces and wetlands, and the second period, in which all evidence of dwellings disappears from the archaeological record (Ōnishi 2014). While the paucity of dwellings in the second period has led to theories about cave-dwelling, the river terraces and wetlands seem to be a continuation of Jōmon settlement

patterns (Ōnishi 2014; Moriya 2015). The pit-houses from the first period were circular with a central hearth (Moriya 2015).

Like the Jōmon before them, the Epi-Jōmon hunted and fished, as evidenced by their bone and stone tools (Moriya 2015). Wild foods, as noted in Ainu folklore referring to the Epi-Jōmon, seem to have primarily included deer, salmon, and lily bulbs (Imamura 1996:200). Due to the prevalence of shell middens, it is believed that marine resources were of particular importance (Okada 1998). It is worth noting that Epi-Jōmon sites often involve short-term occupation or specific processing activities (Crawford 2011; Ōnishi 2014), which may be indicative of seasonal rounds. Particularly, short-term processing sites showing processing of nuts and knotweeds would indicate at least some seasonality to those sites, whether or not they represent seasonal occupation patterns (Crawford 2011:S338). The extent to which plant cultivation played a part in prehistoric Japanese cultures is not well understood, but, since the Jōmon and the Satsumon show evidence of plant husbandry, it may be assumed that the Epi-Jōmon cultivated plants as well (Crawford 2011). What is clear is that nuts, fruits, and "anthropogenic annual plants," including rice, were exploited, though whether these last were imported or cultivated remains unclear (Crawford 2011).

Religion among the Epi-Jōmon is also unclear from the archaeological record, but figures found at Epi-Jōmon sites suggest bear worship (Utagawa 1992). Also, given the variety and long-distant nature of grave goods, it appears that there were distinctions of social status (Okada 1980; 1998). In terms of pottery, the Epi-Jōmon period saw a continuation of and subsequent changes to the Kamegaoka tradition at the end of the Jōmon (Okada 1998).

Satsumon (7th century - 13th century AD; ca. 800-1400 BP)

The Epi-Jōmon period transitioned to the Satsumon period in the 7th century AD (ca. 1400 BP), and the Satsumon lasted until the Ainu tradition started in the 13th century AD (ca. 800 BP)(Ōnishi 2014; Weber et al. 2013). The transition from the Epi-Jōmon to the Satsumon may have been brought about by movement of remaining Jōmon-descended peoples on Honshu being driven into Hokkaido, where the Satsumon culture is found (Crawford 2011). In any case, whether due to movement of peoples or diffusion of cultural traits, the Satsumon is noted as having mainland Japanese cultural influences, such as the style of pit-dwellings and iron tools (Imamura 1996).

Despite these similarities, the Satsumon remained distinct from mainland Japanese culture, enough even for some cultural diffusion to spread from the Satsumon south into Japan (Imamura 1996). In contrast to the continuity between Jōmon and Epi-Jōmon, the Satsumon built their settlements on the floodplain of rivers (Ōnishi 2014). Satsumon houses returned to the early Epi-Jōmon use of pit-houses, though they were rectangular or sub-rectangular in shape (Moriya 2015). These Satsumon houses also contained a unique oven built into a wall, a trait not shared by houses in any other cultural tradition discussed in this paper (Moriya 2015).

While hunting and fishing remained an important part of Satsumon subsistence (Table 4,5), agriculture seems to have become much more intensive than it was in previous periods (Moriya 2015). Site locations especially indicate that river fishing, particularly that of

salmon, remained central to Satsumon subsistence or trade (Ōnishi 2014:290). Cultivated plants from this period include buckwheat, barley, various millets, sorghum, melon, adzuki bean, and hemp (Imamura 1996).

The technological shift from stone to iron tools and the use of more mainland Japanese goods acquired through trade is also an important part of the Satsumon transition (Crawford 2011). While distinctive scraped designs in Satsumon pottery give the period its name, Haji ware from northern Honshu and local pottery with interior lugs, imitating Japanese iron pots, also appear (Hudson 1999; Kodansha 1983; Utagawa 1992). Another probable Japanese influence is the modified Kofun-style burial mounds, though what this says about religion among the Satsumon remains unclear (Kodansha 1983). Kofun are keyhole-shaped burial mounds of powerful elites, such as chieftains and kings, that were present in mainland Japan during the Kofun Period (3rd century – 6th century AD; 1400-1700 BP), and associated with highly stratified society (Tsude 1996). In Hokkaido during the Satsumon period, however, the mounds are found later than in the Japanese mainland, and are much reduced in size and altered in shape, to the point that such tombs may not represent social stratification in terms of classes or elites but rather heads of family (Imamura 1996). Based on this evidence, some authors have claimed that evidence is insufficient to show social stratification (Imamura 1996), while others have determined that the Satsumon had "substantial social differentiation"(Weber et al. 2013).

Ainu (13th Century AD – Present; ca. 800 BP-Present)

The Ainu emerged as a distinct culture in the 13th century AD (ca. 800 BP), and are an ethnic group to this day (Ōnishi 2014; Weber et al. 2013). It must be noted, however, that the ethnographic present of traditional Ainu culture (i.e., before Japanese conquest of Hokkaido and direct involvement with Ainu daily life) is often considered to end in the 19th century AD (Ohnuki-Tierney 1976; Weber et al. 2013). Ainu archaeological sites correlate with historical, ethnographic, and modern populations in Hokkaido, Sakhalin, and the Kuril Islands (Batchelor 1892; Ōnishi 2014). Ainu settlements originally appeared following the Satsumon pattern of "riverside wetlands on the floodplain," (Ōnishi 2014:285) though subsequent forced migration ordered by the Japanese government has led to many Ainu being moved outside of these settlement patterns (Ōnishi 2014; Aoyama 2012).

Ainu settlements were generally built near these rivers and coastlines, and are called *kotan* (Aoyama 2012). *Iwor* is the term for the rest of the world outside of the village, particularly the river, sea, and mountains, where resources were gathered and brought in for use in the *kotan* (Aoyama 2012). Additionally, the Ainu considered the *kotan* to be the place for humans to dwell, while the *iwor* into which the Ainu ventured was the realm of the spirits (Aoyama 2012). Aside from the difference in use and spiritual nature, the physical differences between the two are also important. While the difference between a terrestrial village and a river or the ocean is obvious, it is also worth noting that much of the hunting,

fishing, and gathering took place in the mountains above the coastal plains in which the kotan were built.

It is worth noting that Ainu settlements were relatively permanent in Hokkaido, with only occasional movement due to scarcity of food sources (Ohnuki-Tierney 1976). Men erected temporary hunting huts, but otherwise, there is no evidence of seasonal mobility in Hokkaido (Ohnuki-Tierney 1976). This division between a permanent *kotan* and the surrounding *iwor* may be reflective of a collector-style subsistence, in which sedentary settlements are strategically placed to exploit an uneven distribution of specialized resources (Binford 1980; 1982; Habu 2004). We see this particularly in the location of settlements by rivers and hunting and gathering occurring in forays into the surrounding area (Ōnishi 2014).

Both fishing and hunting, as well as gathering of plant materials, were important (Ohnuki-Tierney 1976). Due to the greater ease of travel involved with plant gathering and hunting than with fishing, settlements were often best situated for access to fish (Ohnuki-Tierney 1976). Hunting, however, remained a significant part of Ainu subsistence, with as much as over half of animal food coming from deer (Ohnuki-Tierney 1976; Watanabe 1968). Important food animals included deer, bear, trout, and salmon (Table 4,5), while plants included leeks, berries, lily bulbs, and other root crops (Ohnuki-Tierney 1976). Fish, particularly salmon, was also a major food source, with some parts of Hokkaido (in the Hidaka Mountains region) reporting salmon availability the year round, excluding the period from January to March (Ohnuki-Tierney 1976). In Hokkaido, while fishing remained important, sea mammal hunting was less important over much of the island, with occasional whaling and other sea mammal hunting limited to certain areas, particularly the Pacific coast

(Ohnuki-Tierney 1976). Also, inland sites would have "had little to do with sea mammals"(Ohnuki-Tierney 1976:304).

Traditional Ainu houses in the ethnographic literature were rectangular pole-and-thatch surface dwellings (Munro and Raglan 1959). Houses had a hearth near the center of the structure, an east-west orientation, and a sacred window in the east wall, opposite the main entrance (Batchelor 1892). Despite a long academic tradition of regarding pre-modern Ainu as hunter-gatherers, flotation samples from Ainu archaeological sites have shown that the Ainu also grew millet and other crops (Crawford 2011; Ōnishi 2014). Also, given historical Japanese legislation, many Ainu were forced to intensify agriculture at the expense of the hunting and gathering aspects of traditional Ainu subsistence (Aoyama 2012). With the transition from the Satsumon period, local pottery was replaced by foreign vessels (Hudson 1999).

Ainu religion is ethnographically well documented, particularly in the works of Batchelor (1892) and Munro (1963). Traditional religious life among the Ainu revolved, and continues to revolve, around interactions with gods who come into the human world for an exchange of benefits with humans (Aoyama 2012; Munro 1963). These interactions were held through the mediation of the household Fire Goddess (Kamui Fuchi), housed in the hearth (Munro 1963:18). Ceremonies include iyomante, in which the god disguised as a bear or sometimes an owl is ritually sacrificed (Aoyama 2012; Batchelor 1892; Munro 1963). These ceremonies are designed to curry favor with or placate gods, as well to preserve spiritual substance in objects (Munro 1963). These objects included skulls of various animals serving as personal protector spirits and treasured stones (Munro 1963:23-24).

Before Japanese rule, the Ainu were politically organized by village, with a patrilineal chief exercising limited government (Munro 1963). While villages would sometimes organize together for warfare, there was no unified nation until the Japanese assimilation in the 19th century (Munro 1963; Ōnishi 2014).

Traditional Ainu culture, as seen in the archaeological and ethnographic records, is distinct from modern Ainu practices due to aggressive assimilation and forced migration under the Japanese government, especially in the 19th and early 20th centuries (Aoyama 2012). Also, given Japanese legislation, many Ainu were forced to intensify participation in agriculture at the expense of the hunting and gathering aspects of traditional Ainu subsistence (Aoyama 2012).

Today, the Ainu in Hokkaido are citizens of Japan. They were recognized recently by the Japanese government as an indigenous people, though much of the traditional Ainu culture has not survived earlier government policies of cultural eradication (Aoyama 2012; Kato 2009:48). There remain problems of discrimination and battles over repatriation of remains to this day, in spite of Japan's agreement to international treaty regarding treatment of and archaeological responsibilities toward indigenous people (Aoyama 2012; Kato 2009:49; Scott 2013).

Cultural Similarities

While there are some notable differences among these cultural periods in Hokkaido which are used to distinguish these periods from each other (Table 5), namely the extent of

plant cultivation (Crawford 2011; Okada 1998), house types (Imamura 1996; Moriya 2015; Okada 1998; Ōnishi 2014), and the shift from stone to iron tools (Ōnishi 2014), there are also similarities. The Epi-Jōmon, in their pottery, subsistence, and early house structures are clearly a continuation of the Jōmon (Okada 1998; Ōnishi 2014). The Satsumon, while showing strong similarities to aspects of the Yayoi culture in northern mainland Japan at the time, are accepted as the immediate ancestors of the Ainu, though the Okhotsk people may have also contributed to the Ainu gene pool (Crawford 2011; Amano 2003; Sato et al. 2007, 2009). There are also similarities in subsistence (Okada 1998; Ōnishi 2014), settlement patterns (Ōnishi 2014), and even a clear stylistic sequence for harpoons from the Epi-Jōmon, Satsumon, and Ainu (Immura 1996). To further connect the Satsumon-Ainu and Jōmon-Epi-Jōmon lineages, genetics have shown important similarities between the Ainu and Jōmon, confirming the widely-held assumption that the Ainu descended from the Satsumon, through the Epi-Jōmon, and ultimately from the Jōmon (Adachi et al. 2009; Matsumura et al. 2006; Sato et al. 2009; Tajima et al. 2004). Transition?

Study Sites

Single and multi-component study sites are located in Central Hokkaido (Table 6; Figure 3). The Chipunii 1 (Ainu and Satsumon layers) and 2 (Ainu and Jōmon layers) sites are located in the Chuo ward of Chitose city, east of the Do-ou National Highway 337 bypass. The two sites are situated in the inland lowlands (22.0 to 26.0 m above sea level) withinin forested areas near unnamed streams. The Kamihoronaimoi site (Ainu, Satsumon,

and Epi-Jōmon layers) is and upland site (58 m above sea level) found in a mountainous area with many unnamed converging mountain streams, which eventually flow into the Atsuma River. The site is near the 235 Highway, southeast of Atsuma Dam in the town of Atsuma. The K39-7 (Satsumon layer) and K39-9 (Satsumon and Epi-Jōmon layers) sites mentioned here are in Sapporo on or immediately adjacent to the Hokkaido University Campus. They are lowland sites (14.0 m above sea level) in the Ishikari River Basin near archaeological rivers and relatively near (about 12.71 km) to an ocean coast (Google Maps).

Table 6. Site locations and elevations.

Site	Component(s)	Municipality	Elevation
Chipunii 1	Ainu, Satsumon	Chitose (Chuo)	26.00
Chipunii 2	Ainu, Jōmon	Chitose (Chuo)	22.00
K39-7	Satsumon	Sapporo (Chuo Ward)	14.00
K39-9	Satsumon, Epi-Jōmon	Sapporo (Kita Ward)	14.00
Kamihoronaimoi	Ainu, Satsumon, Epi-Jōmon	Atsuma	58.00

The sites are situated within or nearby the Ishikari Plain, stretching from Ishikari Bay in the Sea of Japan in the north to the Pacific Ocean in the south (Figure 1,2,3). As is generally expected from previous archaeological research on the relevant time periods, these sites are close to rivers (Ōnishi 2014). Aside from their riverine nature, the sites can be divided into coastal lowland (K39-7 and K39-9), inland lowland (Chipunii 1 and 2), and inland upland (Kamihoronai). Nevertheless, these sites are all relatively low in elevation, with the highest only at 58 m above sea level (Table 6). The lowland sites (Chipunii 1, Chipunii 2, K39-7, and K39-9) all fit within the Quercus mongolica deciduous forest regime

(Ohara 2009; Okitsu 2003). The higher-elevation site, Kamihoronaimoi, sits on the edge of the Yubetsu Mountains (Figure 3), though not at high enough elevation to be in the higher cool-temperate (500-1500 m) or boreal forest zone (Figure 2,3; Okitsu 2003; Qian et al. 2003). It may possibly belong to the Abies sachalinensis-Quercus mongolica mixed forest regime, though resolution from existing maps is unclear (Okitsu 2003). The study area foris in the Temperate Broadleaf and Mixed Forest ecoregion of Hokkaido (PA0423) (see Figure 2,3), therefore fauna present in study site assemblages listed in Table 4 only include fauna from this regime. Non-terrestrial fauna, such as fish and aquatic mammals, are divided into marine and freshwater, as well as species that exist in both. From the study sites, one faunal type (Cyprinidae) is freshwater, one (Marine mammal (M-L size class)) is marine, and four (Salmonidae, Tribolodon, *Hucho perryi*, and *Clupea pallasii*) are both (Table 4).

