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## Where was the PaleoAmerind standstill?

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### ABSTRACT

After many years and much effort searching Beringia for the ancestors of Amerinds (PaleoAmerinds), archaeologists are empty-handed. Beringia certainly was the pathway for later peoples (Na-Dene and Inuit), but there is no persuasive evidence of an archaeological culture in Beringia during the last glacial maximum (LGM) when archaeologists expect an early, pre-Clovis culture group and biologists detect a long period of isolation—the “standstill.” In this article, I show that archaeologists defer to biologists for proof of concept, and biologists use that deference to support their outmoded model that Beringia, or even greater Siberia, was the sole route by which all Native American people entered the hemisphere. I propose that the standstill took place in the Americas and that the pathway taken by PaleoAmerinds was by the Pacific Ocean, possibly from Southeast Asia.

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### 1. Problem: location of the PaleoAmerind standstill

More than 30 years ago, [Greenberg et al. \(1986\)](#) modeled most indigenous people of the Americas as descendants of an early migrating population—PaleoAmerinds. This founding population was later followed by groups of biologically and linguistically distinct Na-Dene speakers and then Eskimo/Aleut speakers. I use this model as a starting point because its bio-linguistic structure continues to be repeated by biologists ([Anderson, 2010:322](#); [Mulligan and Kitchen, 2013](#); [Mulligan et al., 2008](#); [Raghavan et al., 2014](#); [Reich et al., 2012](#); [Schurr, 2004](#); [Tamm et al., 2007](#)). According to these biological studies, the earliest PaleoAmerind group must have been isolated from their direct ancestors, and others, anywhere from 26,000 to 18,000 cal yr BP, essentially during the LGM. This isolation period is referred to as the “Beringian standstill,” or the “Beringian Incubation Model” ([Mulligan et al., 2008](#); [Raghavan et al., 2015](#); [Skoglund et al., 2015](#); [Tamm et al., 2007](#); [Wang et al., 2007](#)). I argue that this standstill did not take place in western or eastern Beringia, submerged or terrestrially, or even in greater Siberia to the west, but rather that it happened in the Americas where multiple environments ideal for population isolation existed at those times.

In this article, PaleoAmerinds are modeled as a single cohesive social group, or multiple connected social groups, who arrived in the Americas sometime before 14,300 cal yr BP. They may have

been forced to out-migrate due to environmental conditions or cultural conflict. Assuming they arrived in the Americas in sufficient numbers to survive and propagate, the earliest people retained their ancestral Asian mtDNA haplotypes and began their genetic divergence during this isolation period. Theoretically, these people should have left archaeological residue or other traces (e.g., skeletal or biomolecular), or both, of their propagation from one or more landfalls. Na-Dene and Eskimo/Aleut-speaking social groups produced archaeological material culture correlates in Beringia *Dyuktai/Denali* and *Paleo-Eskimo* that track their sequential propagations ([Carlson, 1996](#); [Dumond, 1980](#); [Raghavan et al., 2014](#)). However, there is no archaeological correlate for PaleoAmerinds in Beringia, eastern or western, during the LGM as expected by current models, nor is there any such correlate in greater northeast Siberia east of 130° longitude or north of 55° latitude ([Dumond, 2011](#); [Hoffecker, 2011](#); [Kuzmin and Keates, 2005](#); [Vasil'ev, 2011](#)). Nor is there convincing evidence in unglaciated eastern Beringia (i.e., Alaska and Yukon) where a refugium is proposed as the locus of the standstill isolation ([Llamas et al., 2016](#)). There may be evidence on the now-inundated Pleistocene continental shelf, as [Anderson and colleagues \(2013\)](#) have proposed, but there is no evidence of propagation of such a population into the continent. If PaleoAmerinds trekked across the Bering land bridge, then there should be a non-Na-Dene/non-Eskimo/Aleut archaeological culture during the LGM, with evidence of propagation and adaptation southward into North America after 14,300 cal yr BP, and sites in South America should post-date sites to the north.

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The earliest known site in eastern Beringia with Dyuktai/Denali diagnostics is Swan Point, dating to about 14,000 cal yr BP (Holmes, 2011; Potter et al., this volume). The diagnostics include microblades produced from bifacial cores by the Siberian Dyuktai Yubetsu technique. This earliest assemblage at Swan Point is preceded by several sites south of the ice sheets, but especially Amerind mtDNA from coprolites at Paisley Caves, Oregon (Jenkins, 2007); an *in situ* biface and debitage from Page-Ladson, Florida (Halligan et al., 2016); and marine sea weed from a hearth at Monte Verde, Chile (Dillehay et al., 2008). Acceptance of these three sites, what I use as unequivocal examples, and assuming survival and propagation of those people, requires human entry into the Americas sometime before 14,300 cal yr BP, south of the ice sheets, possibly by means of a Pacific Ocean crossing (Faught, 2008).

