

# MEGAFUNA, MAN AND PATHOGENS: INTERNATIONAL TRAVEL IN THE PLEISTOCENE

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This conference is the outcome of a ten-year legal battle between religious fundamentalism and our right of scientific inquiry. What should have been a simple legal action to cause a government agency to follow its own rules quickly developed into an extended confrontation between specialized faith-based groups and many scientists. This decade long legal action would become known as the Kennewick Man case.<sup>1</sup> At risk were the analyses and interpretations of ancient sites and ancient human remains, both in North America and elsewhere.

Even though the Kennewick Man case was decided in favor of scientific inquiry, there are still paleo-American remains at serious risk of burial without ever being studied. Another ancient individual, this time in Nevada, is currently being targeted for burial without further examination by scholars.<sup>2</sup> Like Kennewick Man, the Nevada individual exhibits attributes that argue strongly against any relationship to modern American Indian groups (Owsley and Jantz, 2005:292). Notably, the two ancient individuals do not appear to have a biological relationship to each other. Instead, they seem to be from very different population groups.

The right of scientific study is an issue with global ramifications. The fundamentalist movement is nearly universal, and growing in strength. In the press just weeks ago was a situation that was literally out of Africa. An influential bishop instructed his followers to boycott the exhibition of a 1.6 million year old human skeleton. Authorities were warned that the specimen was at serious risk, as violence had been suggested if the exhibition was not withdrawn.<sup>3</sup> What sad irony that the first hominids were from Africa, yet the study of ancient man is now being boycotted there. A major reason for this conference is to test the boundaries of what we know, or think we know. This extends from considering analytically the “truths” learned in the classroom or delivered to us by the media, to an assessment of the degree to which we are currently able to investigate our subjects. What are the limits of study for each discipline at this time? Are we maximizing the analytical potential of the types of laboratory studies that are currently available to us? Which types of questions and tests are valid, and which are invalid? What types of answers can we actually expect from science, and which results should not be considered to be completely accurate? And, perhaps most importantly,

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<sup>1</sup> Original case 96-1481-JE; going through the courts, and ending as 367 F. 3d 864 (9<sup>th</sup> Circuit).

<sup>2</sup> Case number CV-N-04-466-LRH (RAM)

<sup>3</sup> See <http://www.cnn.com/2007/WORLD/africa/02/06/kenya.fossil.ap/index.html>

what questions have we not asked? What questions, if they were asked, would yield additional information? Further, what types of data recovery will be attainable in the reasonably near future? All of these concerns were raised during preparation of the Kennewick Man case, when a full understanding of what science could and could not tell us had the potential to define the direction of that case, and the probable future of archaeology.

I would like to propose that we pay particular attention to four specific areas of research, all of which are relevant to both megafauna and ancient human populations in North America. These same issues are important to our understanding and interpretation of traveling populations in other parts of the world. This paper, therefore, will focus upon: (1) early migrations, (2) extinction models, (3) replacement populations and (4) biological affinity. In addition, recent geologic and oceanographic data will be considered, in an effort to more accurately develop alternative models.

### Migrations

In considering the migrations of both megafauna and humans, a primary question is whether these events were ever simultaneous. Did megafauna and humans ever actually share the same routes? Or, was there a separation in time and therefore in accessible landforms? Geologic studies have confirmed that during multiple periods, land bridges were not accessible, due to either inundation by water or extensive ice coverage (Bryson and DeWall, 2007; Lange, 2003:17).

The research by investigators of very different disciplines suggests that when the physical evidence is examined, most of the models are wrong. Dates provided by paleontologists for the entry or exit of many species tend to precede human contact, often by thousands to millions of years. Paleoclimate models and the examination of core contents from land bridge areas define periods during which food resources would not have been sufficient to sustain herds of grazing or browsing animals (Grayson, 1993:50; Bryson and DeWall, 2007). Thus, how might continents have been populated during periods when terrestrial routes do not seem to have been accessible?

Examples of problematic migrations include the arrival into North America of two very different South American species. These are the ground sloth and the “terror” bird, both now extinct. The ground sloth, in any of its many forms, does not appear to have been aquatic, and there is obviously nothing in the fossil record to suggest that it had the capability of flight. Yet it arrived before the Panamanian land bridge would have been accessible.<sup>4</sup> Another unexplained arrival is the avian species, *Titanis*. This flightless, > 3 meters tall, predaceous bird, without webbed feet, arrived in North America approximately 5 million years ago.<sup>5</sup> Remains of this species have been identified at multiple North American sites, from Texas to Florida. The examination of multiple specimens eliminates the problem of incorrect speciation due to the misidentification

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<sup>4</sup> The puzzling arrival of the smaller sloths, of the family *Megalonychidae*, are discussed briefly by Lange (2002:19, 20 and 75).