CHAPTER III

THEORY

Evolutionary Archaeology

Evolutionary archaeology takes concepts such as descent with modification, natural selection, diffusion, drift, and speciation from evolutionary biology and applies them to human culture as seen in the archaeological record (Lyman & O'Brien 1998:615-616). It is important to note that, as in much of biology, cultural evolutionary concepts refer to changes over time, often in response to changes in circumstances or contexts, and not a progression from a "lower" to a "higher" set of states. The connections drawn thereby show what aspects of a culture precede which others and what forces likely influenced change between temporally adjacent traits, without claiming any traits to be more "advanced" than any others. Whatever changes that occur are charted on temporal, not qualitative, lines. While biology studies the descent-with-modification of genes, the replicator unit in evolutionary archaeology is the cultural trait (Henrich et al. 2008; Lyman & O'Brien 1998:619). Cultural traits are mental representations within the minds of the humans who are part of a culture (which is the total of such mental representations and meanings), and they are passed to the next generation through cultural transmission (learning) (Henrich et al. 2008; Lyman & O'Brien 1998:619). Since the traits themselves exist only within human minds and are expressed in behaviors, transmission from one human to another involves some degree of error, since we cannot ever fully express our thoughts to one another (Henrich et al. 2008;

Lyman & O'Brien 1998:619). Also, such traits are not visible themselves in the archaeological record (or even ethnography), though the physical manifestations of these traits, in the form of artifacts, make up the cultural phenotype, which we can definitely study to infer cultural continuity and change (Lyman & O'Brien 1998:619; O'Brien et al. 2001:1134). As such, it must be remembered that such inquiry involves inference about culture from cultural material, and that the meanings attached to artifacts may be different to different people (Dunnell 1978) and as such change with transmission.

Cultural transmission can be vertical (from parent to offspring), horizontal (from peers), or oblique (from a non-parent member of a previous generation) (Boyd & Richerson 1985; Cavalli-Sforza & Feldman 1981; Mace & Holden 2005:117; Tehrani & Collard 2009:3). Such transmission can occur through different means, including direct teaching followed by individual experimentation (guided variation), conforming to perceived social norms (conformist transmission), or copying a chosen model's set of traits (indirectly biased transmission) (Eerkens et al. 2006). How these different transmission methods are used can depend on the context in which the culture exists. For example, vertical transmission seems to be most adaptive when the environment is stable and risk of mortality is high, because living long enough to have children is sufficient evidence of the effectiveness of an individual's set of cultural traits (Tehrani & Collard 2009:18). If this is true, it follows that if the environment changes and risk of mortality is low, the children would most benefit by looking around for the most effective models to learn from in oblique or horizontal learning (Tehrani & Collard 2009:19). It is also important to note that any of these modes of transmission can take place within a cultural group or from another group, with peers or non-

parent elders (or even, sometimes, a parent) from other groups transmitting cultural traits (Henrich & Boyd 1998; Hewlett et al. 2002; McElreath & Strimling 2008; Tehrani & Collard 2009:3-4).

The potential for non-vertical transmission is one important difference between biological and cultural evolution (Lyman & Obrien 1998:616). Such blending or reticulation of lineages of cultural traits is not seen in biological genes (Kroeber 1931; Steward 1944), and has led to some criticism of applying evolutionary models to archaeology (Moore 2001; Terrell et al 1997:184). In practice, however, we see that, though blending models sometime best describe certain instances of cultural evolution, branching models are also often appropriate (Collard et al. 2006). In general, we see that cultures tend to remain distinct and transmit most traits vertically, horizontally, or obliquely within the same group (Barth 1969; Collard et al. 2006:53; Durham 1990, 1992; Gil-White 2001; McElreath et al. 2003; O'Brien et al. 2001:1118; Tehrani & Collard 2009:21).

Another notable difference between biological and cultural evolution is the role of intention. Unlike genetic change, cultural change can take place as a result of conscious actions, such as invention (creation of a new trait) and innovation (creation of a new trait that is adopted and passed on) (Lycett 2015:24). Intention, however, is not the only selective force in cultural evolution. Environmental constraints, association of certain traits with individuals perceived to be more model-worthy, natural selection, transmission error, and drift (random chance) all create selective pressures or variation (Henrich et al. 2008:4, 14; Lyman & O'Brien 1998:615, 619-620; Lycett 2015:24; O'Brien et al. 2014:100-101, 115; Eerkens et al. 2006). Furthermore, intention is invisible from the archaeological record, and

thus cannot be addressed (Lyman & O'Brien 1998:618). More importantly, whatever the sources of variation, the fact that descent with modification occurs in cultural traits enables evolutionary models to be applied to cultural change (Lycett 2015). Even invention and innovation are products of cultural evolution, since existing cultural concepts are modified in these cases, and almost never is an entirely new trait invented from nothing (O'Brien et al. 2014:105).

It is worth noting that, as in biology, there may be a high level of variation among individuals of the population, but population-level characteristics reflect the overall cultural group, much as in biological species (Eerkens et al. 2006:6). Cultural groups can be treated similarly to species because cultural groups largely remain somewhat exclusive, and even with intergroup interaction, someone coming into a different culture likely needs to adopt it to some degree to be successful in it (Mace & Holden 2005:116-117). Further, given the stronger tendency for culture groups to bifurcate than to merge, there may be something like a phylogenetic tree of culture groups, as one would expect should cultural evolution take place (Mace & Holden 2005:117).

Given the advantages that any traits adaptive to a given environmental or other context have, we must be careful to note the horizontal transmission of such (Mace & Holden 2005:118-119). "Neutral cultural variants," or cultural traits that do not necessarily offer a selective advantage, are therefore useful in tracing cultural evolution (Mace & Holden 2005:118). An example of this can be stylistic features of artifacts, which should offer no advantage in terms of natural selection (Lyman & O'Brien 1998:621). Not all traits that arise and are passed on are adaptive (Lyman & O'Brien 1998:621). It must be noted, however, that

some traits will be selected for due to societal, historical, or other cultural contexts, such as being associated with individuals of the cultural group that are otherwise successful (Henrich et al. 2008:9-11).

While innovation, selective attraction, intergroup transmission, and other human-driven selective forces impact cultural evolution, it must not be forgotten that humans, like any other organism, are also subject to natural selection (Lyman & O'Brien 1998). Even on the simplest level, when people move through different environments quickly, or there is quick environmental change, learners would seek out individuals that are most successful in their current environment from whom to learn, as opposed to investing in individual innovation (O'Brien et al. 2014:115). In a more biological context, there is evidence and discussion of "gene-culture coevolution," in which the cultural traits/environment of pre-human organisms gave a distinct set of selective forces that other animals did not have, and so the genes and culture of pre-humans and eventually humans evolved concurrently and interactively (Henrich et al. 2008:15). Overall, whether a trait is adaptive to an environmental or a social context, it is clear that it will survive in a culture only as far as it is transmitted, and selective pressures from environment, social associations, or other sources will determine what traits remain over time amid contextual changes (Lyman & O'Brien 1998:623; Mace & Holden 2005:118). It must be noted that cultural traits do not always follow biological notions of adaptability, and they are instead subject to environmental, social, and other circumstantial selective pressures that will determine which traits continue in a cultural group over time and which do not (Henrich et al. 2008; Lyman & O'Brien 1998; Mace & Holden 2005; O'Brien et al. 2014).

More specific to this study, how animals are used in a cultural group is set of cultural traits that may be steered in one direction or another by environmental or societal pressures. Which animals, parts of animals, or in which contexts animals constitute food vary according to cultural group (Fowles 2008:18; Lyman 1979:537). While some of what is and is not eaten will be in part due to efficiency of energy consumption per caloric gain (Cannon 2003), it remains that, even on a single animal, consumed meat will usually be less than all available meat from that animal (Lyman 1979:537). Whether the factors governing which parts are eaten are kinship-driven (Lyman 1979:539) or determined by religious taboo (Fowles 2008), which animals and which parts of them are treated as food constitute cultural traits. As such, they are subject to evolutionary processes as are other cultural traits. The classic example is the Jewish prohibition on pork, as studied particularly in the Levant (Fowles 2008). Whether this prohibition resulted from environmental economic factors (Hesse & Wapnish 1997), out of desire for ethnic demarcation (Finkelstein 1997; Valeri 2000), or other cultural reasons, the injunction against pork consumption developed culturally within historical and environmental contexts and pressures (Fowles 2008). This study analyzes faunal remains to infer the cultural aspects of animal use through time.

CHAPTER IV

METHODS

Data-gathering

This analysis includes faunal data gleaned from site excavation reports in Central Hokkaido carried out and published by Hokkaido University and various local Boards of Education (*Atsuma-cho Kyouiku Iinkai* 2009; *Hokkaido Maizou Bunkazai Sentaa* 2002, 2004; *Sapporo-shi Maizou Bunkazai Sentaa* 2001, 2002). Excavations included assemblages spanning the Jōmon, Epi-Jōmon, Satsumon, and Ainu components. Reports were made available for scanning by Hokkaido University's Central Library Northern Collection and Graduate School of Letters Library Archaeology section in December 2016. I transcribed and translated faunal assemblage data sections from 21 reports, from which I chose a sample of 5 reports covering 5 sites (Table 7). The sample contained all reports that had component, site (including location), and bone weight and/or count data (Tables 8-10).

Table 7. Sites, the components, they cover, their location, their bibliographical references, and the location of the corresponding reports.

Site	Component	Location of Sites	Bibliographic Reference	Location of Reports
Chipunii 1	Ainu, Satsumon	Chitose, Hokkaido, Japan	Hokkaido Buried Culture Center 2002	Hokkaido University Graduate School of Letters Library (Archaeology)
Chipunii 2	Ainu, Jōmon	Chitose, Hokkaido, Japan	Hokkaido Buried Culture Center 2002; 2004	Hokkaido University Graduate School of Letters Library (Archaeology)
K39-9	Epi-Jōmon	Sapporo, Hokkaido, Japan	Sapporo City Buried Culture Center 2002	Hokkaido University Central Library, Northern Collection
K39-7	Satsumon	Sapporo, Hokkaido, Japan	Sapporo City Buried Culture Center 2001	Hokkaido University Central Library, Northern Collection
Kamihoronaimoi	Ainu, Satsumon, Epi-Jōmon	Atsuma, Hokkaido, Japan	Atsuma Town Board of Education 2009	Hokkaido University Graduate School of Letters Library (Archaeology)

Table 8. Total bone counts (and percentages of total assemblage) per faunal type for each site component in the sample. The General faunal types include Fish (made up of Cyprinidae, Osteichthyes, Pisces, and Salmonidae), Mammal (Cervidae, Mammalia, Mammalia S-size class), and Other (Mollusca).

COUNT DATA	Faunal Type							
	Specific					General		
Site component	Mollusca	Cyprinidae	Cervidae	Mammalia (S size class)	Salmonidae	Fish	Mammal	Other
Chipunii 1 - Ainu	476 (27.48%)	0 (0%)	0 (0%)	3 (0.17%)	1253 (72.34%)	3974 (89.22%)	4 (0.09%)	476 (10.69%)
Chipunii 2 - Ainu	0 (0%)	36 (0.04%)	0 (0%)	0 (0%)	97752 (99.96%)	98337 (100%)	0 (0%)	0 (0%)
Kamihoronaimoi - Ainu	1 (0.20%)	129 (25.70%)	277 (55.18%)	0 (0%)	95 (18.92%)	231 (29.84%)	542 (70.03%)	1 (0.13%)
K39-9 - Epi-Jōmon	0 (0%)	3 (2.48%)	0 (0%)	0 (0%)	118 (97.52%)	121 (100%)	0 (0%)	0 (0%)
Kamihoronaimoi - Epi-Jōmon	0 (0%)	12 (2.90%)	380 (91.79%)	0 (0%)	22 (5.31%)	50 (10.62%)	421 (89.38%)	0 (0%)
Chipunii 2 - Jōmon	0 (0%)	0 (0%)	7 (87.5%)	0 (0%)	1 (12.5%)	1 (0.56%)	177 (99.44%)	0 (0%)
Chipunii 1 - Satsumon	39 (0.5%)	0 (0%)	0 (0%)	0 (0%)	39 (0.5%)	165 (80.88%)	0 (0%)	39 (19.12%)
K39-7 - Satsumon	0 (0%)	7 (1.49%)	0 (0%)	0 (0%)	463 (98.51%)	470 (100%)	0 (0%)	0 (0%)
Kamihoronaimoi - Satsumon	0 (0%)	300 (40.16%)	266 (35.61%)	0 (0%)	181 (24.23%)	561 (55.22%)	455 (44.78%)	0 (0%)

Table 9. Total bone weights in grams (and percentages of total assemblage) per specific faunal type for each site component in the sample.

WEIGHT DATA	Faunal Type (Specific)									
Site component	Arthropoda	Aves	Cetacea	Clupeinae	Cyprinidae	Cervidae	Mammalia (M-L)	Mammalia (S-M)	Marine mammal	Salmonidae
Chipunii 1 - Ainu	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	20.13 (100%)
Chipunii 2 - Ainu	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1.1 (2.52%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	42.5 (97.48%)
Kamihoronaimoi - Ainu	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0.8 (11.85%)	1.1 (16.30%)	0 (0%)	0 (0%)	0 (0%)	4.85 (71.85%)
K39-9 - Epi-Jōmon	0.012 (0.03%)	0 (0%)	0 (0%)	0 (0%)	0.011 (0.03%)	0 (0%)	0.656 (1.63%)	0 (0%)	0.058 (0.14%)	39.4998 (98.17%)
Kamihoronaimoi - Epi-Jōmon	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0.15 (10%)	0.05 (03.33%)	0 (0%)	0 (0%)	0 (0%)	1.3 (86.67%)
Chipunii 2 - Jōmon	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	65.67 (99.85%)	0 (0%)	0 (0%)	0 (0%)	0.1 (0.15%)
Chipunii 1 - Satsumon	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0.45 (100%)
K39-9 - Satsumon	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	0 (0%)	1.305 (100%)	0 (0%)	0 (0%)	0 (0%)
K39-7 - Satsumon	0 (0%)	0.84 (0.94%)	0.63 (0.71%)	0.01 (0.01%)	0.05 (0.06%)	1.18 (01.32%)	0 (0%)	0.51 (00.57%)	0 (0%)	85.89 (96.39%)
Kamihoronaimoi - Satsumon	0 (0%)	0 (0%)	0 (0%)	0 (0%)	5.7 (15.04%)	26.9 (70.98%)	0 (0%)	0 (0%)	0 (0%)	5.3 (13.98%)

Table 10. Total bone weights in grams (and percentages of total assemblage) per general faunal type for each site component in the sample. The general faunal types include Fish (made up of Clupeinae, Cyprinidae, Osteichthyes, Pisces, and Salmonidae), Land Mammal (Cervidae, Mammalia, and Mammalia S-M and M-L size classes), and Other (Arthropoda, Aves, Cetacea, and Marine Mammals).