Most researchers reject the probability, or even possibility, of peopling of the Western Hemisphere via late Pleistocene ocean crossings, especially across the Pacific. One reviewer of this article called the idea “far-fetched.” Meltzer called its crossing “... very doubtful” (Meltzer, 2009 pp. 195). Madsen (2015 pp. 229) discounts it out of hand, and Anderson (2010) and Auerbach (2007) do not consider it at all. The Pacific is daunting. I understand and accept the arduous nature of crossing wide expanses of water, as well as the requirement that the migrants must have included quite a large number of people. Nevertheless, this alternative warrants consideration.

## 2. Short background: Its Hrdlicka's Fault

The way and tempo of the peopling of the Americas has confounded European scholars since the sixteenth century (Huddleston, 1967). They reviewed the books of the times and found several potential sources, the most popular being the Lost Tribes of Israel and Plato's narrative about Atlantis. Nevertheless, by the mid-nineteenth century, it was accepted that the New World was peopled from Asia via the Bering Strait. This connecting route into the Western Hemisphere gained dominance in the twentieth century with the particular influence of Ales Hrdlicka and his many influential publications, including *Shovel-Shaped Teeth* (1920), *The Origin and Antiquity of American Indians* (1925), *The Race and Antiquity of the American Indian* (1926), *Melanesians and Australians and the Peopling of America* (1935), and *The Problem of Man's Antiquity in America* (1942). Alternative migration theories were dismissed because of his authoritative power as Physical Anthropologist at the Smithsonian Institution. According to Hrdlicka, native people came late, and they came by way of Beringia. W.W. Howells, one of Hrdlicka's students, put it succinctly:

“Where did the Indians come from? ... Of course they came from Asia, where their racial cousins are, and they came over the Bering Strait. They could have come from nowhere else. They did not originate in the New World. They did not come from Europe, nor from Africa. And they assuredly did not cross the Pacific Ocean itself; the Indians, nowhere good boatmen, cannot be imagined, in a long-ago era before seaworthy boats had been invented, as having made a series of voyages which were too much for the mighty Polynesians ...” (Howells, 1945 pp. 259)

Hrdlicka held that northeast Asia was the only place from which Native Americans originated and the Bering Land Bridge was the only possible route based on the phenotypic similarities among peoples living in Northeast Asia, Alaska, and the northwest coast of North America. The concept of walking across the Bering Strait was confirmed when archaeologist Nelson (1937) reported similarities between microblade core and blade production in northeast Asia

and Alaska. Identification of differences among the various Beringian lithic assemblages resulted in the terms *Dyuktai* by Mochanov for those located at sites in northeast Asia and *Denali* by West for those located at sites in Alaska (Carlson, 1996; Slobodin, 2011).

Hrdlicka would have dismissed any attempt to model a potential Pacific Ocean crossing, as shown by his interpretation of robust dolichocephalic morphologies in some Amerinds:

“The only conclusion that appears possible in view of all the facts is that the hypothesis of either Melanesian or Australian, and even that of recognizable Polynesian, presence on the American continent is not demonstrable, nor even probable, that the dolichocephalic cranium is not extraneous but represents one of the several cranial types of both the Indian and the Eskimo; and that whatever cultural or other resemblances may appear to exist between the pre-Columbian Americas and the South Seas must have other explanations than any material accession of the peoples of the latter parts of the world to the American populations” (Hrdlicka, 1935 pp. 48–49).

Nevertheless, Neves et al. (2007) and Powell (2005 pp. 198), among others, continue to find craniofacial similarities between some PaleoAmerinds and Polynesians (Auerbach, 2007 pp. 40). However, craniofacial morphologies are the result of a complex interplay of genetic and environmental conditions that can include climate, diet, activity, and other factors, in addition to representing ancestor-descendant relationships (Green, 2012). The point is that Hrdlicka's opinions and influence remain, to this day, as subtext for much of the discipline of anthropology and biology.