<sup>5</sup> Some estimates for the arrival of this bird into North America extend to 8 mya. See Lange (2002:17-18) and multiple news articles for the first quarter of 2007.

of a single bone. Like the sloth, this bird arrived from South America, with no known route of travel.

How did these and other non-aquatic species arrive from South America, when their migrations occurred at least two million years before the Panamanian Land Bridge became accessible? The only hypotheses thus far seem to be limited to difficult options, such as these species utilizing floating mats of vegetation as their primary method of travel.

The eventual emergence of the Panamanian Land Bridge would have allowed for movement into newly accessible lands, increasing contact between animal populations from both the north and the south. But prior to terrestrial access to this geologic feature, arrivals into North America occurred that we are unable to explain. All we know is that species that were not maritime adapted came and went, and they did so in the absence of humans. It was still too early for human entry into the Americas.

The next area of interest is the northern migration route across the Bering Strait and into North America. Despite the lack of recognition by all but paleontologists, the Bering Land Bridge would actually have been a two-way corridor (Martin and Klein, 1984; Lange, 2002:20; Orr and Orr, 1999). When this landform was accessible, animals traveled east to west, and west to east. A successful pedestrian crossing of the north Pacific route, however, would have been exceedingly demanding. A number of challenging variables would have existed to the north that would not have been factors to the south.

The northern means of access required timing and Arctic adaptation. The fossil record indicates that multiple migrations occurred over time, with most land mammals traveling millennia before humans crossed into North America.

As was true for the animals, a human entry into North America via the Bering Land Bridge would have been treacherous, when it was possible at all. If migrating people were not Arctic adapted, they would not have survived long enough to adapt. They would have arrived without the necessary clothing, and their subsistence strategies would not have been adequate for survival in the harsh Arctic environment. If they were already Arctic adapted, they would have developed successful subsistence strategies. They would also most probably be a maritime economy, living primarily upon fish, shellfish, marine mammals and the occasional terrestrial mammal. They would have had boats to access fish and marine mammals. Thus, even when the Land Bridge was accessible for pedestrian travel, why would they walk? Further, with boats, they would not have needed to haul as far north as the Bering Strait to travel west to east or east to west.

The paleoclimate models clearly define a late Pleistocene Arctic that was very cold and very dry (see figure 1). With high temperatures in the minus 20 degree range, and with almost no precipitation, this would have been a very unforgiving environment (Bryson and DeWall, 2007). If travelers were not Arctic adapted, they would not live long enough to develop survival strategies.

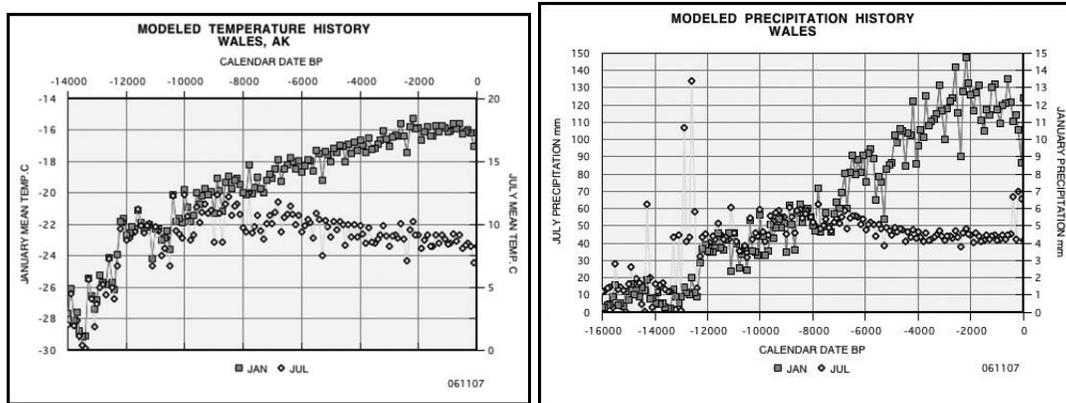


Figure 1. Excessively dry and cold conditions are suggested by these paleoclimate models. Courtesy of Dr. Reid Bryson, CCR.