WEIGHT DATA	Faunal Type (General)		
Site component	Fish	Land Mammal	Other
Chipunii 1 - Ainu	20.13 (100%)	0 (0%)	0 (0%)
Chipunii 2 - Ainu	46.6 (100%)	0 (0%)	0 (0%)
Kamihoronaimoi - Ainu	13.8 (8.25%)	153.45 (91.75%)	0 (0%)
K39-9 - Epi-Jōmon	39.5108 (74.92%)	13.212 (25.05%)	0.012 (0.02%)
Kamihoronaimoi - Epi-Jōmon	1.9 (0.43%)	438.35 (99.57%)	0 (0%)
Chipunii 2 - Jōmon	0.1 (0.12%)	83.76 (99.88%)	0 (0%)
Chipunii 1 - Satsumon	0.73 (100%)	0 (0%)	0 (0%)
K39-9 - Satsumon	0 (0%)	1.305 (100%)	0 (0%)
K39-7 - Satsumon	85.95 (93.50%)	5.14 (5.59%)	0.84 (0.91%)
Kamihoronaimoi - Satsumon	15.05 (2.07%)	711.15 (97.93%)	0 (0%)

Within this sample, entries missing any of the above information or faunal taxonomic information were excluded. Taxa with uncertain assignments, those marked in reports as a specific taxon assignment with the addition of a question mark, were assumed to have been identified correctly and assigned to the taxon indicated. These data were then organized into specific faunal types: Arthropoda (crustaceans), Aves (birds), Cetacea (generally whales, dolphins, and porpoises), Clupeinae (herrings, sardines, and sprats), Mollusca, Cyprinidae (carps and minnows), Cervidae, Mammalia (size class Small to Medium), Mammalia (size class Medium to Large), Marine mammals (size class Medium to Large) (which could include cetaceans, as well as seals, sea lions, manatees, and sea otters, but is constrained as being Medium to Large size), and Salmonidae

(salmon, trout, and char). In most cases, these categories represent the most specific

classifications of remains identified in the reports. In some cases, further specific

distinctions appeared in reports, but represented such a small number that they were

added to a more general category. While other groups of fauna are notable to Hokkaido

and particularly to Ainu culture, such as the brown bear (*Ursus arctos yesoensis*) or fox

(*Vulpes vulpes*), they did not appear or were not identified in the reports. These data and

any other entries that had less specific identification were also included in a separate

dataset of general faunal types of Fish, Land Mammals, and Other, since a large number

of unidentified mammals and fish were present in reports that could not be identified to a

more specific taxon. Taxa represent all specifically-identified entries that had both taxon

and weight and/or count information, except for one case, where a site component was

represented by a single entry of mammal bone, which was disregarded due to its skewing

of results and poor representation of site or component (see Tables 8-10).

Since many report entries had either bone weight or bone count data, weight and

count make up separate datasets. The weight data were compiled into weight totals (in

grams) of remains of each faunal type at each site component. The count data were

compiled into total numbers of bones (or numbered bone fragments) of each faunal type

at each site component. This was beneficial because both weight and count data have

biases inherent in archaeological material, and using both should help to arrive at a more

accurate understanding of the assemblages (Lyman 1979). Other measures of faunal

assemblages, such as Minimum Number of Individuals (MNI) and estimates of meat

weight were not used due to lack of data and the highly fragmentary nature of the remains

(Lyman 1979). While imperfect and prone to biases, using only bone weight and bone count allowed me to use more of the available data.

Using bone weight data is an imperfect way to measure faunal remains at a site, partially because of problems with preservation. The bones, in losing some of their mass to weathering, will not represent the full weight that they initially held, and weathering will favor the preservation of larger bones, biasing the sample toward larger bones and underrepresenting smaller animals (Lyman 1979). In contrast, bone count will favor fragmentary bones, usually from smaller animals. For example, the many small bones of a fish as compared to the fewer large bones of a deer will lead to overrepresentation of fish in a sample. Fragmentation further compounds the problem, since many pieces of bones that cannot be readily fit back together will each be treated as single bones, and fragmentation will occur more readily on smaller bones (Lyman 1979). Given these two competing biases, using both weight and count should help to develop a more accurate picture of the faunal assemblages of these different sites.

Cladistic Analysis

Cladistics was developed in the 1940s by Willi Hennig (1950, 1965, 1966) and has now replaced other methods as the primary method by which biologists measure evolutionary relationships (Buchanan & Collard 2008; Cap et al. 2008; Lycett et al. 2007; Mallegni 2007; O'Brien et al. 2001; O'Brien et al. 2014; O'Leary & Gatesy 2008; Schuh 2000; Smith & Grine 2008). Due to the evolutionary nature of culture, in which cultural traits descend with modification from transmission sources, archaeologists have begun to

use cladistics as well to measure cultural evolutionary relationships (Henrich et al. 2008; Lyman & O'Brien 1998:619). Cladistic analysis is used to establish a hypothetical evolutionary relationship among objects of study called taxa (Buchanan & Collard 2008:1685-1688; Coward et al. 2008:43; O'Brien et al 2014:104; 2015; Tehrani & Collard 2009:12). To do this, states of a chosen set of characters, or characteristics that can be assigned states for each object of study, from each taxon are compared to determine which taxa share a common ancestor to the exclusion of others. A character state is an attribute of a specific feature of the item under study (Hennig 1950). For example, a feature may be hair and an attribute is presence or absence of hair. Taxa with a common ancestor will share character states. It is important to note that "common ancestors" spoken of here need not be actual, but may be theoretical. For example, a pair of taxa sharing one character state that is not present in a third will be represented as having a common ancestor that the third taxon does not descend from, even though that common ancestor with the package of character states theorized may not exist. This creates a set of relationships in which taxa will be grouped according to how recent a common ancestor they share. This set of relationships is expressed graphically in a cladogram, with each node of branches representing a common ancestor and each branch line representing where changes in character states may have taken place. Taxa grouped together by branching from a single node are called a clade, and more inclusive clades (i.e. clades with more nodes and branches) descend from less recent ancestors. Out of all possible configurations of branches, the cladogram with the least number of changes is considered the most parsimonious and therefore more likely to be accurate.

To establish these relationships, it is necessary to determine which states are ancestral (plesiomorphies) and which are derived (apomorphies) (O'Brien et al. 2014:104). The most common way to achieve this is through including an outgroup, which is presumed to be descended from a common ancestor of the entire ingroup, while being excluded from the ingroup clade. Any states shared between the outgroup and the ingroup will therefore be seen as ancestral, descending in both groups from a root ancestor (Arnold 1981; Buchanan & Collard 2008:1685; Maddison et al. 1984).

Cladistic analysis distinguishes between informative and uninformative character state changes (O'Brien et al. 2014:104-105). In cladistic analysis, changes that occur due to parallelism (independent evolution along similar lines), convergence (independent evolution of the same or similar set of traits), or reversion to a previous ancestral state, called homoplasies, are not used to determine evolutionary relationships, since they do not inform on descent with modification from a common ancestor. Other types of character states that are not considered are symplesiomorphy, where the ancestral state remains in the end taxa, or where only one taxa shows a change (autapomorphy). In the case where no configuration will remove all homoplasy, the cladogram with the least homoplasy will be considered most parsimonious, and therefore most likely. This is seen in the tree length, or number of changes in character states needed to produce a given topography of clades. Out of all possible configurations of branches, the one tree with the least number of changes is considered the most parsimonious (O'Brien et al. 2015:235). For my analysis, I used the PAUP* (Version 4.0a, build 153) program by Swofford (2002), which contains algorithms for finding the most parsimonious trees and other

important cladistic information, such as cladogram statistics (tree length, Consistency Index, Retention Index), PTP tests, and bootstrapping.

Gap Weighting and Generalized Frequency Coding

Given that cladistic analysis uses changes between states of characters, I used Generalized Frequency Coding (GFC) (Smith and Gutberlet 2001) methods to code continuous numerical data, percentages of fauna type represented in each site during each component, into discrete states. While the GFC method has been recognized as a more robust way to deal with morphometric data than Thiele's (1993) Gap-weighting method, both have been shown to be useful and legitimate methods and are explained here (Lawing et al. 2008; Smith and Gutberlet 2001). Given that the topologies of the cladograms were similar between the two methods, and that the GFC method is accepted as being more reliable (Lawing et al. 2008), I have chosen for the analysis and discussion in the article to only consider the GFC-coded data and corresponding cladograms and analyses.

Since cladistics measures changes between states, the coding method used needs to preserve distance between values. Without this preservation, a change from a very low to a very high value, for example, would be measured as the same amount of change as between two closer values. This would mean a loss of important information for determining the most likely cladistics relationship, as well as an incomplete presentation of the assemblages. Both gap weighting and GFC are designed to code meristic data or continuous morphological data from samples of different taxa. In this study, however, my

data are percentages of fauna type represented in each site during each component (ex., Salmonidae makes up 97.48% of the Chipunii 2 Ainu faunal assemblage), and as such, there are no sample frequency distributions. Therefore, I have modified the methods presented by Thiele (1993) and Smith and Gutberlet (2001) accordingly.

Gap Weighting

For Thiele's (1993) gap-weighting method, fauna type percentages, rounded to the whole percent, are used instead of finding a mean to represent distributions for each character state. Next, the data is range-standardized within each character following this formula:

$$x_s = \frac{x - \min}{\max - \min} \times n,$$

"where n is the maximum number of ordered states allowable by the algorithm used (32 for PAUP…)" (Thiele 1993:284). The maximum and minimum values are those found within each character, and so each percentage value in my initial matrix was entered as the x value in this formula using the maximum and minimum values for the character in which the value was found. In my data, given that there were 0's present, and given that PAUP* allows a maximum of 32 ordered states, I used 31 for my n value, to allow for 0 as a 32nd state. These range-standardized values were rounded to the nearest integer and the resulting character matrix, with its coded states, was input into PAUP* for analysis. The characters must be set as ordered for analysis, since this is the mechanism by which the distance between states is preserved for analysis. For example, if a change

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is observed between states 4 and 20 with no intervening states present for the character, this change would be viewed as a single change between unordered character states. If, however, the states are set as ordered, there would be 16 changes between 4 and 20, given the order of possible states.

Generalized Frequency Coding

With GFC (Smith & Gutberlet 2001), my data is considered within this new framework. Instead of multiple characters containing percentages, as traditionally used in GFC, I must consider my data to consist of the single character Total Faunal Remains for the different site components present. This character is then divided into subcharacters (my original faunal type division), each of which is then expressed as percentages of the total. Since the subcharacters in this study are not ordered in any way (i.e., "Salmonid" is not a logical subsequent step from "Marine Mammal" as "4 scales present" would be to "3 scales present"), I use this initial percentage data rather than transforming it into cumulative frequencies for each subcharacter. Then, the data are assigned to frequency bins, where the range of percentages from 0 to 100% are divided into 25 letters, each corresponding to a range of whole percentages. For my data, I rounded the percentages to the nearest whole percentage and assigned each to its letter. I input this ordered character data into PAUP*. The next step is important to make sure that the characters are weighted so they are not inflated, particularly because the data by definition will be nonindependent (Smith and Gutberlet 2001:160). For each subcharacter, the maximum number of steps, the number of steps between the lowest and the highest value, is

calculated. Also, whether or not the subcharacter is cladistically informative is determined by the presence or absence of multiple states. For example, if a subcharacter only contains one state, or contains one state for all taxa but one (autapomorphy), it is noninformative. Given PAUP*'s maximum weight value of 32,767, this method assigns weights to each subcharacter following the formula:

$$\text{weight} = \frac{\dfrac{32767}{\text{range of frequency bins}}}{\text{number of informative subcharacters}}$$

Noninformative subcharacters are excluded, since the resulting weight would be undefined. These weights are then assigned in PAUP* for each subcharacter, with the default weight of 1 left for the noninformative subcharacters.

Cladograms

Four sets of data were coded with these two methods (gap weighting and GFC) for a total of eight resulting cladograms. For each method, I used Specific Weight data (weight data divided into specific faunal types), General weight data (weight data divided into general faunal types), Specific Count data and General Count data. Using the PAUP* program (Swofford 2002), I ran these sets of coded character states through a heuristic tree search algorithm using Jōmon as the outgroup, since a branch-and-bound tree search algorithm returned no cladograms. Jōmon was chosen as the outgroup on the basis that it is chronologically the oldest component in the sample.

Robustness and Goodness-of-Fit: Bootstrapping, Permutation Tail Probability Tests,

Consistency Index, Retention Index

For any cladogram, it is necessary to determine how robust it is and how good a fit the data are to it (i.e., how strong a phylogenetic signal is present in the data). Robustness can be measured by a bootstrap test and goodness-of-fit by Permutation Tail Probability (PTP) tests, though both of these tests, while useful, must be treated as heuristic and not statistical devices (Buchanan & Collard 2008:1686-1688). Goodness-of-fit can be more reliably measured with Consistency and Retention Indices (Farris 1989).

Bootstrap tests produce a large number (10,000 here) of "pseudo-datasets" through sampling with replacement from the original dataset and measuring the percentage of these datasets that produce the same clades as found in the original dataset (Buchanan & Collard 2008:1688; Tehrani & Collard 2009:15). From this test, each clade can be evaluated for robustness and degree of conflicting phylogenetic signal (Buchanan & Collard 2008:1688; Efron 1979; Felsenstein 1985; Tehrani & Collard 2009:15).

In the PTP test, the dataset is reshuffled a large number of times (in this case, 10,000), the most parsimonious trees are found for each, and the tree lengths thereof are compared to that of the most parsimonious tree from the original data (Archie 1989; Buchanan & Collard 2008:1686; Faith 1990; Faith & Cranston 1991; Jordan & Shennan 2003:63). If the actual data tree has a lower tree length value than 95% of permutations (producing a p-value of less than 0.05), the data have a significant phylogenetic signal,

which means it will fit a tree well (Buchanan & Collard 2008:1686; Jordan & Shennan 2003:63).

Other important measures of goodness-of-fit are the Consistency Index (CI) and Retention Index (RI) (Farris 1989). These two statistics both measure character changes, with CI measuring homoplasies (where multiple taxa share a derived character state that resulted from convergence or other processes not resulting from descent) and RI measuring homologies (taxa sharing derived character states that are the result of descent) (Buchanan & Collard 2008:1687-1688; O'Brien et al. 2015). In both cases, the values will range from 0 to 1, with low values showing poor fit and high values showing good fit (Buchanan & Collard 2008:1687). The former, while useful, reflects autapomorphies in the data, while the latter does not, and can be used to compare different data sets, making RI a more meaningful statistic (Buchanan & Collard 2008:1688).

Statistical Analysis

To better assess the groupings by character state in the cladograms, Chi-squared and Spearman's rank correlation coefficient were performed on the faunal assemblage datasets using Microsoft Excel (Version 1707) according to accepted methods (Ebdon 1985; McGrew 2014; Verschuuren 2013).

Chi-square Analysis

Chi-square analysis and adjusted residuals was performed on bone count data for specific and general faunal types against site and component for four matrices in total. Chi-square analysis is a well-established method for examining frequency data, so this method was chosen over other statistical tests. These four matrices were each tested for deviation from a random distribution using a chi-square analysis in an effort to determine whether the overall distributions of faunal remains by type were as would be expected should there be no significant difference between each site or component. Given the large sample sizes (101,860 in the Specific dataset, 106,025 in the General dataset), an additional set of analyses was performed excluding Salmonidae data (which accounted for 98.1% of the Specific dataset and 94.25% of the General dataset).

To further determine how these distributions of faunal remains varied from a random distribution, I found adjusted residuals for each value in the matrices. Again, I performed this analysis for both the sets of data including and excluding Salmonidae. In all analyses, I observed trends based on direction and magnitude of significant deviation from a random distribution and grouped sites and components according to similar distributions.