Consequently, most archaeologists start with Hrdlicka's supposition that the Bering Land Bridge was the sole pathway for the peopling of the Americas. Whether appealing to osteological or genomic evidence, specialists assume that the earliest New World inhabitants trekked across the Bering Strait from northeast Asia. However, none have identified an LGM archaeological culture in northeast Asia and all appeal to biological references to fill the gap (Goebel et al., 2008; Graf et al., 2015; Hoffecker et al., 2016; Meltzer, 2009; Pitblado, 2011). The geneticists consider *a priori* a Beringian (or greater Siberian) route for all indigenous Americans, but in particular the hypothetical PaleoAmerind standstill group. A few make this clear in their title (Fagundes et al., 2008a; Perego et al., 2009; Scott et al., 2016; Tamm et al., 2007), many in the abstract (Achilli et al., 2013; Fagundes et al., 2008b; Reich et al., 2012), and most in the first paragraph or two. Wang et al. (2007) stated as their research question, “... what records of the original colonization from Siberia are retained in Native American genetic variation?” Tamm et al. (2007) begin with, “Native Americans derive from a small number of Asian founders who likely arrived to the Americas via Beringia ...” More recently, Skoglund and Reich (2016) note, “The first unambiguous evidence of modern humans in the Americas ... was likely the consequence of migration from Beringia.” Madsen (2015) provides additional examples.

Paradoxically, some geneticists now cite the above-mentioned archaeological literature as if archaeology supports their models (Achilli et al., 2013; Fagundes et al., 2008a, 2008b; Perez et al., 2009; Tackney et al., 2015). Apparently they are unaware, or unconcerned, that archaeologists cannot identify an archaeological culture during the LGM in Beringia where it is needed. Researchers surely must recognize that a LGM archaeological culture in Beringia or Siberia is required to support either a terrestrial ice-free corridor (IFC) route or a Pacific coastal route into the Western Hemisphere (Anderson and Bissett, 2015; Erlandson and Braje, 2011).

This situation is a classic example of affirming the consequent (Dincauze, 1984) or, in this case, beginning with the conclusion. One result of beginning with the conclusion is that it narrows the choice of out-groups when seeking biological relationships. Comparing samples from only northeast Asia or eastern Siberia

ignores the possibility of migrations from other geographic regions. For instance, Reich et al. (2012 pp. 371) show Amerinds as phylogenetically related to groups in both Southeast Asia and Siberia. They focus, however, only on the Siberians (Khanty, Ket, Selkup, Yukaghir, Tundra Nentsi, Nganasan, Dolgan, Evenki, Yakut, Buryat, Mongolian, Altaian, and Tuvian) and ignore the southern Asians (Yi, Han, Cambodia, and Japanese) (Reich et al., 2012 pp. 371). If Native Americans are related to either group, then their late Pleistocene ancestors could have come from Southeast Asia instead.

Beginning with the conclusion also influences models of population expansion and propagation that employ spatial algorithms with different initial population numbers, varying birth rates, and environmental variables, but always with eastern Beringia as the point of origin and always the direction of propagation from north-to-south (e.g., Hamilton and Buchanan, 2010; Lanata et al., 2008; Steele, 2009; Steele et al., 1998; Surovell, 2003). Anderson and Gilliam's (2000) least-cost pathway is a useful approach, but their propagation direction remains north-to-south, assuming Beringian origins. What if the models started in Central or South America? How different would the resulting patterns or estimated peopling chronology be then?

### 3. An absence of archaeological evidence: No pre-Dyuktai in Beringia

One late Pleistocene archaeological culture that propagates from Northeast Asia into Alaska is Dyuktai, a Siberian chipped-stone technology dominated by Yubetsu microblade production (Slobodin, 2011) and Denali represents the assumed descendant technological tradition in Alaska. The producers of Dyuktai/Denali assemblages have both pre-Clovis and Clovis-contemporary ages (Faught, 2008; Goebel and Buvit, 2011; Graf et al., 2015) and microblade-making archaeological cultures propagated along the northwest coast later in the early Holocene (Chatters, 2010). These later microblade assemblages have been inferred by regional specialists to have been made by the ancestors of Na-Dene ethnic groups: the Tlingit, Haida, and Athabaskans (Carlson, 1996; Fedje et al., 2011; Meltzer, 2009 pp. 193–194).

However, in western Beringia and greater Siberia, there is a lack of evidence for people adapting to the cold LGM environments between ca. 26,000 cal yr BP and 18,000 cal yr BP, where the pre-Clovis PaleoAmerind standstill archaeological culture is expected (Kuzmin and Keates, 2016). Goebel et al. (2008 pp. 1500, Fig. 3) illustrate this lacuna with a dashed line and query marks beginning with Yana RHS at ca. 32,000 cal yr BP in north central Siberia (Pitulko et al., 2004, 2016) and skipping 18,000 years to Swan Point, Alaska, at 14,000 cal yr BP (Goebel et al., 2008; Holmes, 2011). While the archaeological records at Yana RHS and Nikita Lake, east of Yana RHS, demonstrate the human capacity to adapt to high Arctic latitudes before and after the LGM, they do not show occupation during when the standstill is supposed to be occurring biologically (Kuzmin and Keates, 2016; Pitulko et al., 2016).