Totally apart from Bryson and DeWall’s findings, other researchers have now stated that the ice field was not solid across the Bering expanse. Importantly, open water divided the landmasses of the east and west (Lange, 2002:47). This would have prevented a pedestrian crossing, of course, and it would have exposed the Aleutian Trench.<sup>6</sup> There would be no way for pedestrians to travel across this obstacle when it is exposed, and not ice covered.

The earliest site dates in North America also argue against a peopling of the continent by way of the Arctic. The oldest sites actually cluster well away from any north Pacific entry. Significantly, the oldest firmly dated sites thus far are in South America, and the eastern portion of North America. When a listing of ancient sites was compiled, the more recent examples proved to be located from California northward to Alaska (Stanford et. al., 2005; Time, 2006:11).

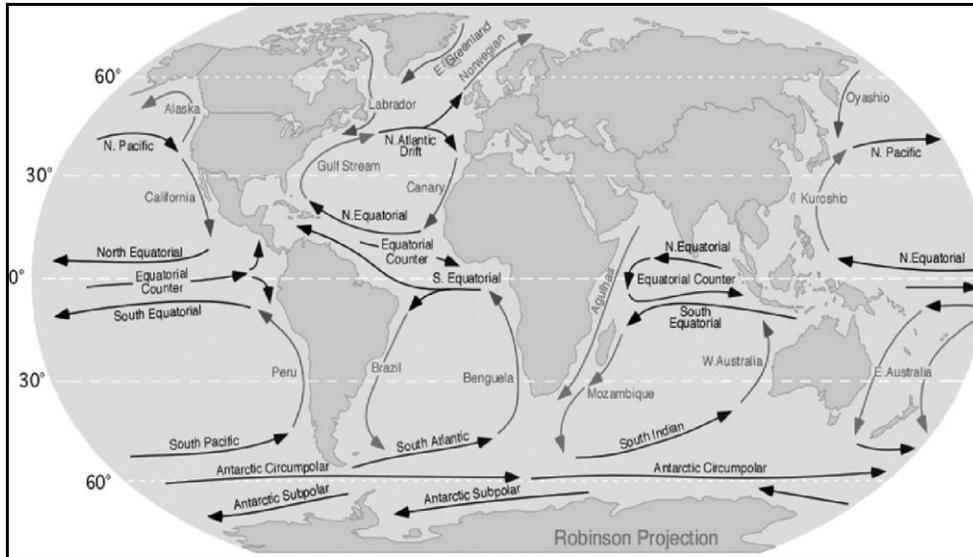
Boat travel is a logical option. For maritime adapted explorers or migrating people, crossing the north Pacific or the north Atlantic by boat may have been far easier than pedestrian travel. Ocean travel would have eliminated the need to traverse a landform forged by Arctic conditions. One suggested migratory route utilizes the near shore kelp beds of the Pacific in its model (Erlandson, 2006). This course would have allowed maritime people to avoid the most severe Arctic conditions, imposed by the open exposure of the Bering land bridge. It would also have eliminated the need to traverse the ocean, away from the shallows. But other travel options exist.

Prevailing currents allow for many travel scenarios (see figure 2). Significant studies of pathogens certainly argue for routes far south of the Bering Land Bridge (Jett, 2006; Montenegro et al, 2006). The data demonstrate that specific pathogens arrived in South America from the East, mutating after arrival, and thus defining a different primary origin than that of the New World. These pathogens are temperature sensitive enough that survival far north of their current localities

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<sup>6</sup> The depth of this feature allows submarines to travel under the ice from the North Pacific to the Arctic Ocean.

would not have been possible (Montenegro et.al:2006:193-199). A number of researchers are now using parasite biology and infection dynamics to track the movement of populations over time.<sup>7</sup>



*Figure 2. Travel from east to west, as well as from west to east, is possible merely by utilizing ocean currents.*