Spearman's Rank Correlation Coefficient

Spearman's rank correlation coefficient was performed for Specific and General faunal type bone weight data comparing both sites and components. The weight dataset includes a different set of faunal types than does the count dataset, and so these different types will be seen in the analysis. These analyses determine which sites or components significantly differ from the others in terms of the shape of their distributions. Since weight is continuous data, and the total weights from each site or component differ in scale, it was necessary to compare rank distributions of faunal remains across faunal types (general and specific) for each site or component. Also, given that the distribution, rather than some measure of central tendency, was the focus of this analysis, and the assumption that the data would not necessarily follow a normal distribution, I chose Spearman's rank correlation coefficient. In doing so, I compared each distribution (ranked distribution of faunal remains by type for each component or site) against each other within each matrix and produced matrices of the resulting values, with indications of which values were statistically significant. These analyses show which sites (or components) significantly differ from which others in terms of the shape of their distributions, and which do not. These analyses also determine which sites or components differ significantly from the others in terms of the shape of their distributions and whether component or site is more powerful in determining differences in assemblages.

Results presented in the article in the next section include cladograms, consensus trees (where applicable), bootstrap data, PTP data, and tree length, CI, and RI statistics

utilizing the PAUP* program, as well as chi-square adjusted residuals and Spearman's ranked correlation coefficient data. In the article, due to similarities across Specific and General datasets and analyses, only the Specific datasets will be discussed. From this data, trends in groupings found in the cladograms and supporting trends in the statistical analyses are described and discussed.

CHAPTER V
JOURNAL ARTICLE

TRACING AINU AND PRE-AINU CULTURAL CONTINUITY THROUGH CLADISTIC ANALYSIS OF FAUNAL ASSEMBLAGES

Abstract

Cladistics (Hennig 1950, 1965, 1966), a method for establishing evolutionary relationships, is used to compare faunal assemblages from Jōmon (14,000-500 BC; 14,000–2700 cal. BP), Epi-Jōmon (3rd – 7th century; 2700-1500 cal. BP), Satsumon (7th century - 13th century AD; ca. 1500-800 cal. BP), and Ainu (13th century AD – present) period components (Habu et al. 2011; Matsumura 2006; Ōnishi 2014; Weber et al. 2013) from sites in Central Hokkaido, Japan using Generalized Frequency Coding methods (Smith & Gutberlet 2001). Groupings of site components follow geographic rather than temporal trends, showing similarities in animal use across these time periods but differentiated between coastal lowland, inland lowland, and inland upland areas. Statistical analyses confirm the trends found in cladistic analysis. These findings suggest some level of cultural continuity across these time periods and important local environmental forces at work in shaping animal use.

Introduction

Throughout the world, indigenous archaeology, or archaeology conducted concerning and by indigenous peoples, faces issues of colonial history and perceptions of "who has the right to control the past"(Kato 2009:47-49; Nicholas 2010; Smith & Wobst 2005). The Ainu, an indigenous people and ethnic minority in Japan and especially Hokkaido, the island of Sakhalin, and formerly the Kuril Islands in the north Pacific (Figure 1), face problems inherent to indigenous archaeology (Kato 2009). In particular, the incomplete archaeological picture and unclear origins of Ainu people and culture lend to a cultural identity incomplete in its reach into the past (Hudson 2006:423). Aside from a general dearth of ethnography in studies of Ainu archaeology, current Ainu cultural concerns and insights seem often to be ignored (Kato 2010). While there are important studies charting cultural changes between adjacent temporal periods in Hokkaido (see Hudson 1999), no examinations of cultural transitions cutting across the Jōmon (14,000-500 BC; 14,000–2700 cal. BP), Epi-Jōmon (3rd – 7th century; 2700-1500 cal. BP), Satsumon (7th century - 13th century AD; ca. 1500-800 cal. BP), and Ainu (13th century AD – present) periods have been undertaken (Habu et al. 2011; Matsumura 2006; Ōnishi 2014; Weber et al. 2013). Furthermore, none have specifically entailed tracing cultural continuity or changes using faunal remains from across these time periods, and cultural aspects of animal use in general has also been neglected in cladistical archaeological studies. Tracking animal use and substance changes is especially important for understanding sedentary hunter-gatherer populations with a history of animal-based religion (Batchelor 1892; Munro 1963; Ohnuki-Tierney 1976; Utagawa 1992).

Figure 4. Map showing historical range of Ainu settlement (red) and probable range (pink) based on linguistic evidence (dots) (Kwamikagami 2011).

A cohesive look at faunal assemblages across Central Hokkaido is a valuable addition to our understanding of the area's prehistory, which cannot be obtained solely from site-by-site reports and studies. Similarly, including a broader temporal range can give insight into larger-scale cultural evolution. Understanding how Ainu culture articulates with previous cultural traditions will also help provide a more unified historical basis and greater respect for the Ainu in modern Japanese society as a whole in that it will more firmly establish the Ainu as an indigenous people of long duration and

with indigenous rights, particularly in terms of traditional animal use practices (Siddle 1995:73-4). Finally, cladistics, while extensively used in evolutionary archaeology for studies of human-made objects, has yet to be used for traces of food culture, or of animal-human interface in general.

To address these gaps in our current understanding, this article synthesizes archaeological evidence of animal use across time periods and geographic locations in Central Hokkaido. We examine excavated faunal assemblage data from archaeological sites on Hokkaido including the Jōmon, Epi-Jōmon, Satsumon, and Ainu time periods. Cladistic analysis is used to determine similarities in faunal distributions and how they change over space and time. This study reveals continuity in animal use over time in Central Hokkaido, thereby adding evidence to claims of traditional animal use practices for modern Ainu.

Background

Biophysical Context

The island of Hokkaido is bordered by the Okhotsk Sea to the north, Pacific Ocean to the east, and Sea of Japan to the west (Figure 1). Lower sea levels during the Pleistocene meant that Hokkaido was connected to present day Sakhalin and mainland Asia until about 15,000 BP (Millien-Parra & Jaeger 1999; Nakazawa et al. 2011), thus affecting plant and animal distributions on Hokkaido (Dobson & Kawamura 1998; Igarashi 2013). Hokkaido today is noted for its cold, snowy winters and mild summers, due to Tsushima and Soya Warm Currents and the Okhotsk and Siberian Highs (Aoyama 2012; Igarashi 2013).

In Hokkaido, the forest is divided between boreal and cool-temperate in an elevation-based deciduous-coniferous gradient (Igarashi 2013; Okitsu 2003)(Figure 2; Table 1). The study area for this article is in the Temperate Broadleaf and Mixed Forest ecoregion of Hokkaido (PA0423) (Figure 2, 3). Most sites in this study fall under the lowland deciduous regime, with some cool-temperate mixed forest at one upland site (Kamihoronaimoi). Neither Japanese beech forests nor boreal coniferous forests are present in the study area (Figure 2,3).
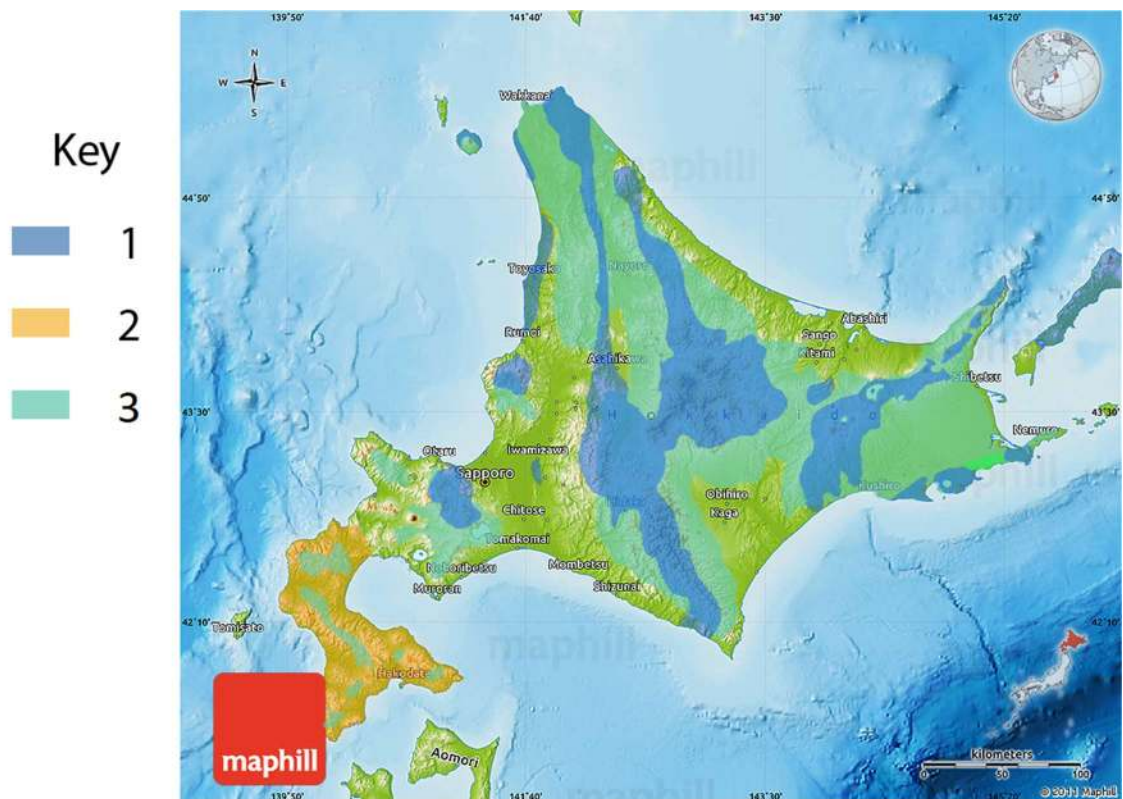
Figure 5. Map of Hokkaido compiled from Igarashi (2013), Maphill (2011), and the World Wildlife Fund (2017b). 1 – Boreal coniferous forest; 2 – *Fagus crenata* forest and Nihonkai montane deciduous forest ecoregion (PA0428)(World Wildlife Fund 2017c); 3 – Hokkaido montane coniferous forest ecoregion (PA0510)(World Wildlife Fund 2017a). The remaining land makes up the Temperate Broadleaf and Mixed Forest of Hokkaido (PA0423)(Yumiko 2017).

Table 11. Main tree species in Hokkaido forests (Igarashi 2013; Ogawa et al. 2006).

	Scientific name	Common name
Southwest Hokkaido		
	Fagus crenata	Japanese beech
Boreal		
	Picea jezoensis	Yezo Spruce
	Picea glehnii	Glehn's spruce
	Abies sachalinensis	Sakhalin fir
Cool-temperate		
	Quercus crispula	Mongolian oak
	Quercus mongolica var, *grosseserata*	Mongolian oak
	Acer mono	Painted maple
	Tilia japonica	Japanese lime
	Fraxinus mandshuria var. *japonica*	Japanese Manchurian ash
	Phellodendron amurense	Amur cork-tree
	Sasa kurilensis	Chishima dwarf bamboo
	Alnus spp.	Alder shrubs
Pacific coast		
	Betula ermanii	Erman's birch

Figure 6. Map of the study area and sites included in the study in Central Hokkaido.

The land bridge to mainland Siberia during glacial periods has affected the

mammalian fauna in Hokkaido, distinguishing it as boreal Eurasian fauna as opposed to

the more Indo-Malayan fauna in the rest of Japan (Dobson 1994:91; Dobson &

Kawamura 1998). The Hokkaido brown bear (*Ursus arctos yesoensis*), foxes (*Vulpes*

spp.), owls (Strigiformes), deer (*Cervus nippon*), salmon (Salmonidae), and seals

(Pinnipedia) have been notable in archaeological and ethnographic Ainu diet, religion,

and trade hunting (Aoyama 2012; Batchelor 1892; Hudson 1999; Munro 1963; Ohnuki-Tierney 1976).

Since study area is in the Temperate Broadleaf and Mixed Forest ecoregion of Hokkaido (PA0423), it only includes fauna from this regime (Figures 2,3; Table 2). Non-terrestrial fauna, such as fish and aquatic mammals, can be divided into marine and freshwater, as well as species that exist in both. Fauna present in assemblages of study sites are listed in Table 3, and a list of fauna from select sites of the Ainu and Satsumon periods comprises Table 4 (Nishimoto 1985).

Table 12. Animal species noted by the World Wildlife Fund as found in the Temperate Broadleaf and Mixed Forest of Hokkaido (PA0423) and Temperate Coniferous Forest of Hokkaido (PA0510) ecoregions (Yumiko 2017; World Wildlife Fund 2017) with select Hokkaido Fauna as determined by Dobson & Kawamura (1998) and Ohdachi & Aoi (1987) denoted by *. Species reported in all references are denoted by **.

Temperate Broadleaf and Mixed Forest (PA0423) and Temperate Coniferous Forest (PA0510)	
Common Name	**Scientific Name**
Birds	
Stellar's Sea eagle	*Haliaeetus pelagicus*
Common merganser	*Mergus merganser*
Tufted Puffin	*Lunda cirrhata*
Hazel grouse	*Tetrastes bonasia*
Three-toed woodpecker	*Picoides tridactylus*
Willow tit	*Parus palustris*
Japanese crane	*Grus japonensis*
Blakiston's fish owl	*Keputa blakistoni*
Microbats	
Rodents	
Dsinezumi shrew	*Crocidura dsinezumi* *
Laxmann's shrew	*Sorex caecutiens* *

TABLE 2 (CONTINUED)

Temperate Broadleaf and Mixed Forest (PA0423) and Temperate Coniferous Forest (PA0510)	
Common Name	**Scientific Name**
Slender shrew	*Sorex gracillimus* *
Long-clawed shrew	*Sorex unguiculatus* *
Red squirrel	*Sciurus vulgaris* *
Siberian chipmunk	*Tamias sibiricus* *
Siberian flying squirrel	*Pteromys volans* *
Grey red-backed vole	*Clethrionomys rufocanus* *
Northern red-backed vole	*Clethrionomys rutilus* *
Rabbits/Hare (Lagomorphs)	
Mountain hare	*Lepus timidus* *
(Small Mustelids)	
Mammals	
Red fox	*Vulpes vulpes*
Sika deer	*Cervus nippon yesoensis*
Hokkaido brown bear	*Ursus arctos yesoensis* **
Temperate Coniferous Forest (PA0510)	
Common Name	**Scientific Name**
Pika (Northern Pika)	*Ochotona hyperborea yesoensis* **
Sable	*Martes zibellina brachyuran* **

Table 13. Faunal remains by component present in study sites.

Component	Faunal Remains Present
Ainu	**Mammal**
	Cervus nippon (Sika deer)
	Fish
	Cyprinidae (minnow and carp); Tribolodon (redfin dace)
	Salmonidae (Salmonids); *Hucho perryi* (Sakhalin taimen)
	Mollusc
	Ezohelix gainesi gainesi (terrestrial mollusc)
	Clausliidae (door snail); Snail
Satsumon	**Mammal**
	Cervus nippon (Sika deer)
	Cetacea (whale, dolphin, porpoise family)
	Fish
	Cyprinidae (minnow and carp); Tribolodon (redfin dace)
	Salmonidae (Salmonids); *Hucho perryi* (Sakhalin taimen)
	Clupeinae (Clupea pallasii) (sardine)
	Mollusc
	Snail; Clausliidae (door snail)
Epi-Jōmon	**Mammal**
	Cervus nippon (Sika deer)
	Marine mammal (M-L size class)
	Fish
	Cyprinidae (minnow and carp); Tribolodon (redfin dace)
	Salmonidae (Salmonids); *Hucho perryi* (Sakhalin taimen)
	Crustacean
	Arthropoda (Crustacean)
Jōmon	**Mammal**
	Cervus nippon (Sika deer)
	Sus scrofa leucomystax (Japanese boar)
	Fish

TABLE 3 (CONTINUED)

Component	Faunal Remains Present
Jōmon	**Mammal**
	Salmonidae (Salmonids)

Table 14. Species present in select Hokkaido sites divided by component, from Nishimoto (1985).