Goebel (2011), Graf et al. (2015), and others have characterized Nenana technology in Alaska as a possible non-Denali, Clovis progenitor archaeological culture (Goebel et al., 1991; Pitulko et al., 2016). The Nenana assemblages contain blades and bifaces without microblades, along with distinctive, thinned but not fluted, trianguloid Chindadn bifaces (Goebel et al., 1991). The recent report of Chindadn points at Nikita Lake at 13,800–13,600 cal yr BP (Pitulko et al., 2016) and at the Dry Creek site slightly later (Graf et al., 2015) link the groups living in these two widely separated regions, but they have not been found to be early enough to represent the expected Beringian LGM standstill population.

Graf et al. (2015 pp. 690) state that Beringia has more well-dated pre-Clovis sites than any other region in the Americas, but the

ancestor/descendant relationships are not convincing and the tally of pre-Clovis sites in the Western hemisphere is growing. Regardless, there is no other archaeological culture in eastern or western Beringia that reflects an isolated, pre-Clovis, pre-Dyuktai, pre-Nenana, LGM standstill population propagating into the Western hemisphere (*sensu* Greenberg et al., 1986; Mulligan et al., 2008; Tamm et al., 2007; etc.).

### 4. PaleoAmerinds on the landscape before 14,300 cal yr BP

My interpretation of the relevant archaeological data is that Northeast Asian culture groups were contemporaries and possibly interacting with social groups already on the landscape to the south as they migrated into Alaska (Faught, 2008). The Beringians are indicated by the earliest Denali site, Swan Point, at ca. 14,200 cal yr BP (Holmes, 2011), and PaleoAmerinds are indicated by Paisley Caves in Oregon at ca. 14,200 cal yr BP (Jenkins et al., 2012, 2013); Page-Ladson in Florida at ca. 14,300 cal yr BP (Dunbar, 2006; Halligan et al., 2016); and Monte Verde in Chile at ca. 14,300 cal yr BP (Dillehay, 2000, 2002; Dillehay et al., 2008; Meltzer et al., 1997). PaleoAmerinds are indicated at Paisley Caves because two of five Amerind mtDNA haplotypes, A2 and B2, are recognized in the earliest coprolites (Gilbert et al., 2008). It is important in this regard to see critiques by Poinar et al. (2009), Fiedel (2014), and the additional research and evidence presented by Jenkins et al. (2013). Sistiaga et al. (2014) have recently shown that one of the supposed human coprolites is more likely a herbivore mammal specimen and not human. Clearly, more sampling is called for. Regardless, A2 and B2 are Amerind and B2 is immediately Southeast Asian related, not Northeast Asian as I describe below, and A haplogroups are present in southern latitudes of Asia as well.

These three sites are not the only pre-Clovis sites I could list. Additional pre-Clovis sites include Buttermilk Creek in Texas, estimated at 15,000 cal yr BP (Waters et al., 2011), and Miles Point and Parsons Island in Maryland around 20,500 cal yr BP (Collins et al., 2013; Lowery et al., 2010). Gonzalez et al. (2014) have reviewed evidence for pre-Clovis in the Basin of Mexico; Aceituno et al. (2013) and Maggard (2015) have reported sites in Colombia; and Lourdeau (2015) and Roosevelt et al. (1996) have reported sites in Brazil. It will remain to be seen which of these continue to demonstrate trustworthy examples. Conceivably, there should be more pre-Clovis-aged sites closer to the PaleoAmerind landfall(s) (Surovell, 2003).

On the other hand, PaleoAmerind propagation may be indicated by the numbers of early archaeological culture groups forming as populations survived and grew in numbers. Historically, Clovis was considered the singular archaeological progenitor from which all later archaeological cultures arose (Barton et al., 2004; Fiedel, 2000; Goebel et al., 2008), but shortly before the onset of the Younger Dryas (YD) climatic episode, ca. 13,000 cal yr BP, there were multiple, distinct lithic tool traditions contemporaneous with, but not related to, Clovis (Madsen, 2015:218–223). Two were in North America (Denali and Western Stemmed Point [Beck and Jones, 2010; Davis and Schweger, 2004; Faught, 2008; Graf et al., 2015]) and possibly as many as four in South America (Abriense, Itaparica, Paijan, and fluted point related Magellan [Borrero, 2015; Dillehay, 2000; Lourdeau, 2015; Maggard, 2015]).