Extensive work by disciplines as diverse as oceanography and anthropology further substantiate models of transoceanic travel in prehistory. Physical experiments have validated circum-Pacific and direct island-to-mainland floatation, without the need of additional propulsion (Ebbesmeyer, 2006). Utilizing materials that were tracked in journeys across the ocean, routes from departure to landing were accurately plotted. Wind-current models illustrate the same findings.<sup>8</sup> Archaeological evidence also suggests trans-Pacific travel. The similarities between the ancient cultural materials of Japan, China and Ecuador provide a compelling argument for oceanic travel in prehistory (Meggers, 2006). There is a nearly overwhelming commonality between some very diverse elements of South American and Asian culture. Similarities are identifiable in sculpture, religious beliefs, writing, and the ritual importance of jadeite, cinnabar and nephrite (Xu, 2002:9). The number of parallels, and the diversity of subjects, suggests similarities that are beyond the limitations typically identified for independent invention. New World materials documented in ancient sites outside of South America also argue for transoceanic contact. The appearance of maize in prehistoric China and India is difficult to explain. The friezes of some ancient buildings in both lands support motifs

<sup>7</sup> See “Parasites, Paleoclimate, and the Peopling of the Americas” which synthesizes the work of six scientists, whose research on this topic is extensive.

<sup>8</sup> Refer to multiple research papers and computer models by Renee Hetherington.

that include maize (Thompson, 2006).<sup>9</sup> Cocaine, documented in the wrapping of an Egyptian mummy, caused the examination of subsequent wrapped specimens from that region. The majority of the specimens evidenced cocaine within the physical remains of the bodies (Jett 2002:297-313). Some areas that tested positive for the drug could not have been contaminated through prior examination, due to the location of the cocaine.

These prehistoric and protohistoric exchanges in material culture could not have occurred between such distant populations by walking from one area to another. Expanses of ocean needed to be crossed for transfer to occur, whether in the transmission of parasites or processed alkaloids such as cocaine.

It is puzzling that people of the 21<sup>st</sup> century embrace the concept of South Seas open ocean travel by the Polynesians and the Marquesans, yet the concept of boat travel by more northerly populations is still rejected. Most people concede that South Seas Islanders traveled to Rapa Nui, off the South American coast.<sup>10</sup> Yet, open ocean travel to or from the Americas by pre-industrialized populations is still viewed as impossible by many Westernized populations.<sup>11</sup>

Another issue that is often ignored is the existence of previously exposed landforms, other than in the north Pacific. During the last two glacial maximums, if not during all previous glacial maximums, pedestrian travelers could certainly have traversed such regions as the area between Japan and the mainland (see figure 3).<sup>12</sup> Contemporary maps demonstrate that significant shallow areas still exist to the south of this region, as well as elsewhere. Travel over extensive areas through shallow waters, during Pleistocene and now Holocene times, is obviously feasible.

One way to identify previously exposed landforms and areas of shallow water would be to extract cores. By analyzing the subsurface material from terrestrial and marine locations, many issues could be resolved. The sediment layers can obviously be dated, and defined by type. The structure of any soil strata can then be used to explain more about ancient landscapes, both in their formation and structure. As pollens are often transported over long distances by wind, they are not immediate indicators of vegetation. However, the prior identification of sediment types can aid in validating or refuting the existence of pollen indicated flora. Through even these basic lines of inquiry, it is possible to gain a comprehensive understanding of coastal and inland migration probabilities.

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<sup>9</sup> See publications by Gunnar Thompson, as well as various articles in *Pre-Columbiana*.

<sup>10</sup> Maritime researchers and other archaeologists in Hawaii and Polynesia, including Ben Finney, discriminate between the early populations of Polynesia and the Marquesas.

<sup>11</sup> Notably, the populations of China and northern India have narratives describing travel over vast expanses of ocean. Some of these accounts are written, and most describe the recipient populations. The transcripts of voyages to Fusang are one example. Some recipient populations, who came into contact with the maritime travelers, have oral histories about their arrivals. American Indian stories from some N.W. Coast Tribes retain such stories.

<sup>12</sup> See Chard (1974) and Jumsai (1988).

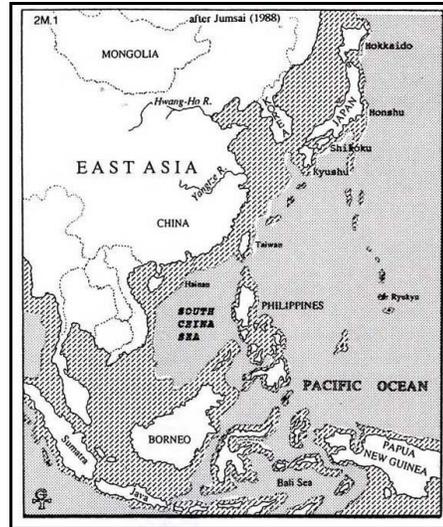


Figure 3. This map illustrates the areas between Japan and the mainland that were exposed during the major glacial periods of the Pleistocene. The shallow or exposed regions are depicted with diagonal lines. Chard's findings were nearly identical. Adapted from Jumsai (1988).