Component	Scientific name (Common name), *Marine, **Brackish-water, †Freshwater, ‡Both Marine & Freshwater
Satsumon & Ainu	Mammal: *Ursus arctos yesoensis* (Hokkaido brown bear), *Canis lupus familiaris* (Dog), *Canis lupus hattai* (Hokkaido wolf), *Vulpes vulpes schrenki* (Ezo red fox), Felis (Cats), Equus (Horses), *Cervus nippon yesoensis* (Yezo sika deer), *Nyctereutes procyonides albus* (Ezo tanuki/raccoon dog), *Lepus timidus ainu* (Ezo mountain hare), *Martes zibellina brachyura* (Japanese sable), Cetacea (Whales, dolphins, porpoises)*, Dolphins*, *Eumetopias jubatus* (Steller sea lion)*, Phocidae (Earless seal)*, *Zalophus japonicus* (Japanese sea lion)*, Arctocephalinae (Fur seal)*
	Bird: Laridae (Gulls & Terns), Diomedeidae (Albatross), *Gavia arctica/pacifica* (Arctic or Pacific loon), Phalacrocoracidae (Cormorant), Uria (Murres)
	Fish: *Gadus macrocephalus* (Pacific cod)*, *Paralichthys olivaceus* (Olive flounder)*, Thunnus (Tuna)*, *Xiphias gladius* (Swordfish)*, Pleuronectiformes (Flatfish)‡, Tribolodon (Dace)‡, Salmonidae (Salmonids)‡, Scorpaeniformes (Scorpionfish, rockfish, sculpins, etc.)‡
	Reptile: Chelonioidea (Sea turtle)*
	Mollusc: *Margaritifera laevis* (Freshwater pearl mussel)†, *Mercenaria stimpsoni* (species of venus clam)*, *Saxidomus purpurata* (Purple butter clam)*, *Spisula sachalinensis* (species of surf clam)*, *Haliotis discus discus* (Black abalone)*, *Patinopecten yesoensis* (species of scallop)*, *Barbitonia arthritica* (a sea snail)*
	Echinoidea: Echinoidea (Sea urchin)*
Satsumon	Mammal: Felis (Cats),

TABLE 4 (CONTINUED)

Component	Scientific name (Common name), *Marine, **Brackish-water, †Freshwater, ‡Both Marine & Freshwater
Satsumon	Fish: Thunnus (Tuna)
Ainu	Mammal: *Lutra lutra nippon* (Japanese river otter)
	Bird: Accipitriformes (Eagles and hawks), Anatidae (Ducks, swans, and geese), Corvidae (Crows, ravens, jays, magpies)
	Fish: Elasmobranchii (Sharks, skates, rays, sawfish)*, *Pagrus major* (Red seabream)*, *Pleurogrammus azonus* (Okhotsk atka mackerel)*, *Seriola quinqueradiata* (Japanese amberjack)*, *Eleginus gracilis* (Saffron cod)‡, *Clupea pallasii* (Pacific herring)‡, *Hucho perryi* (Sakhalin taimen)‡, Acipenseridae (Sturgeon)‡, Cottus (Freshwater sculpins)†
	Mollusc: *Glycymeris albolineata* (species of bittersweet clam)*, Mytilus (Mytilus (certain mussels)*, *Gomphina melanegis* (species of venus clam)*, *Crassostrea gigas* (Pacific oyster)*, *Mytilus galloprovincialis* (Mediterranean mussel)*, *Meretrix lusoria* (Hamaguri / Common Orient clam)*, *Corbicula japonica* (Japanese basket clam)**
	Crustacean: Brachyura (Crabs)‡

Cultural Context

Archaeological studies in Hokkaido distinguish between the Jōmon, Epi-Jōmon, Satsumon, and Ainu time periods (*Atsuma-cho Kyouiku Iinkai* 2009; *Hokkaido Maizou Bunkazai Sentaa* 2002, 2004; *Sapporo-shi Maizou Bunkazai Sentaa* 2001, 2002). It must be noted that the time periods here are modern categories assigned based on differences in cultural materials, rather than a set of distinctions made by the peoples living in the time periods themselves. Broadly, the transitions between these time periods are marked by changes in cultural materials, where some material types disappear and others appear for the first time. While the transition between Jōmon and Epi-Jōmon seems to be more one of small-scale change marked mostly by the lack of replacement by Yayoi cultural features, the transitions from Epi-Jōmon to Satsumon and from Satsumon to Ainu are more clear-cut (Hudson 1999; Kodansha 1983; Okada 1998; Utagawa 1992). Features used to define these time periods, in terms of house type, level of plant cultivation, pottery, and tools will be discussed further in this section and in Table 5.

Table 15. Summary of cultural traits for the Jōmon, Epi-Jōmon, Satsumon, and Ainu periods mentioned in this study.

Time Period	Subsistence	Settlement	Society
Jōmon (14,000–2,700 cal. BP)(Ōnishi 2014)	• Hunting-Fishing-Gathering • Emphasis on marine resources (Habu 2004; Minagawa & Akazawa 1992; Takahashi et al. 1998) • Seasonal rounds (Habu 2004) • Plant Gathering & Cultivation (Crawford et al. 1976; Habu 2004)	• Sedentary (Habu 2004; Hudson 2007) • Pithouses on river terraces and wetlands (Crawford 1976; Hudson 2007; Ōnishi 2014)	• Some possible social stratification (Nakamura 1999; Pearson 2004) • Some of the oldest pottery in Asia (Adachi et al. 2009)
Epi-Jōmon (2,700-1,500 cal. BP)(Weber et al. 2013)	• Hunting-Fishing-Gathering (Moriya 2015) • Ainu folklore: Deer, Salmon, & Lily Bulbs (Imamura 1996) • Seasonal processing of nuts and weeds (Crawford 2011; Ōnishi 2014) • Little evidence of plant cultivation (Crawford 2011)	• Pithouses on river terraces on wetlands → no evidence of dwellings (Ōnishi 2014; Moriya 2015) • No evidence of seasonal occupation (Crawford 2011)	• Possible bear worship (Utagawa 1992) • Some social status distinctions (Okada 1980; 1998) • Pottery similar to Jōmon (Okada 1998)

3

TABLE 5 (CONTINUED)

Time Period	Subsistence	Settlement	Society
Satsumon (ca. 800-1400 BP)(Weber et al. 2013)	• Hunting-Fishing-Gathering • Agriculture (Imamura 2016; Moriya 2015)	• Pithouses on river floodplains (Moriya 2015; Ōnishi 2014) • Wall ovens (Moriya 2015) • Settlement locations determined by salmon fishing (Ōnishi 2014)	• Cultural diffusion between Hokkaido and northern Honshu (Crawford 2011; Imamura 1996) • Appearance of iron tools (Crawford 2011) • Kofun-style burial mounds – Possible social stratification (Imamura 1998; Weber et al. 2013) • Scraped-design, interior-lug, and imported Haji pottery (Hudson 1999; Utagawa 1992)
Ainu (ca. 800 BP-Present)(Ōnishi 2014; Weber et al. 2013)	• Hunting-Fishing-Gathering (Ohnuki-Tierney 1976) • Plant cultivation (Crawford 2011; Ōnishi 2014)	• Surface dwellings on riverside wetlands and floodplains (Aoyama 2012; Munro & Raglan 1959; Ōnishi 2014) • Relocation rare, no seasonal mobility (Ohnuki-Tierney 1976)	• Religion – interaction with gods, especially those in animal disguises (Aoyama 2012; Munro 1963) • Ritual animal sacrifice (Batchelor 1892) • Patrilineal chief had limited government over the village (Munro 1963) • Local pottery absent, imported vessels (Hudson 1999)

Populations associated with each of the cultural periods addressed in this article (Table 5) are often assumed to be related to one another (Sato et al. 2009). It is generally accepted that the Epi-Jōmon and subsequent Satsumon populations descended from the Jōmon, though Satsumon human remains are rare (Adachi et al. 2009; Matsumura et al. 2006; Sato et al. 2009). Using mtDNA haplogrouping, comparisons of Ainu mtDNA with that of Jōmon and other human remains show that the Ainu have close genetic similarities with the Jōmon, including the N9, D1, and G1 haplogroups (Sato et al. 2009). The Ainu also share Y-haplogroup D with other groups thought to have descended from the Jōmon, such as the modern Japanese (Tajima et al. 2004). Some differences between modern Japanese and Ainu Y-haplogroups have been traced to outside of the Japanese archipelago (such as O-M122 from China), suggesting that later imported genetic markers altered in modern Japanese what they once shared with the Ainu, which suggests Jōmon ancestry (Tajima et al. 2004). Overall, while there remain questions as to the exact descent and genetic contributions, the Ainu are strongly theorized to have descended from the Jōmon people. While the genetic connections reveal some evidence of biological connections (Adachi et al. 2009; Sato et al. 2009; Tajima et a. 2004), it is also clear that certain cultural similarities exist between the Jōmon, Epi-Jōmon, Satsumon, and Ainu traditions.

Cultural Similarities

The cultural periods in Hokkaido included in this study show some important

differences, by which they are in part distinguished, but also show significant similarities.

Cultural differences among these periods include extent of plant cultivation (Crawford

2011; Okada 1998), house types (Imamura 1996; Moriya 2015; Okada 1998; Ōnishi

2014), and the shift from stone to iron tools (Ōnishi 2014). Plant remains indicate some

limited cultivation during the Jōmon period, little or no local cultivation in the Epi-

Jōmon, significant cultivation (though not the main focus of subsistence) in the

Satsumon, and some cultivation during the Ainu period (Crawford 2011; Okada 1998).

House types can be divided into pithouses for the first three periods and surface dwellings

for the Ainu period (Imamura 1996; Moriya 2015; Okada 1998; Ōnishi 2014). Pithouses

in the Jōmon and in the Epi-Jōmon are round with central hearths, while Satsumon

pithouses were rectangular with wall ovens (Imamura 1996; Moriya 2015; Okada 1998;

Ōnishi 2014). The shift from stone to iron tools occurred at the beginning of the

Satsumon (Ōnishi 2014).

Nevertheless, there are also similarities. The Epi-Jōmon, as seen in pottery,

subsistence, and early round pithouse structures, are clearly a continuation of the Jōmon

(Okada 1998; Ōnishi 2014). The Satsumon, while showing strong similarities to aspects

of the Yayoi culture in northern mainland Japan at the time, are accepted as the

immediate ancestors of the Ainu, though the Okhotsk people may have also contributed

to the Ainu gene pool (Crawford 2011; Amano 2003; Sato et al. 2007, 2009). A pattern of

hunting-fishing-gathering subsistence, with the addition of plant cultivation at least in the

Jōmon, Satsumon, and Ainu periods, is apparent (Crawford 2011; Imamura 1996; Okada

1998; Ōnishi 2014). There is even a clear stylistic sequence for harpoons from the Epi-

Jōmon, Satsumon, and Ainu (Immura 1996). Settlement along riverside areas, including

wetlands in the Jōmon, Epi-Jōmon, and Ainu periods and floodplains in the Satsumon

and Ainu periods, is the rule in Hokkaido during these periods (Ōnishi 2014).

In particular, the sedentary settlement patterns present in all periods may indicate

either abundant resources or a collector subsistence strategy, in which unevenly

distributed resources are exploited from a strategic central location (Binford 1980; 1982;

Habu 2004). Genetics have also shown important similarities between the Ainu and

Jōmon, confirming the widely-held assumption that the Ainu descended from the

Satsumon, through the Epi-Jōmon, and ultimately from the Jōmon (Adachi et al. 2009;

Matsumura et al. 2006; Sato et al. 2009; Tajima et al. 2004).

Study Sites

Single and multi-component study sites are located in Central Hokkaido (Table 6;

Figure 3). These sites all sit within or near the Ishikari Plain, stretching from Ishikari Bay

on the Sea of Japan on the north to the Pacific Ocean on the south (Figure 2,3). As is

generally expected from all of the relevant time periods, these sites are close to rivers

(Ōnishi 2014). Aside from their riverine nature, the sites can be divided into coastal

lowland (K39-7 and K39-9), inland lowland (Chipunii 1 and 2), and inland upland

(Kamihoronai). Nevertheless, these sites are all relatively low in elevation, with the

highest at only 58 m above sea level (Table 6). The lowland sites (Chipunii 1, Chipunii 2, K39-7, and K39-9) all fit within the *Quercus mongolica* deciduous forest regime (Ohara 2009; Okitsu 2003). The higher-elevation site, Kamihoronaimoi, sits on the edge of the Yubetsu Mountains (Figure 2,3), though not at high enough elevation to be in the higher cool-temperate (500-1500 m) or boreal forest zone (Figure 2,3; Okitsu 2003; Qian et al. 2003). It may possibly belong to the *Abies sachalinensis-Quercus mongolica* mixed forest regime, though resolution from existing maps is unclear (Okitsu 2003). The study area for this article is in the Temperate Broadleaf and Mixed Forest ecoregion of Hokkaido (PA0423) (see Figure 2,3), therefore fauna present in study site assemblages listed in Table 6 only include fauna from this regime. Non-terrestrial fauna, such as fish and aquatic mammals, are divided into marine and freshwater, as well as species that exist in both. From the study sites, one faunal type (Cyprinidae) is freshwater, one (Marine mammal (M-L size class)) is marine, and four (Salmonidae, Tribolodon, *Hucho perryi*, and *Clupea pallasii*) are both (Table 3).

Table 16. Site Locations and Elevations.

Site	Component(s)	Municipality	Elevation
Chipunii 1	Ainu, Satsumon	Chitose (Chuo)	26.00
Chipunii 2	Ainu, Jōmon	Chitose (Chuo)	22.00
K39-7	Satsumon	Sapporo (Chuo Ward)	14.00
K39-9	Satsumon, Epi-Jōmon	Sapporo (Kita Ward)	14.00
Kamihoronaimoi	Ainu, Satsumon, Epi-Jōmon	Atsuma	58.00

Evolutionary Archaeology

Evolutionary archaeology takes concepts such as descent with modification, natural selection, diffusion, drift, and speciation from evolutionary biology and applies them to human culture as seen in the archaeological record (Lyman & O'Brien 1998:615-616). It is important to note that, as in much of biology, cultural evolutionary concepts refer to changes over time, often in response to changes in circumstances or contexts, and not a progression from a "lower" to a "higher" set of states. The connections drawn thereby show what aspects of a culture precede which others and what forces likely influenced change between temporally adjacent traits, without claiming any traits to be more "advanced" than any others. Whatever changes that occur are charted on temporal, not qualitative, lines. While biology studies descent-with-modification of genes, the replicator unit in evolutionary archaeology is the cultural trait (Henrich et al. 2008; Lyman & O'Brien 1998:619). Cultural traits are mental representations within the minds of the humans who are part of a culture (which is the total of such mental representations and meanings), and they are passed to the next generation through cultural transmission (learning) (Henrich et al. 2008; Lyman & O'Brien 1998:619). It must be noted that cultural traits do not always follow biological notions of adaptability, and they are instead subject to environmental, social, and other circumstantial selective pressures that will determine which traits continue in a cultural group over time and which do not (Henrich et al. 2008; Lyman & O'Brien 1998; Mace & Holden 2005; O'Brien et al. 2014). Also, such traits are not visible themselves in the archaeological record (or even ethnography), though the physical manifestations of these traits, in the form of artifacts, make up the

cultural phenotype, which we can study (Lyman & O'Brien 1998:619; O'Brien et al. 2001:1134). As such, it must be remembered that such inquiry involves inference about culture from cultural material, and that the meanings attached to artifacts may be different to different people (Dunnell 1978) and as such change with transmission.