### 5. The search for PaleoAmerind roots

If there is no PaleoAmerind archaeological culture in Beringia during the LGM, and Asiatic-derived PaleoAmerinds were already in the Americas when late Pleistocene Dyuktai/Denali artifact-making people propagated into Alaska, then pre-Clovis PaleoAmerinds must have gotten to the Western Hemisphere from

somewhere other than Beringia. I have argued previously (Faught, 2008) that this was necessarily by an ocean route(s), and others have listed the same as possibilities (Anderson, 2010; Erlandson and Braje, 2011; Surovell, 2003 pp. 580). But if not Beringia, where was the Asiatic PaleoAmerind homeland and why did they leave it?

One motivation might have been global climate change. After 40,000 cal yr BP, during marine isotope stage (MIS) 3, global warming and deglaciation caused significant sea level rise. Glaciation and sea level regressions returned during the LGM in MIS 2 until ca. 18,000 cal yr BP when sea levels rose again during MIS 1, especially with meltwater pulse 1a (MWP 1a) that occurred ca. 14,400 cal yr BP (Blanchon, 2011; Lambeck et al., 2014; Simms et al., 2009). These sea level fluctuations and landscape changes at the end of the Pleistocene may have caused demographic shifts (Anderson and Bissett, 2015; Anderson et al., 2013; Hill et al., 2006; Lambeck et al., 2014).

The extent of Asian and Southeast Asian fluctuating continental shelf areas during these times around Indonesia, China, and the East Asian coastline is substantial, especially around Japan, Okinawa, and along the Japanese (Ryukyu) Archipelago. Lithic traditions in Southeast Asia during the late Pleistocene include pebble and flake technologies, as well as biface technologies (Bellwood, 1997 pp. 171–190; Fujita et al., 2016). The point is that there is plenty of evidence for humans in East Asia before and during the LGM, and people could have been displaced from these more southerly latitudes. But could people have made it across the Pacific Ocean from there in the late Pleistocene? I believe so. Maritime adaptations and sea-faring capacity in Oceania is well documented before the LGM in Australia, especially after 35 kya in Melanesia, Okinawa, and the Japanese Archipelago (Erlandson, 2002 pp. 69; Erlandson and Braje, 2011; Fujita et al., 2016). While these examples do not prove that a viable population sailed thousands of kilometers across the Pacific to the Americas, they do suggest that people had the capacity to do so (Wyatt, 2004).

Where people from Asia most likely crossed the Pacific and reached land in the Americas depends on late Pleistocene wind gyres and ocean currents (Montenegro et al., 2006a). Today, there is a southern route that has taken historic and modern sailors from Australia to southern South America, and it is called the “roaring 40’s.” While it is not gentle, it is a plausible route. However, New Zealand is in the way, and people didn’t settle there until about 1250 CE. A direct crossing at the Equator is possible, but the distance is about 17,000 km. The shortest, most likely route, at about 9000 km, is via the Kuroshio Current that flows into the North Pacific Current from southern Japan across to the northwest coast of North America (Callaghan, 2003). This route might account for the presence of the Western Stemmed tradition (Beck and Jones, 2010; Callaghan, 2003; Erlandson et al., 2011; Erlandson and Braje, 2011; Jenkins, 2007).

On the other hand, Montenegro et al. (2006a) have concluded that drift crossings in tropical latitudes would have been more likely in the late Pleistocene than today due to higher sea surface temperatures and fewer storms, especially during the LGM, and that ocean currents would have been depressed toward the Equator, away from glacial margins. These conditions would have made arrivals in southern North America or Central America, or even South America, possible. At this time, I can only speculate about the particulars of the voyage process, including the sorts of vessels used and necessary water and food supplies (Wyatt, 2004).

How can we identify the place where PaleoAmerinds lived during their presumed standstill? Assuming the ancestral PaleoAmerind entity was a cohesive social group (or set of related groups), there should be more pre-Clovis sites near landfall(s), and there should be evidence of social group propagation from those

places (Surovell, 2003). South America is of interest because of numerous alleged pre-Clovis aged sites, including confirmed, proposed, and equivocal examples (Aceituno et al., 2013; Boeda et al., 2014; Dillehay, 2000, 2002; Maggard, 2015). In addition, there are Clovis-aged, but distinct, lithic traditions in South America that imply social group divergence by the time Clovis-like Magellan (fishtail) assemblages occur (Borrero, 2015; Dillehay, 2000; Faught, 2008; Madsen, 2015; Miotti et al., 2003).