### Extinctions

Extinctions are one of the most discussed but least understood events in recent geologic history. While climate change was initially considered the sole cause of the megafaunal die-off, predation by humans was later suggested as a primary cause.<sup>13</sup> Some historic analogies, however, suggest very different reasons for the extinction events that plagued the terminal Pleistocene and early Holocene. Before these alternative explanations are explored, however, the two primary extinction models--which identify either humans or climate change-- should be addressed.

There are several significant arguments against climate change being the sole causal element in late Pleistocene extinctions (Stenger, 2004). These points are also lines of reason that suggest an adaptability of many species over time, rather than assuming the fragility of most megafauna. Three of these primary issues are:

- Many species survived full & little Ice Ages before going extinct, and some of these prior glacial events terminated very abruptly.
- Some species of megafauna have survived. Not all went extinct.
- The dietary requirements of some of the animals that did survive appear to be the same as the resource needs of the animals that went extinct.

One other issue should also be considered. In what ways would a slightly moister and warmer climate be negatively impacting, especially to grazing and browsing species?

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<sup>13</sup>See Martin's many publications, including "Quaternary Extinctions".

There is no question that climate change would have forced independent animal populations into diminishing or distant refugia. Further, numerous earlier migration models suggested that animals would have been trapped between the north-south trending mountain ranges in North America and the east-west trending ranges of Europe.<sup>14</sup> These theories of insurmountable barriers have now been proven invalid.

Although the responses below reflect the topography and herd responses of North America, most can be applied to other parts of the world, as well.

- Recent work has shown that many of the larger species were not trapped, especially in their movement east and west within North America.<sup>15</sup>
- If habitat was the only limiting factor, then species between the Rocky and Allegheny Mountains should have survived the longest, due to their access to substantially more available range. And this is not the case.
- It is probable that food resources were problematic in some areas. However, while the birthrate would have dropped as a response to this stressor, the result would have been fewer animals competing for limited resources. Unless the birthrate dropped precipitously throughout the continent, and globally, the megafauna should have been able to rebound.

Something else had to happen, beyond climate change and altering habitats. These species had survived both glacial and interglacial periods, and in many cases, they had thrived. What happened at the end of the Pleistocene that they were not able to endure?

The next most often stated reason for the late Pleistocene extinctions is human predation. Supposedly man, with his burgeoning population and vastly improved tool kit forced the megafauna into extinction. It is generally assumed that humans hunted non-predatory species. While this would have caused an imbalance in the predator to prey ratio that still needs to be explored, there is evidence that some late Pleistocene carnivores and omnivores may have gone extinct prior to their prey.<sup>16</sup>

Hunting by humans could certainly have put more stress upon animal populations, both directly and indirectly, within limited areas. But there are major problems associated with the hypothesis that humans were such a primary component in the die-offs that occurred. Further, whether this model of human induced extinctions is applied to the North American continent, or universally, the following issues remain.

Unless humans communicated globally, how were they able to exterminate selected species world wide, within a finite period?

Importantly, not all humans had improved tool kits, so many groups were hunting with old-style equipment. No geographic location has yet been identified where the human population was large enough in the Pleistocene to cause the extinction of selected species of megafauna through hunting.

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<sup>14</sup> North American features include the Coast Range, the Cascade Range, the Rocky Mountains, and the Appalachian Mountains. In Europe, ranges such as the Alps are regularly listed.

<sup>15</sup> Personal communication with Larry Agenbroad, Houston, 2/26/07.

<sup>16</sup> Available radiocarbon dates for the most recent die-offs of various species indicate that some predator species, such as the American Cheetah (*Acinonyx*) or short faced bear (*Arctodus*) occurred long before the last of their prey species went extinct. See Lange (2002:183).

The eradication of far too many mammalian groups occurred during the late Pleistocene for even a burgeoning hominid population to be identified as the primary destructive element. This is especially true in North America. When the geographic distribution and frequency of ancient human remains are studied, the results are surprising. The actual number of individuals is very low, and the locations they are associated with are not in close proximity to each other. Where are the human remains from these supposedly vast populations of hominid hunters? More directly stated, where are the bodies of all of these people?