More specific to this study, animal use is a set of cultural traits that may be influenced by environmental or societal pressures. Which animals, parts of animals, or in which contexts animals constitute food vary according to cultural group (Fowles 2008:18; Lyman 1979:537). While some of what is and is not eaten will be in part due to efficiency of energy consumption per caloric gain (Cannon 2003), it remains that, even on a single animal, consumed meat will usually be less than all available meat from that animal (Lyman 1979:537). Whether the factors governing which parts are eaten are kinship-driven (Lyman 1979:539) or determined by religious taboo (Fowles 2008), which animals and which parts of them are treated as food constitute cultural traits. As such, they are subject to evolutionary processes as are other cultural traits. The classic example is the Jewish prohibition on pork, as studied particularly in the Levant (Fowles 2008). Whether this prohibition resulted from environmental economic factors (Hesse & Wapnish 1997), out of desire for ethnic demarcation (Finkelstein 1997; Valeri 2000), or other cultural reasons, the injunction against pork consumption developed culturally within historical and environmental contexts and pressures (Fowles 2008). This study analyzes faunal remains to infer the cultural aspects of animal use.

Cladistics was developed in the 1940s by Willi Hennig (1950, 1965, 1966) and has now replaced other methods as the primary method by which biologists measure evolutionary relationships (Buchanan & Collard 2008; Cap et al. 2008; Lycett et al. 2007;

Mallegni 2007; O'Brien et al. 2001; O'Brien et al. 2014; O'Leary & Gatesy 2008; Schuh 2000; Smith & Grine 2008). Due to the evolutionary nature of culture, in which cultural traits descend with modification from transmission sources, archaeologists have also begun to use cladistics to measure evolutionary relationships between cultural materials (Henrich et al. 2008; Lyman & O'Brien 1998:619). Cladistic analysis is used to establish a hypothetical evolutionary relationship among objects of study called taxa (Buchanan & Collard 2008:1685-1688; Coward et al. 2008:43; O'Brien et al 2014:104; 2015; Tehrani & Collard 2009:12).

To do this, states of a chosen set of characters, or characteristics that can be assigned states for each object of study, from each taxon are compared to determine which taxa share a common ancestor to the exclusion of others. Taxa sharing a common ancestor share character states. Through such consideration, taxa are grouped according to how recent a common ancestor they share. It is necessary to determine which states are ancestral (plesiomorphies) and which are derived (apomorphies) (O'Brien et al. 2014:104). The most common way to achieve this is through including an outgroup, which is presumed to be descended from a common ancestor with the entire ingroup, while being excluded from the ingroup clade (Farris 1982; Kitching et al. 1998; Watrous & Wheeler 1981). Any states shared between the outgroup and the ingroup therefore are seen as ancestral, descending in both groups from a root ancestor.

This set of relationships can be graphically expressed in a cladogram, with each node of branches representing a common ancestor and each branch line representing where changes in character states may have taken place. Taxa grouped together by branching from a single node are called a clade, and more inclusive clades (i.e. clades

with more nodes and branches) descend from less recent ancestors. Out of all possible configurations of branches, the cladogram with the least number of changes is considered the most parsimonious.

Materials and Methods

This analysis includes faunal data gleaned from site excavation reports on Central Hokkaido carried out and published by Hokkaido University and various local Boards of Education (Atsuma-cho Kyouiku Iinkai 2009; Hokkaido Maizou Bunkazai Sentaa 2002, 2004; Sapporo-shi Maizou Bunkazai Sentaa 2001, 2002). Excavations included assemblages spanning the Jōmon, Epi-Jōmon, Satsumon, and Ainu time periods. This sample includes reports from the Chipunii 1 (Ainu and Satsumon period), Chipunii 2 (Ainu and Jōmon), K39-7 (Satsumon), K39-9 (Epi-Jōmon), and Kamihoronaimoi (Ainu, Satsumon, and Epi-Jōmon) sites. All of these reports contain information about time period, site data, and bone weight and/or bone count, though entries missing any of this information or faunal taxonomic information were excluded. These data were then organized into specific faunal types: Arthropoda (crustaceans), Aves (birds), Cetacea (whales, dolphins, and porpoises), Clupeinae (herrings, sardines, and sprats), Molluscs (snails), Cyprinidae (carps and minnows), Cervidae (deer), Mammalia (size class Small to Medium), Mammalia (size class Medium to Large), Marine mammals (size class Medium to Large) (which could include cetaceans, as well as seals, sea lions, manatees, and sea otters, but is constrained as being Medium to Large size), and Salmonidae (salmon, trout, and char). While other groups of fauna are notable to Hokkaido and

particularly to Ainu culture, such as the brown bear (*Ursus arctos yesoensis*) or fox (*Vulpes vulpes*), they did not appear or were not identified in the reports.

Since many report entries had either bone weight (weight in grams of remains of each faunal type at each site-time period) or bone count (total numbers of bones or numbered bone fragments of each faunal type at each site-time period) data, weight and count make up separate datasets. Other measures of faunal assemblages, such as Minimum Number of Individuals (MNI) and estimates of meat weight were not used due to lack of data and the highly fragmentary nature of the remains (Lyman 1979). While imperfect and prone to biases, using only bone weight and bone count allowed us to use more of the available data. Bone weight data tend to favor the preservation of larger bones, biasing the sample toward larger bones and underrepresenting smaller animals (Lyman 1979). In contrast, bone count favors fragmentary bones, usually from smaller animals. Using both should convey a more accurate understanding of the faunal assemblages.

Cladistic Analysis

Given that cladistic analysis uses changes between states of characters, we used Generalized Frequency Coding (GFC) (Smith and Gutberlet 2001) methods to code continuous numerical data, percentages of fauna type represented in each site during each time period, into discrete states. It should be noted that GFC is designed to code meristic data or continuous morphological data from samples taken of different taxa. Methods presented by Smith and Gutberlet (2001) were modified in this study since data is a set of

percentages taken from a set of totals, and as such, there are no sample frequency distributions to convert.

Using the PAUP* (Version 4.0a, build 153) software program (Swofford 2002), we used a heuristic tree search algorithm on these sets of coded character states, since a branch-and-bound tree search algorithm returned no cladograms. Jōmon was chosen as the outgroup because it is chronologically the oldest time period in the sample.

For any cladogram, it is necessary to determine how robust it is and how good a fit the data are to it. Robustness can be measured by a bootstrap test and goodness-of-fit by Permutation Tail Probability (PTP) tests, though both tests, while useful, must be treated as heuristic and not statistical devices (Buchanan & Collard 2008:1686-1688). Goodness-of-fit can be more reliably measured with Consistency (CI) and Retention Indices (RI) (Farris 1989). These two statistics both measure character changes, with CI measuring homoplasies (where multiple taxa share a derived character state that resulted from convergence or other processes not resulting from descent) and RI measuring homologies (taxa sharing derived character states that are the result of descent) (Buchanan & Collard 2008:1687-1688; O'Brien et al. 2015). In both cases, the values will range from 0 to 1, with low values showing poor fit and high values showing good fit (Buchanan & Collard 2008:1687). The former, while useful, reflects autapomorphies in the data, while the latter does not, and can be used to compare different data sets, making RI a more meaningful statistic (Buchanan & Collard 2008:1688).

Statistics

To better assess groupings by character state in the cladograms, Chi-square and Spearman's rank correlation coefficient were performed on the faunal assemblage datasets using Microsoft Excel (Version 1707) according to accepted methods (Ebdon 1985; McGrew 2014; Verschuuren 2013).

Chi-square and adjusted residuals analysis was performed on bone count data for faunal types against site and time period. These matrices were each tested for deviation from a random distribution using a chi-square analysis in an effort to determine whether the overall distributions of faunal remains by type were as would be expected should there be no significant difference between each site or time period. Trends were observed in residual analyses based on direction and magnitude of significant deviation from a random distribution and grouped sites and time periods according to similar distributions. Spearman's rank correlation coefficient was performed for bone weight data comparing both sites and time periods. These analyses determine which sites or time periods differ significantly from the others in terms of the shape of their distributions.

Results

Cladistic Analysis

Parsimony analysis of the two sets of data resulted in two cladograms (Figure 4). In terms of goodness-of-fit of the data to a tree, the strength of phylogenetic signal, I measured tree statistics (CI, RI, and tree length) and performed PTP tests in PAUP* 4.0. It is clear from the CI and RI values that there is a strong phylogenetic signal, with both showing above 0.8 for each statistic (Buchanan & Collard 2008:1687; Table 7). This trend is not conclusively confirmed by the p-values returned by the PTP tests, in which the weight data showed a value greater than 0.05, which would indicate an insignificant phylogenetic signal, while the count data showed a value less than 0.05 (Buchanan & Collard 2008:1686). It must be noted, however, that the CI and RI are generally accepted as more reliable, and PTP is to be treated more as a heuristic device than a meaningful statistic (Buchanan & Collard 2008:1686). Therefore, it is clear from the CI, and RI statistics that these datasets show significant phylogenetic signal.

Figure 4. Cladograms of Weight (a) and Count (b) data coded with the GFC method.
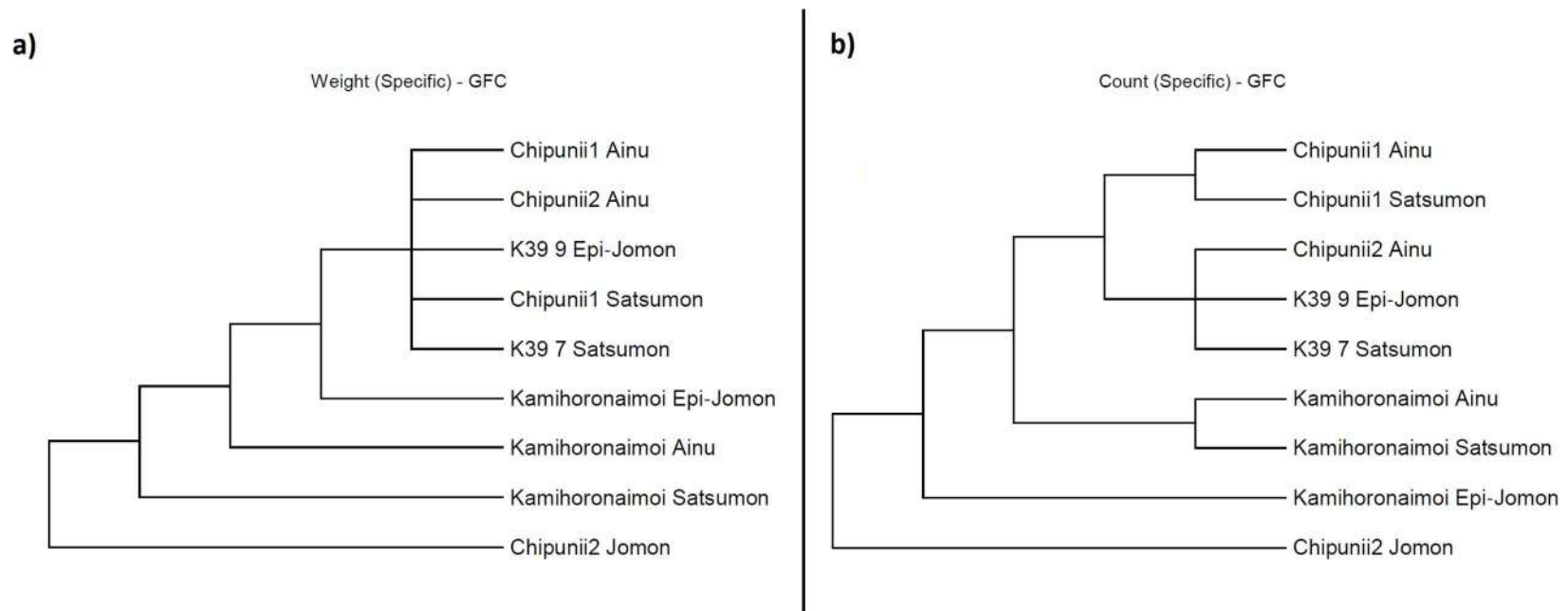
Table 7. Tree Statistics for cladograms.

Measurement Type	Faunal Specificity	Tree Length	CI	RI	PTP P-value	Tree Type
Weight	Specific	40048.56	0.82	0.81	0.1711	Heuristic
Count	Specific	37834.23	0.87	0.88	0.0061	Heuristic

The bootstrap analyses using 10,000 replicates performed on each dataset yielded 50% majority-rule bootstrap consensus trees which each matched closely with the most parsimonious cladograms used in the analysis (Figure 5). The clades present in both trees were all supported 100% in the bootstrap analyses, showing high robustness in both analyzed cladograms. It must be remembered, however, that bootstrap analysis is more of a heuristic than a statistical measure of robustness, though its usefulness has been well established (Buchanan & Collard 2008:1688).
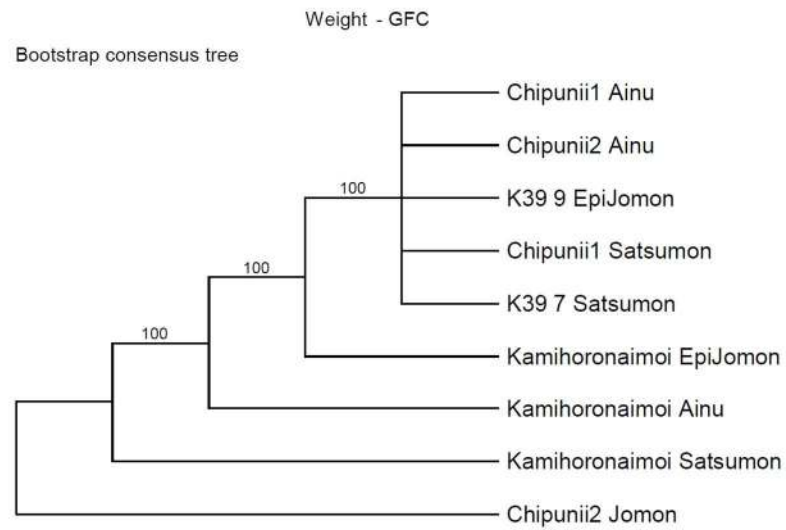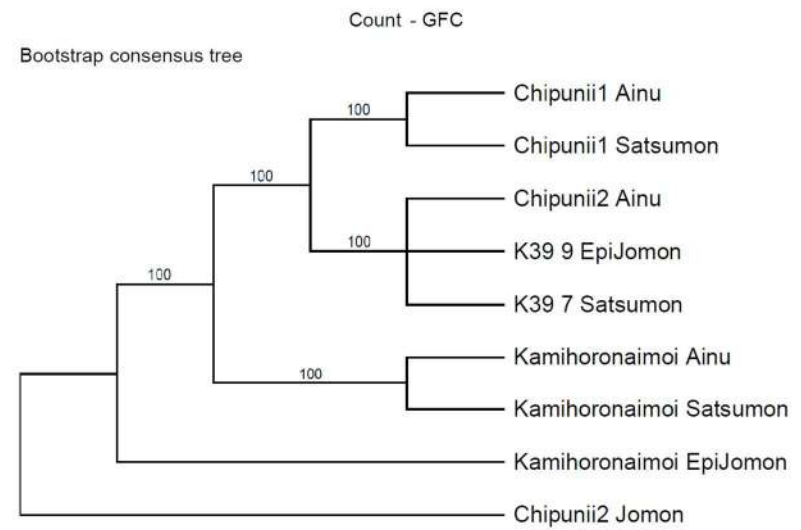
Figure 5. Bootstrap Cladograms of Weight and Count data coded with the GFC method.