Late Pleistocene-Early Holocene settlers in some tropical regions of the Americas (i.e., Mesoamerica, Colombia, Amazonia) were involved in early plant domestication, indicating familiarity with and adaptation to those environments. This is not expected of Arctic-adapted PaleoAmerinds coming from Beringia, but is not inconsistent with Southeast Asian ancestry (Aceituno and Loaiza, 2015; Piperno, 2011; Roosevelt et al., 1996). In addition, there are early village settlements (Dillehay et al., 2003; Stothert et al., 2003) and early social complexity in South America (Pozorski and Pozorski, 2008). These sites imply longevity of occupation and social group propagation. However, are biological data in accord with Asians coming from more southerly latitudes in the late Pleistocene?

## 6. Importance of biology: could PaleoAmerinds have come from Southeast Asia?

Regardless of where the standstill took place, biological characteristics and relationships are fundamental to reconstruct the peopling of the Western Hemisphere (Anderson, 2010; Greenberg et al., 1986; Scott et al., 2016; Skoglund and Reich, 2016; Zegura, 1985). One avenue of research includes postcranial body dimensions that have been used to identify adaptations to Arctic environments as would be expected for standstill Beringians, but the results are equivocal and contradicting. Specific characteristics identified include rounder and larger crania, wider faces, narrower nasal apertures, longer torsos, wider bodies, shorter limbs, and higher body masses when compared to other populations (Auerbach, 2007:88; Jantz et al., 2010). Auerbach (2007) studied physical characteristics of 2749 pre-Contact adult skeletons, mostly from North America, and concluded that the earliest of these ( $n = 2$ ) had wider bodies, as did all samples from all time periods, but he noted that limb dimensions were more indicative of sea-faring populations (Auerbach, 2007:452), and other indices were more consistent with adaptations to temperate climates (Auerbach, 2007:467). Indeed, Jantz et al. (2010:292) reported “... larger, wider bodies are found in warmer temperatures, the opposite of ecological expectations ...” and “... (n)ative American limb proportions are more consistent with those of ancestors originating in the lower to mid-latitudes of East and Southeast Asia.”

A different source of evidence comes from discovery of intestinal parasites (helminths), specifically *Ancylostoma duodenale* and *Necator americanus* in some North and South American human remains. These hookworm species are endemic to tropical and subtropical climates, but cannot survive Arctic conditions. To complete the lifecycle, the larvae must pass from the intestines to soils with temperatures between 17 °C (62.6 °F) and 35 °C (95 °F) for eggs to evolve into infective larvae before they return back to the host. They perish at temperatures lower than 14 °C (57.2 °F; Araújo et al., 2008). Montenegro et al. (2006b:194) state that the minimal survival conditions for these parasites are at least five days with temperatures no lower than 17 °C (62.6 °F), which excludes Beringia as a viable habitat. They report the presence of parasites in South America (northern Brazil, Peru, and Chile) as well as in North America, but so far the oldest samples are about 7000 cal yr BP. However, it remains possible that the helminths were already present in the New World, as parasites of other mammals, before

humans arrived, or these parasites could have been introduced by trans-Pacific drifters through time. Even Hrdlicka (1926:9) noted the potentials for (male) drifters.

Less equivocal evidence for a trans-Pacific migration from, and possibly to, more tropical latitudes would include detection of direct biological relationships with Southeast Asians, or an explanation of how gene pools may have migrated and changed during the Holocene, or both. For instance, craniofacial analyses continue to indicate that some ancient Americans exhibit morphological similarities with Southeast Asians, Australians, or even Africans, rather than with Northeast Asians (Brace et al., 2001; Hubbe et al., 2015; Neves et al., 2003, 2007; Powell, 2005). The problem is that these morphological similarities can have environmental as well as phylogenetic explanations (Green, 2012).

On the other hand, molecular analyses of NRY (paternal) and mtDNA (maternal) genetic material result in unequivocal relationships, as well as phylogenies useful for reconstructing direct ancestries. I will not discuss in detail the relevant NRY data, because Karmin et al. (2015) have shown that the phylogeny of NRY (paternal) DNA exhibits numerous bottlenecks over the millennia, and there are fewer samples than those of mtDNA (Karmin et al., 2015; Zegura et al., 2004, Table 1). I focus instead on mtDNA molecules because they have experienced fewer bottlenecks, they are the data cited as evidence for the standstill, and there is a phylogeny that can be accessed by non-expert genealogical researchers (van Oven and Kayser, 2009:Build 17). Whether modern or ancient, there are five main Amerind mtDNA haplogroups which stem from three macro-haplogroups that migrated out of Africa around 70,000 cal yr BP. Haplogroups C and D mutated from Haplogroup M, haplogroups A and X mutated from haplogroup N, as did haplotype B, but it cleaved from haplogroup R (a sister group to A and X). Macaulay et al. (2005) model the dispersal of these early humans along the tropical coasts of the Indian Ocean to Southeast Asia and Australasia, where the majority of descendant clades of these macro-haplogroups reside today.