Another problem with an anthropogenic model is the lack of actual kill sites. Where are the Pleistocene sites that evidence massive species devastation? At least within North America, kill sites are predominately of early to late Holocene age, and generally exclude Pleistocene megafauna. Instead, they will evidence the remains of Holocene species such as *Bison bison*, rather than *Bison latifrons* or even *Bison antiquus*.<sup>17</sup>

We do observe sites evidencing natural entrapment, most often without indications of a human component. These sites include caves--often with animals entering from above due to collapsed ceilings, limestone sinks, asphalt seeps, and so on. Only occasionally are there signs of a human presence. In these natural catchment environments, the level of human involvement is unclear. We are generally unable to tell whether the animals were herded into such an environment or whether humans located them only after entrapment occurred. In either case, indications of human activity are extremely rare. Butchering marks on Pleistocene remains, for example, are not commonly observed.

If man caused this many species to go extinct, where is the evidence of so much killing? Where are the bone yards, the bone beds of ground sloth, ancient horse, camel, or other now-extinct species? Even sites in Europe that evidence mammoth and mastodon butchering are very limited in the number of actual sites and the number of animals represented.

Another argument against human predation as the primary element in the extinction of Pleistocene megafauna is that many species went extinct long before contact with humans could have occurred. Earlier mammalian species of many types did not survive long enough to have been exposed to humans.<sup>18</sup> The fossil record of numerous other regions suggests a similar temporal separation between specific extinctions and the appearance of humans. Work by a number of researchers suggests that prior to five hundred years ago, the number of human associated extinctions was actually minimal or even non-existent (MacPhee, 2006).

An alternative explanation for species extinctions is needed. In putting aside old ideas and biases, and investigating contemporary analogies, an answer emerges. In then considering historic analogies, with documented histories spanning several centuries, the same causality is revealed. A feasible explanation for the Pleistocene and early Holocene extinctions is disease. Not a single disease, but multiple opportunistic pathogens, as exist in our environment today.

While some diseases are species specific, others have the capability of developing into pandemics, effecting multiple species and regions. All that is needed is the right

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<sup>17</sup>A transitional species of bison, as yet unnamed, appears at the early Holocene kill sites.

<sup>18</sup>Extinction in North America of the chalicothere and the rhinoceros, for example, occurred long before humans entered the continent (Orr and Orr, 1999; Martin and Klein, 1984).

combination of environmental conditions. Further, many pathogens exist within the soils or the host organisms, and need only the right circumstances to become highly destructive. In addition, we see individuals succumbing to diseases to which they were initially immune, once mutations are factored in.

If disease is to be considered as a viable solution to the question of extinctions, however, critical thinking is essential. How well does a disease model hold up when pathogens of early historic times are considered? Do modern diseases, singly or in combination, have the ability to cause extinctions? Are there examples where species terminations would have occurred without medical intervention? Are there examples where only isolation stopped an outbreak from spreading? The answer to all of these questions is yes.

The plagues of 14<sup>th</sup> and 15<sup>th</sup> C. Europe generally come first to mind, with one of the best-known being the bubonic plague. Pandemics, however, have occurred in many areas of the world. Those events are well documented, and need to be considered in the assessment of a hyperdisease model for extinction. Emerging diseases that have only been limited by their isolation, such as Ebola, should also be included for consideration.

The list of species threatening pathogens is long, and ever increasing. In a more intensive study than is provided here, potential pandemic pathogens should be grouped into specific categories for a better projection of transmission viability and potential fatality. Mutated pathogens and methods of transmission should be considered at some length.<sup>19</sup> Initial and secondary contact between previously isolated populations consistently results in a large number of casualties. A very well documented example involves primary and secondary contact between Euroamericans and American Indians of the Pacific Northwest. Using a time period of one hundred years, extending from 1770-1870, up to 98% of the American Indian population of the Pacific Northwest died from introduced diseases (Boyd 1985:69-70, 215-229). Thus, within 100 years of contact, an estimated 98% of the entire recipient population (Indians in the region) died from Old World diseases. In 1805, Lewis and Clark commented on the very high number of Indians in the Pacific Northwest. Within 65 years of that statement being made, local Tribal populations had nearly gone extinct. Only two per cent of the population survived the diseases that followed contact.

Interestingly, when skeletal materials that were several centuries older and from other regions were examined, those human remains evidenced several Old World diseases (Jett, 2006; Boyd, 1985:39) Thus, when the Euroamericans arrived in the Northwest, they reintroduced diseases, but in mutated form. The local inhabitants apparently had no immunity to the mutated form of these diseases.