In all cladograms analyzed (Figure 4), both the Chipunii 1 Ainu and Satsumon components and Chipunii 2 Ainu component are clustered close to one another. More specifically, the Chipunii 1 Ainu and Chipunii1 Satsumon components are paired in the Count cladogram, and in polytomies (groupings of multiple branches or taxa with no greater resolution to show further clade distinctions) with the Chipunii 2 Ainu component in the Weight cladogram. The K39 components are grouped together in polytomies in both cladograms. All three components (Epi-Jōmon, Satsumon, Ainu) from the Kamihoronaimoi site are also generally clustered together. It is clear that sites determine close associations on the cladograms rather than components, and that the differences in faunal assemblages likely follow geographic more than temporal lines.

The associations were produced due to similarities in proportions of each type of fauna. Count and weight data for each site component are presented in Tables 8 and 9. The site components in the tables are arranged from top to bottom according to how they are arranged on the cladograms. It is clear that the relative percentages of different fauna types, especially Salmonidae and Cervidae, influence cladogram construction. Within Weight data (Table 8), clade construction generally begins with the Chipunii 2 Jōmon component containing nearly 100% Cervidae. With each subsequent clade there is a step-wise increase in Fish and decrease in Land Mammals until the clade containing Ainu and Satsumon components at Chipunii 1, the Ainu component at Chipunii 2, the Epi-Jōmon component at K39-9, and the Satsumon component at K39-7 are composed almost entirely of Salmonidae. In the Count data, clades follow a similar pattern but specific families include variability of Cervidae (deer), Cyprinidae (carp and minnow),

Salmonidae, and Mollusca (Table 9). Clade construction begins with the Chipunii 2

Jōmon component that contains over 85% Cervidae. The next grouping includes all three

components of the Kamihoronaimoi site, which include relatively high proportions of

Cervidae, with an increase in fish including both Salmonidae and Cyprinidae. The next

clade contains high proportions of Salmonidae and lower proportions of Cervidae, though

both components of the Chipunii 1 site form their own clade based on the addition of

Mollusca. Overall, similarities and differences, even in terms of distance between

percentages, determine how site components are grouped on the cladograms.

Table 8. Total bone weights in grams (and percentages of total assemblage) per specific faunal type for each site component. This data corresponds to Cladogram a in Figure 1. The Other category includes weight and percentages totaled from the Arthropoda, Aves, Cetacea, Clupeinae, Mammalia S-M size class, and Marine mammal faunal categories.

WEIGHT DATA	Faunal Type				
Site-Component	Cyprinidae	Cervidae	Mammalia (M-L)	Salmonidae	Other
Chipunii 1 - Ainu	0 (0%)	0 (0%)	0 (0%)	20.13 (100%)	0 (0%)
Chipunii 2 - Ainu	1.1 (2.52%)	0 (0%)	0 (0%)	42.5 (97.48%)	0 (0%)
K39-9 - Epi-Jōmon	0.011 (0.03%)	0 (0%)	0.656 (1.63%)	39.4998 (98.17%)	0.07 (0.17%)
Chipunii 1 - Satsumon	0 (0%)	0 (0%)	0 (0%)	0.45 (100%)	0 (0%)
K39-7 - Satsumon	0.05 (0.06%)	1.18 (01.32%)	0 (0%)	85.89 (96.39%)	1.99 (2.23%)
Kamihoronaimoi - Epi-Jōmon	0.15 (10%)	0.05 (03.33%)	0 (0%)	1.3 (86.67%)	0 (0%)
Kamihoronaimoi - Ainu	0.8 (11.85%)	1.1 (16.30%)	0 (0%)	4.85 (71.85%)	0 (0%)
Kamihoronaimoi - Satsumon	5.7 (15.04%)	26.9 (70.98%)	0 (0%)	5.3 (13.98%)	0 (0%)

TABLE 8 (CONTINUED)

WEIGHT DATA	Faunal Type				
Site-Component	Cyprinidae	Cervidae	Mammalia (M-L)	Salmonidae	Other
Chipunii 2 - Jōmon	0 (0%)	65.67 (99.85%)	0 (0%)	0.1 (0.15%)	0 (0%)

Table 9. Total bone counts (and percentages of total assemblage) per faunal type for each site component. This data corresponds to Cladogram b in Figure 1.

COUNT DATA	Faunal Type				
Site-Component	Mollusca	Cyprinidae	Cervidae	Mammalia (S)	Salmonidae
Chipunii 1 - Ainu	476 (27.48%)	0 (0%)	0 (0%)	3 (0.17%)	1253 (72.34%)
Chipunii 1 - Satsumon	39 (0.5%)	0 (0%)	0 (0%)	0 (0%)	39 (0.5%)
Chipunii 2 - Ainu	0 (0%)	36 (0.04%)	0 (0%)	0 (0%)	97752 (99.96%)
K39-9 - Epi-Jōmon	0 (0%)	3 (2.48%)	0 (0%)	0 (0%)	118 (97.52%)
K39-7 - Satsumon	0 (0%)	7 (1.49%)	0 (0%)	0 (0%)	463 (98.51%)
Kamihoronaimoi - Satsumon	0 (0%)	300 (40.16%)	266 (35.61%)	0 (0%)	181 (24.23%)
Kamihoronaimoi - Ainu	1 (0.20%)	129 (25.70%)	277 (55.18%)	0 (0%)	95 (18.92%)
Kamihoronaimoi - Epi-Jōmon	0 (0%)	12 (2.90%)	380 (91.79%)	0 (0%)	22 (5.31%)
Chipunii 2 - Jōmon	0 (0%)	0 (0%)	7 (87.5%)	0 (0%)	1 (12.5%)

For this analysis, cladistics was chosen due to an expectation that the site components would follow a temporal pattern and the resulting cladograms would show a strict evolutionary relationship over time between time periods represented as

components of different sites. When this proved not to be the case, with the cladograms showing instead trends based on similarity and difference between site components, statistical tests were performed to further explain the differences seen in the cladograms.

Statistical Analysis

Results of Chi-square and Spearman's ranked correlation coefficient analysis corroborate the scenario presented in the cladograms. Analyses were aimed at revealing whether differences could be seen overall by comparing fauna remains by site and by component.

Chi-Square Analyses

Results of Chi-square analysis indicate the difference between the observed distribution and that expected from random variation was highly significant across faunal categories by sites and components (Table 10). Adjusted residuals are within the bounds of a normal distribution if between -1.96 and 1.96 (a 5% significance level). Overall, Chipunii 1, Chipunii 2, and Kamihoronaimoi diverge from expected distribution (Table 10). Distributions vary based on amounts of fish to other types of animals. Specifically, it is the amount of Salmonidae against other types of fauna that is driving these relationships (Table 10). Chipunii 2 contains more Salmonidae than all other Specific types of fauna, as does Chipunii 1, though with more Mollusca and small Mammals, while Kamihoronaimoi has more Cervidae (deer) and Cyprinidae (carp and

minnow)(Table 10). It is clear that Salmonidae remains are more plentiful in the

Satsumon and especially the Ainu periods, and most in lowland sites (Chipunii and K39),

though not ever absent from the upland site (Kamihoronaimoi).

Table 10. Chi-square and adjusted analysis data for the Sites and Components dataset.

Sites		Faunal Frequency					Total
		Mollusc a	Cyprinid ae	Cervida e	Mammalia (S)	Salmonid ae	
Chipunii 1	Obs	515	0	0	3	1292	1810
	Exp	9.17	8.65	16.53	0.05	1775.6	
	Adj. Res.	**168.98**	**-2.98**	**-4.12**	**12.88**	**-84.00**	
Chipunii 2	Obs	0	36	7	0	97753	97796
	Exp	495.41	467.57	892.89	2.88	95937.24	
	Adj. Res.	**-111.71**	**-100.16**	**-149.11**	**-8.50**	**212.88**	
K39-9	Obs	0	3	0	0	118	121
	Exp	0.61	0.6	1.1	0	118.7	
	Adj. Res.	**-0.79**	**3.19**	**-1.06**	**-0.06**	**-0.47**	
K39-7	Obs	0	7	0	0	463	470
	Exp	2.38	2.25	4.29	0.01	461.07	
	Adj. Res.	**-1.55**	**3.19**	**-2.09**	**-0.12**	**0.65**	
Kamihoronaim oi	Obs	1	441.00	923.00	0.00	298.00	1663
	Exp	8.42	7.95	15.18	0.05	1631.39	
	Adj. Res.	**-2.59**	**155.22**	**235.98**	**-0.22**	**-241.44**	
Total		19	487	930	3	99924	10186 0
* X²= 109024.26; df=20; p-value=0.00							

TABLE 10 (CONTINUED)

Components		Fauna Frequency					Total
		Mollusca	Cyprinidae	Cervidae	Mammalia (S)	Salmonidae	
Ainu	Obs	477	165	277	3	99100	100022
	Exp	506.69	478.21	913.22	2.95	98120.93	
	Adj. Res.	**-9.84**	**-106.88**	**-157.45**	**0.23**	**168.78**	

Components		Fauna Frequency					Total
		Mollusca	Cyprinidae	Cervidae	Mammalia (S)	Salmonidae	
Satsumon	Obs	39	307	266	0	683	1295
	Exp	6.56	6.19	11.82	0.04	1270.39	
	Adj. Res.	**12.78**	**121.96**	**74.74**	**-0.20**	**-120.30**	
Epi-Jōmon	Obs	0	15	380	0	140	535
	Exp	2.71	2.56	4.89	0.02	524.83	
	Adj. Res.	**-1.65**	**7.82**	**170.96**	**-0.13**	**-122.17**	
Jōmon	Obs	0	0	7	0	1	8
	Exp	0.04	0.04	0.07	0	7.85	
	Adj. Res.	**-0.20**	**-0.20**	**25.75**	**-0.02**	**-17.73**	
Total		516	487	930	3	99924	101860
* X^2= 50985.92; df=12; p-value=0.00							

Turning to Component data, all components diverge from expected distributions again in terms of Salmonidae and Cervidae. Ainu has more Salmonidae and less Cervidae than expected, while all other components have more Cervidae and less Salmonidae than expected (Table 10). Jōmon, Epi-Jōmon, and Satsumon again have less Salmonidae and

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more Cervidae than expected, while the opposite is true for Ainu components (Table 10). The other types of fish, Cyprinidae (carp and minnow), however, diverge significantly between Satsumon (more than expected) and Ainu (less than expected) components (Table 10).

The trends present in the adjusted residuals analyses of the datasets follow those seen in the cladistic analysis. For components, there is less variation, with the Satsumon, Epi-Jōmon, and Jōmon periods showing similar distributions and the Ainu period decidedly different. This reveals an overall similarity between most components, which would provide a smaller impact in groupings. It is noteworthy that the Ainu period, and not the outgroup Jōmon period, is the odd component. For sites, there is a high degree of variability, but with certain associations evident even in the adjusted residuals distributions. The K39 sites are similar, and they are grouped together in the cladograms. Also, Chipunii 1 is similar to Chipunii 2, with some important differences in Salmonidae and Mollusca, in their distributions, and we see them close but not paired together in the cladograms. Kamihoronaimoi is distinct in its distribution, and its components are often grouped together in the cladograms. So far, the chi-squared and adjusted residual analyses of the Count data reinforce the concept that sites, because they vary more, predict site component clustering more than the more similar components do.

Turning specifically to the Salmonidae data (Table 10), it is clear that the Jōmon and Epi-Jōmon are similarly low in Salmonidae remains, and the amount of remains in the Satsumon, though higher than normal, were dwarfed by those found in the Ainu period. The Chipunii sites are similar in that they are the only sites to have large amounts of Salmonidae remains, while all others did not. The values driving the results of this

analysis were two extremely large values, one from Chipunii 2 Ainu and the other from Chipunii 1 Ainu. This clearly shows that the inland lowland site assemblages from the Ainu period have a heavy emphasis on Salmonidae, though not much other information about other sites or times is available from this analysis.

<center>*Spearman's Rank Correlation Coefficient Analysis*</center>

The Spearman's rank correlation coefficients were compared against critical values for a two-tailed test at a significance level of 0.05, which, given 10 faunal types (and therefore 10 pairs of ranks compared), was 0.648 (Ebdon 1985:219). Any r_s values above 0.648 or below -0.648 are considered to show significant difference in distributions of faunal remains between the compared sites or components. Given the high number of tied ranks, especially the number of instances of absence of a given faunal type in the component or site, a correction for tied ranks was used (Ebdon 1985:101).

By Sites, r_s values ranged from -0.2945 to 1, with most between 0.4997 and 0.6265 (Table 11). Only the comparison of Kamihoronaimoi and Chipunii 2 were significantly correlated, and here, perfectly so at a r_s value of 1. This makes sense given that the rank distributions of each match perfectly with Cervidae (deer), Salmonidae, and Cyprinidae (carp and minnow) at the top (Table 12). These fauna are important at most of the other sites. Salmonidae is represented as either the most or second most abundant at all sites (Table 12). Cervidae was also highly ranked except at Chipunii 1 and K39-9. K39-7 and K39-9 sites were the only sites to contain several different types of fauna beyond Salmonidae, Cervidae, and Cyprinidae (Table 12). Most sites are similar, given

the high prevalence of Salmonidae, Cervidae, and Cyprinidae, as well as the exclusivity of any other faunal types to individual sites. The higher instance of deer than salmon use makes sense for inland sites, given the greater distance from the ocean and therefore more opportunity for salmon depletion downstream, but one inland site, Chipunii 1, only contains Salmonidae remains. Given the presence of Mollusca and small mammal remains from the count data, however, it may be more of a problem of complete record-keeping (the recording of bone counts but not weights) rather than an indication of sole dependence on Salmon at Chipunii 1.

Table 11. Spearman's rank correlation coefficient (r_s) values for comparisons of site and component weight distributions. Significant correlation marked in bold.

SITES - SPECIFIC - Spearman's r				
	Chipunii1	Chipunii2	K39-9	K39-7
Chipunii2	0.499745	-	-	-
K39-9	0.557086	0.151132	-	-
K39-7	0.528681	0.626544	-0.29452	-
Kamihoronaimoi	0.499745	**1**	0.151132	0.626544
TIMES - SPECIFIC - Spearman's r				
	Ainu	Satsumon	Epi-Jōmon	
Satsumon	**0.807714**	-	-	
Epi-Jōmon	**0.656187**	0.184063	-	
Jōmon	**0.723691**	**0.691786**	**0.862044**	

Table 12. Weights and ranks of faunal remains by type per site and component.