To be more Amerind-specific, A- and B-related haplotypes are well represented in people of Southeast Asia (*sensu lato*) including people from Southern China, Japan, Melanesia, and Indonesia (Jinam et al., 2015; Mona et al., 2009; Peng et al., 2011; Tabbada et al., 2010). In fact, the clade that is closest phylogenetically to Amerind B<sub>2</sub> is haplotype B<sub>4b1</sub>, and this clade has been found in Austronesian speakers of eastern Indonesia, Filipinos, aborigines of Taiwan and Hainan, as well as people in southern China (Kumar et al., 2011; Peng et al., 2011; Mona et al., 2009; Tabbada et al., 2010). The distribution of these B haplotypes provides strong support for a Pacific crossing, followed by the A haplotypes that are frequent in Japan and East Asia.

Peng et al. (2011) have identified haplogroups A, B, C, and D in Taiwan, mainland southern China, and Vietnam, but in general, haplogroups C and D are not as well represented in Southeast Asia—in modern populations—but instead are dominant in northern latitudes as expected by the Beringian model. Regardless,

these modern distributions have post-Pleistocene coalescence estimates (Derenko et al., 2007, 2010; Lee et al., 2016; Zhong et al., 2011), and the archaeology indicates replacement of Dyuktai by the Sumnagin archaeological culture, as well as later migrations in the Holocene (Slobodin, 2011:106). This evidence suggests that those haplotypes may have come from more southerly latitudes where they may have been present earlier in the late Pleistocene.

The distribution of X haplotypes is more perplexing. Haplogroup X is one of 11 nodes of N, equivalent in phylogenetic position (age) with A haplotypes, and older (higher up the phylogeny) than the B haplogroup in Southeast Asia. The modern distribution of these haplotypes is in Turkey, Central Asia, Western Europe, and the Western Hemisphere (Oppenheimer et al., 2014; Raff and Bolnick, 2015). No X haplotypes have yet been found in Northeast or Southeast Asia. In the Western Hemisphere, X haplotypes (of the North American-specific X2a clade) are mostly found in modern Algonquian-speaking populations around the Great Lakes (Brown et al., 1998; Dornelles et al., 2005; Oppenheimer et al., 2014; Raff et al., 2011). A basal variant of X2a has been identified in Kennewick Man from Washington (Rasmussen et al., 2015).

Regardless, all of the earliest ancient DNA (aDNA) samples analyzed so far from North America nest are within one of five Amerind phylogenies, consistent with those remains as progeny of PaleoAmerinds, the standstill group. The oldest aDNA samples analyzed at the time of this manuscript are listed in Table 1. Regarding haplogroup D4h3, found in the Anzick and On Your Knees Cave individuals in Table 1, Perego et al. (2009:5) note: “the fact that it is very rare in North America and mainly found in South America with deep variation needs some explanation.” They consider this evidence of coastal migration from Beringia (Bodner et al., 2012), and I consider it as evidence the standstill occurred in the Western Hemisphere.

## 7. Numbers of migrating groups and holocene landfalls

While the preceding discussion has been focused on the three wave model of Greenberg et al. (1986) with a singular standstill PaleoAmerind social group, two recent publications, Raghavan et al. (2015) and Skoglund et al. (2015) present alternative interpretations. Both made comparisons using whole genomes and state of the art molecular analyses with Bayesian statistical algorithms. Skoglund et al. (2015) propose two migration streams for South and Central America, whereas Raghavan et al. (2015) propose a single founding group that includes Athabascan-speaking Na-Dene as Amerinds (Raghavan et al., 2015:aab3884-4).