Some pathogens that jump species are listed in the chart below (see Table 1). Included are examples where two or more species are involved. Insects are often common vectors, as are birds. Ross MacPhee has introduced the possibility of man and domesticated animals bringing hyperdisease into North America with them (2007). Even considering the few examples listed here, it becomes apparent that such a scenario is

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<sup>19</sup>Transmission concerns include aerosol, direct contact, and indirect contact through a mobile vector such as the deer tick. For information on these aspects of contagion, see Drexler (2002).

Pathogen	Primary Host & Vector	Recipient & Lethality
1918 Flu	Avifauna to arthropods or other avifauna	Humans Y
Bird Flu now	Avifauna to arthropods or avifauna (fatal to host)	Humans Y
Ebola	Unknown reservoir. Possibly primates to arthropods	Humans Y
Marburg	Primates to arthropods	Humans N
Aids	Primates	Humans Y
Plague(s)	Rodents to arthropods	Humans Y
Haunta	Deer & other artiodactyla to arthropods	Humans Y
Yellow Fever	Primates to arthropods	Humans Y
Lyme	Deer & other artiodactyla to arthropods	Humans N
TB	Mammals to arthropods	Humans Y
Malaria	Mammals to arthropods	Humans Y
Malaria– Avian	Birds to arthropods	Humans Y
Distemper	Mammals to arthropods	Humans Y

*Table 1. Examples of diseases that can migrate from one species to another are listed above. Lethality tends to occur in the recipient population, and not the host.*

entirely possible. An interesting side note is that ancient man seems to have gone extinct soon after the megafauna, at least in North America.

Species specific diseases include the examples listed below (see Table 2). There are many more, of course. But, by considering the diseases that affect only a single sector of the mammalian population, it is then easy to understand the extinction only of specific groups. The remaining animal population could remain unaffected or only marginally disrupted.

<b>CANINE GROUP</b>	<b>FELINE GROUP</b>	<b>EQUINE GROUP</b>
<b>Distemper</b>	<b>Feline Leukemia</b>	<b>Strangles</b>
<b>Canine Influenza</b>	<b>Feline HIV/AIDS</b>	<b>E.I.A. (Anemia)</b>
<b>Parvovirus</b>	<b>F.I.P.</b>	<b>Rhinopneumonitis</b>
<b>Hepatitis</b>	<b>Feline Herpes</b>	<b>Encephalitis</b>
<b>Coronavirus</b>	<b>Calicivirus</b>	<b>Equine piroplasmosis</b>

*Table 2. Some pathogens are species specific. Disease may push one species to the brink of extinction, while exposure to that same pathogen has no effect upon the surrounding animal population.*

Now consider groups of like species that have never before come into contact with each other. Contemporary examples include competitive exhibitions of felids, canids, or equids. The close proximity of previously discrete populations of a single species can put all of the animals at risk. Even with inoculations, disease often follows, as not all pathogens will be anticipated. Further, the spread of disease does not require direct contact. Vectors such as arthropods or avifauna have proven quite successful in spreading multiple types of pathogens.

In situations of limited available range, as is often proposed for the late Pleistocene, distinct herds of a single species could be forced to share a single habitat. Exposure to new, or mutated, forms of diseases would occur, with neither group possessing immunity to the other's diseases. Direct contact might not even be necessary, when transmission is possible through carriers such as insects or birds, or through the soil.

How would most species be able to avoid disease? Isolation before exposure or isolation of a surviving population would be a successful strategy. In some isolated locations such as islands, humans shared the landscape with the megafauna. Yet ancient humans went extinct while some megafaunal species, in dwarfed form, lived for about 8,000 more years! So much for over-hunting.

The same pattern for extended survival seems to have occurred in the Mediterranean, as it did off the West Coast of North America. Mammoth, in pygmy or dwarf form, survived for an extended period in numerous locations within the Mediterranean. Each was an island and thus isolated from the mainland (Agenbroad, 1998:10). The same pattern of survival is documented outside of the Mediterranean, and for other species. Other long term survivors include the pygmy water buffalo (*Bovidae bovini*) of Cebu Island in the Philippines, and several species of ground sloth in the West Indies.<sup>20</sup>

While we do not know at what point within the exposure cycle these animals became isolated, we do know that the survival of these species generally extended far longer in situations of isolation. The mainland extinctions seem consistently to predate the demise of the island isolate groups, in some cases by more than 5,000 years.