	Weight in g (Rank)								
	SITES					COMPONENTS			
Faunal Types	Chipunii 1	Chipunii 2	K39-9	K39-7	Kamihoronaimoi	Ainu	Satsumon	Epi-Jōmon	Jōmon
Arthropoda	0 (5)	0 (4)	0.012 (7)	0 (2)	0 (4)	0 (4)	0 (1.5)	0.012 (5)	0 (4.5)
Aves	0 (5)	0 (4)	0 (3)	0.84 (8)	0 (4)	0 (4)	0.84 (6)	0 (2.5)	0 (4.5)
Cetacea	0 (5)	0 (4)	0 (3)	0.63 (7)	0 (4)	0 (4)	0.63 (5)	0 (2.5)	0 (4.5)
Clupeinae	0 (5)	0 (4)	0 (3)	0.01 (4)	0 (4)	0 (4)	0.01 (3)	0 (2.5)	0 (4.5)
Cyprinidae	0 (5)	1.1 (8)	0.011 (6)	0.05 (5)	6.65 (8)	1.9 (9)	5.75 (8)	0.161 (8)	0 (4.5)
Cervidae	0 (5)	65.67 (10)	0 (3)	1.18 (9)	28.05 (10)	1.1 (8)	28.08 (9)	0.05 (6)	65.67 (10)
Mammalia (M-L size class)	0 (5)	0 (4)	1.961 (9)	0 (2)	0 (4)	0 (4)	1.305 (7)	0.66 (9)	0 (4.5)
Mammalia (S-M size class)	0 (5)	0 (4)	0 (3)	0.51 (6)	0 (4)	0 (4)	0.51 (4)	0 (2.5)	0 (4.5)
Marine mammal	0 (5)	0 (4)	0.058 (8)	0 (2)	0 (4)	0 (4)	0 (1.5)	0.058 (7)	0 (4.5)
Salmonidae	20.58 (10)	42.6 (9)	39.50 (10)	85.89 (10)	11.45 (9)	67.48 (10)	91.64 (10)	40.80 (10)	0.1 (9)

By Component, r_s values ranged from 0.535 to 0.862, with significant positive correlation between all components except Satsumon and Epi-Jōmon (Table 11). The significant correlations arise from the high level of Salmonidae (highest in all components except Jōmon), Cervidae, and Cyprinidae (Table 12). In this distribution, all sites include Salmonidae and Cervidae as highly ranked fauna types (Table 12). Likewise, Cyprinidae has a high rank in all except the Jōmon components (Table 12). This follows the general trend seen in the Site data. Other types of fauna are found only in the Epi-Jōmon or Satsumon components, which makes sense given that these faunal types are also exclusive to the K39-9 and K39-7 sites. The low correlation between Satsumon and Epi-Jōmon is due to high levels of exclusive faunal types in each of these components, though they both show high levels of Salmonidae, Cervidae, and Cyprinidae.

Overall, similar trends emerged in from both datasets. There were high levels of Salmonidae, Cervidae, and Cyprinidae throughout the sites and components. The K-39 sites showed more variety than did the others, with faunal types exclusive to K39-9 Epi-Jōmon, K39-9 Satsumon, and K39-7 Satsumon (Table 12). The Chipunii sites are somewhat dissimilar, even though both include an Ainu component. Kamihoronaimoi fits the overall trend, only containing Salmonidae, Cervidae, and Cyprinidae. This pattern for the sites fits with that seen in the chi-square adjusted residuals. Likewise, rankings by components are similar, especially when accounting for the exclusive faunal types. This

also matches the chi square residuals, though the ranked weight data (Table 12) shows difference only really in the exclusive fauna and order of the three high-level fauna types, while the chi-square residuals show broad similarity except for in the Ainu period in the General data and the Jōmon in the Specific data.

Discussion

Ancestry by time was not the driving force behind the formation of the cladograms. Instead, geographic location may be more of a predictor (Figures 4 and 6). The Ainu and Satsumon components of Chipunii 1 are always paired or in a polytomy together. The Satsumon and Epi-Jōmon components of the K39 sites are also either paired, in a polytomy, or adjacent to each other in a clade. The Ainu component of Chipunii 2 is always close to Chipunii 1 and K39 components that are represented by different components (Figure 4). The Kamihoronaimoi components were also generally grouped together. In all of these cases, the components are mixed. Therefore, the site takes precedence over component in cladogram construction.

In the statistical analyses, component distributions showed less variability and more similarity than site distributions did. These results make sense in the context of the trends seen in the cladograms. If there is little variation, or high similarity, across components, except for in the Jōmon outgroup (which we already know will be different in important ways), the component will not affect the grouping much, while the sites, which show less similarity, will show up in grouping trends, given that the cladistic

association is based changes present in the data. This all supports the concept that site is a more important predictor of evolutionary associations than component in this sample. Using these statistical analyses based only on broad categories such as components or by sites alone would not have revealed the complex associations that the cladograms illustrated. However, the data associated with the construction of cladograms (as in Table 8 and 9) must also be explored to understand which character state changes are driving cladogram construction and, ultimately, significant archaeological patterns.

Furthermore, this study has illuminated the fact that weight and count faunal data provide very similar results. Only the top-most clades of all cladograms differed by count and weight data (Figure 6). Similar conclusions were also drawn between the Chi-square analysis based on bone count data and Spearman's r coefficient based on bone weight data. This may indicate that both types of data are equally reliable in this context, and so either type of data may be incorporated in future studies.
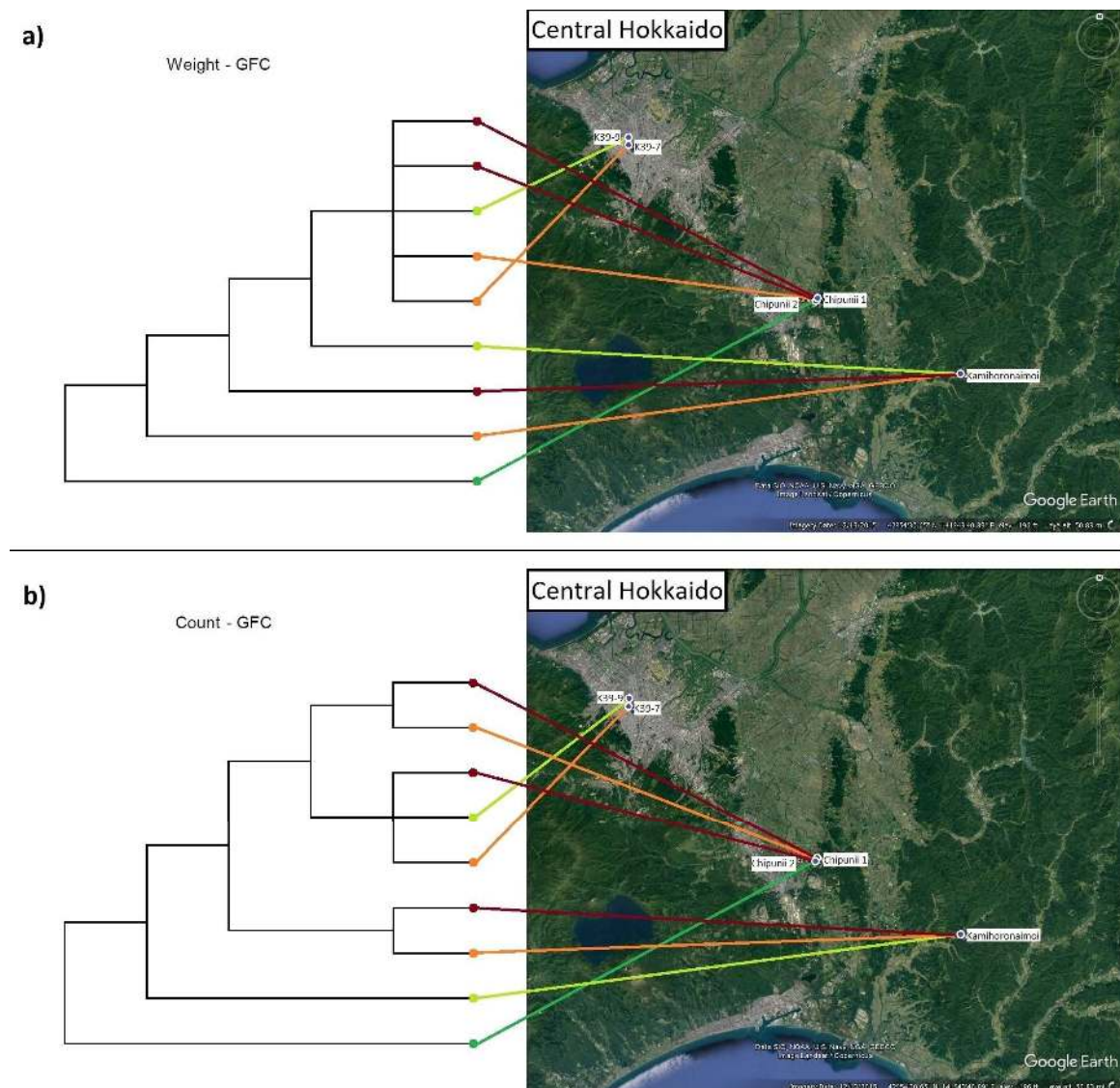
Figure 6. Cladograms mapped on sites in Central Hokkaido for Weight data (a) and Count data (b). Dark red=Ainu component, Orange=Satsumon component, Light Green= Epi-Jōmon component, and Green=Jōmon component.

What does this mean for the archaeology of the study area? While there may have been a shift towards increased fish exploitation over time (as suggested by the chi-square analysis and percentages by component), trends of animal usage in Central Hokkaido

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differed more across space than across time (Figures 6). Certain localities, perhaps with certain characteristics, are associated with certain proportions of different types of animals. Given the importance of environment in creating selective pressures which affect cultural adaptation, action, and evolutions (Dunnell 1978:62; Kassa & McCutcheon 2016:81; Lyman & O'Brien 1998:621), it would make sense that these different locations provided different constraints or opportunities which led to different trends across space but relative stability across time. Importantly, salmon and deer were important resources exploited especially from the Epi-Jōmon into the Ainu periods.

This makes sense given the environmental differences between the associated sites in the cladograms (Figures 6). The Chipunii sites are very close together in an inland lowland riverine environment, at an elevation of 22-25.99 m above sea level. Except for the Jōmon layer in Chipunii 2, the assemblages at these sites are almost entirely made up of Salmonidae remains. The Kamihoronaimoi site is an inland upland riverine site, at an elevation of 58 m above sea level. This site's assemblages are mostly made up of Cervidae remains, though there are some significant fish remains as well. The K39 sites are close together in a coastal riverine environment, at an elevation of 13.99 m above sea level. The assemblages from these sites are made up mostly of Salmonidae, though there are some land mammal remains. The fact that these are all riverine sites is in harmony with established understanding of habitation patterns during all of these components (Ōnishi 2014), but the differences in elevation and distance from the coast are potentially seen in the faunal assemblages. We see this, not only in the distinction between upland and lowland in terms of deer taking precedence in the former and fish in the latter, but

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additional differences between coastal and inland lowland sites, especially visible in the Count data analyses, further shows that geographical location predicts animal use more than time period. It is notable, however, that throughout all time periods sedentary hunter-gatherers located their settlements near rivers where they exploited similar resources. This suggests that the pattern of the interplay of the *kotan*, traditional Ainu settlements on the "riverside wetlands on the floodplain," (Aoyama 2012; Ōnishi 2014:285), and *iwor*, the term for the rest of the world outside of the village, particularly the river, sea, and mountains, where resources were gathered and brought in for use in the kotan, may possibly be extended through prehistory as well (Aoyama 2012).

While similarity across components and difference across environments cannot be definitive either way, it seems that either the same groups of people, with cultural changes other than animal use, inhabited the same areas over time, or different groups of people moved in and adopted similar animal use patterns. In any case, it seems that environmental pressures were significant enough to maintain stable animal use patterns across time in these different locations. It could also be that, given the characteristics of these different sites, they were exploited seasonally by people either genetically related or culturally convergent. However, for the Ainu period, at least, ethnographic accounts show little seasonality (Ohnuki-Tierney 1976). While there is likely to be some seasonality in terms of what resources were exploited at what time of the year, it seems that there was no corresponding movement of habitation, and even in terms of animal use, it seems that a mainstay of Ainu harvest was salmon, which was available for most of the year (Ohnuki-Tierney 1976). The importance of fish to the Ainu, and particularly

salmon, seen in ethnography is borne out in the data from this study. What does not quite fit the data is the idea reported ethnographically that deer was a mainstay of Ainu diet, and possibly the main source of animal food (Ohnuki-Tierney 1976). This may, however, be due to different sample populations observed in ethnography and potential problems in using count and weight data in this study. For example, if Ainu populations were largely sedentary and upland populations were studied, it may be that deer would be inflated in importance, while our data, which only has one upland site, would not match. The Ainu component of the one upland site of Kamihoronaimoi does, however, favor deer (55% of the Count data) above all other types of fauna (Table 13). Also, given the weaknesses of only using bone or bone fragment count or weight, perhaps a more detailed study of available meat weight would be more useful in determining how Ainu diet would have been broken up (Lyman 1979). While extrapolating such patterns further into the past may be of questionable validity without further evidence, it seems that seasonality may not have had much impact on animal use in these periods and locations.

Table 13. Total bone counts (and percentages of total assemblage) per faunal type for each site components in the sample.

COUNT DATA	Faunal Type				
Site Component	**Mollusca**	**Cyprinidae**	**Cervidae**	**Mammalia (S size class)**	**Salmonidae**
Chipunii 1 - Ainu	476 (27.48%)	0 (0%)	0 (0%)	3 (0.17%)	1253 (72.34%)
Chipunii 2 - Ainu	0 (0%)	36 (0.04%)	0 (0%)	0 (0%)	97752 (99.96%)
Kamihoronaimoi - Ainu	1 (0.20%)	129 (25.70%)	277 (55.18%)	0 (0%)	95 (18.92%)
K39-9 - Epi-Jōmon	0 (0%)	3 (2.48%)	0 (0%)	0 (0%)	118 (97.52%)
Kamihoronaimoi - Epi-Jōmon	0 (0%)	12 (2.90%)	380 (91.79%)	0 (0%)	22 (5.31%)
Chipunii 2 - Jōmon	0 (0%)	0 (0%)	7 (87.5%)	0 (0%)	1 (12.5%)
Chipunii 1 - Satsumon	39 (0.5%)	0 (0%)	0 (0%)	0 (0%)	39 (0.5%)
K39-7 - Satsumon	0 (0%)	7 (1.49%)	0 (0%)	0 (0%)	463 (98.51%)
Kamihoronaimoi - Satsumon	0 (0%)	300 (40.16%)	266 (35.61%)	0 (0%)	181 (24.23%)

Conclusions

This study indicates importance in site location in determining animal usage, as well as continuity in animal usage over time. It may be that this pattern shows some level of cultural continuity across time at these locations, or that the local environment

pressured convergence. While time is an important factor in evolution, this cladistic analysis did not show relationships primarily based on temporal sequence. Instead, geographic location was a stronger factor. Even with a clear trend toward increased fish, and particularly salmon, use over time, culminating in high levels in the Satsumon and especially Ainu, the cladistic relationships and overall differences in faunal type distributions in assemblages from different components of sites showed associations based more on location. As such, this analysis is not to be treated as a chart of cultural evolution from a root ancestor as much as an analysis of similarity across space-time, showing in this case how important geography and associated natural resource bases is to animal usage. Perhaps a more inclusive cladistic analysis including other cultural markers, such as house shape or hearth placement, could help to establish evolutionary relationships between component traditions.

Also, while this study shows the importance of environment in a culture's animal use, it is drawn from a small sample of all available data, especially the Jōmon component. Additional studies incorporating more data from more sites should help to clarify and round out any observations made here. Until then, it seems clear that, at least in terms of faunal use, there are clearly traceable cultural similarities between the Ainu and the Satsumon, Epi-Jōmon, and Jōmon cultures that preceded them in Hokkaido.

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