Biologically, speakers of Na-Dene (i.e., Haida, Tlingit, and Athabascans) share genes with both Northeast Asians and Amerinds. These shared genetic characteristics can be indicating ancestor/descendant relationships or reticulation between them. In some cases, biological relationships between Na-Dene and Amerinds (particularly Athabascan and Algonquin speakers) have been shown to be the result of Holocene reticulation rather than

**Table 1**  
Earliest human remains with ages and ancient DNA determinations.

Sample	Age	mtDNA	NRY	Citation
Paisley Caves	14.3 kya	A2, B2		Gilbert et al., 2008
Hoyo Negro	12.9 kya	D1		Chatters et al., 2014
Anzick	12.7 kya	D4h3a	Q-L54* (xM3)	Rasmussen et al., 2014
Upward Sun	11.3 kya	C1b and B2		Potter et al., 2014; Tackney et al., 2015
On Your Knees Cave	11.2 kya	D4h3a	Q-M3	Kemp et al., 2007
Wizards Beach	11.3 kya	C		Kaestle, 1998; Kaestle and Smith, 2001
Kennewick	9.3 kya	X2a	Q-M3	Rasmussen et al., 2015
Hour Glass Cave	9.1 kya	B		Stone and Stoneking, 1998

common descent (Schanfield, 1992; Szathmary, 1985:84–85). On the other hand, recent analyses suggest that Athapaskans are essentially Amerinds genetically, with relatively minor (about 15 percent) admixture with PaleoEskimos (i.e., Saqqaq) (Flegontov et al., 2016). This admixture would have occurred ca. 6000–5000 cal yr BP, and this date might suggest Athapaskan cultural and linguistic derivation from Siberian Neolithic groups. Nevertheless, the mother of the On Your Knees Cave individual (*Shuka Kaa*) was clearly Amerind (mtDNA haplotype D4h3a), as were the mothers of the two Upward Sun children (mtDNA haplotypes B2 and C1b) (Tackney et al., 2015). I see these examples as indicating interactions in the Holocene between Denali/Na-Dene and Amerinds.

Both Skoglund et al. (2015) and Raghavan et al. (2015) detect a phylogenetic relationship of some Amerinds in Amazonia and the Aleutian Islands with Australasian/Melanesians that might point to Southeast Asia as the geographic source of some PaleoAmerinds, in support of my thesis in this article. In addition, Skoglund and Reich (2016) have incorporated additional samples of native North Americans, and they report that Algonquian speakers in northern North America sample may represent a separate migration wave. This population includes people with the X2a haplogroup. It actually could be that PaleoAmerinds may have evolved from multiple social groups of distinct origins that came into biological and social interactions from earliest times in the Western Hemisphere.

Another variable to consider is that human navigational capabilities increased throughout the Holocene, adding to the likelihood of genes being transferred via watercraft across the Pacific. In southern California, there is compelling evidence after ca. 1100 CE for interactions with Polynesian seafarers (Jones and Klar, 2005; Jones et al., 2002). These data include planktonic boats (*kamul*) and related linguistic elements indicating cross-cultural learning of techniques and vocabulary. The presence of mtDNA M haplotypes in two mid-Holocene burials from British Columbia (Malhi et al., 2007) may indicate the presence in northern North America of Asian-derived haplotypes that disappeared before contact. This could indicate a contact with Asia after the original PaleoAmerind migration.

A final example of genetic data that may indicate pre-Columbian contact is reported by Roewer et al. (2013). They identified a cluster of YSNP (paternal) lineages of C-M217 (C3\*) in coastal South America. This male lineage is virtually absent from North and Central Americas, but occurs with frequency in Asia. They conclude that this C3\* haplotype arrived in South America no more than 6000 years ago, perhaps via a trans-Pacific route.

## 8. Conclusion

The assumption that PaleoAmerinds inhabited most of the Americas before Na-Dene and Eskimo/Aleut people entered has underpinned most biological studies. However, the standstill or incubation model that places the ancestral PaleoAmerinds in Beringia for thousands of years before Dyuktai/Denali is not supported by the evidence. There is sparse archaeological evidence in Beringia or greater Siberia during the LGM, the place and time of the putative pre-Clovis PaleoAmerind standstill. Sites in North and South Americas are older than the oldest known sites in Alaska, indicating that people were already living south of the ice sheets when the first Dyuktai artifact-making people arrived. Even though many scientists begin with the *a priori* conclusion that Beringia is the only viable pathway for migration, it has not been demonstrated archaeologically or biologically.

In this paper, I have modeled PaleoAmerinds as a cohesive social group (or related groups) out-migrating due to environmental motivations in the late Pleistocene. I propose that they arrived in

sufficient numbers to survive and propagate. Their arrival and standstill isolation occurred either along the west coast of southern North America, Central America, or perhaps South America via a Pacific crossing by one or more groups of people. The human capacity for navigation and the ocean currents, wind gyres, and other environmental conditions necessary for long-distance ocean travel would have been necessary for such an early entry into the Americas. Although the model is inferential and speculative, it may be useful in directing future research. If we accept pre-14,300 cal yr BP sites south of the ice sheets, then we must search for alternatives to Beringia as the sole pathway to the hemisphere.

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