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<sup>20</sup> See *Fossil Remains of a New, Diminutive Bubalus (Artiodactyla: Bovidae: Bovini) From Cebu Island, Philippines* (2006) and *Asynchronous Extinction of late Quaternary sloths on continents and islands* (Steadman, et. al, 2005).

How can the existence of disease be proven? The most direct way would be to examine the remains for indications of disease. This might be identified through cranial or post-cranial scarring, or through evidence at the molecular level. An effort should be made to examine specimens for viral DNA. Soft tissue excavated from Pleistocene sites could easily hold snippets of DNA from recognizable pathogens. Previously unidentified pathogens might also be observed. Another issue of importance is the testing for specific and for non-identifiable antibodies. Especially within pygmy and dwarf populations, indications of immunity could prove especially important, both in suggesting past disease and in helping to explain the longevity of isolated species.

There is an additional issue regarding pathogens. This involves the attempt by some researchers to bring back species of megafauna that are currently extinct. The possibility of the survival of selected pathogens is an issue that needs to be addressed. Although the viability of disease over this long a period is in question, the possibility still exists that survival has occurred.<sup>21</sup> The issue changes from the hypothesized demise of all pathogens, to the possible reintroduction of a disease that is still virulent, or at least viable. Researchers could be reintroducing the specific diseases to which the megafauna originally succumbed. Further, what effect would these pathogens have upon modern species? Contemporary animals can not be expected to have immunity to pathogens that have been inactive for millennia. Could long dormant pathogens reemerge within animal populations, and eventually also infect humans? Or, by first identifying ancient pathogens, could we develop a response to the disease and then successfully reintroduce some species?

### Replacement Populations Among Humans

The replacement of human populations over time is a topic that has become politically incorrect in many parts of North America. Despite a general acknowledgement of changes in animal populations, and of radically altered environments over time, the emerging position of many Tribes is that they have always been here. The accounts of brave people and arduous journeys have simply been erased.<sup>22</sup>

Even when researchers do ignore the older oral histories of the Tribes, the preponderance of the physical evidence still argues against a stationary population for much of prehistoric North American. Thus, to consider the issue of changing populations over time, a standardized set of questions should be applied to each line of evidence. Further, these lines of inquiry should reflect a multidisciplinary approach.

The following four questions might be utilized in a structured and balanced assessment of this issue. While they are designed to address human entry into North America, they could also be useful in the investigation of the peopling of other countries.

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<sup>21</sup> Gilbert, personal communication via email and at the International Science Conference. He suggests a low probability of pathogenic survival over such a long period, adding that a very specific environment would be crucial.

<sup>22</sup> One Tribal group, for example, now claims that their people were made from mud, and that they have always been where they are now (Time, 2006).

- From the physical evidence so far available, what people were first here?
- When were they here?
- How did they get here?
- Who replaced the first Americans? This last question, of course, brings up the same four questions, with regard to subsequent populations. When did the new people arrive, where did they come from, how did they get to North America, and then who subsequently replaced them?

The physical proof of replacement populations extends from molecular biology to physical anthropology. There is substantial evidence that different groups of people have occupied the landscape over time. In some cases, population movement and settlement can be associated with the last few centuries.

There are specific cranial differences between population groups and between time periods. Kennewick Man is an excellent example of physical evidence that refutes any suggested relationship between modern Indians and the ancient Americans that have been studied. While contemporary Indian groups from this region are N.E. Asian or Siberian in origin, Kennewick Man is physically associatable with Polynesian or S.E. Asian ancestry.<sup>23</sup> Importantly, this early specimen and some others like him negate the suggestion of a Bering Strait migration. The origin of these early people is far to the south.

This anthropological evidence of changing populations over time is supported by archaeological data. Some of the most conspicuous indicators of replacement populations include substantially different house types, changes in burial traditions, disparities in subsistence strategies, and radically different tool types—especially when they appear for a very limited period of time. Another important indicator is cultural material or actual house types that can not be associated within the region (Time, 2006:10).

When viewed singly, any of the changes just mentioned may merely be suggestive of a shift within a single culture. However, when multiple cultural differences are evidenced, a change in populations needs to be considered. One example is the ceramics culture that suddenly emerged in the Pacific Northwest. Prior to the arrival of the ceramics makers, and after their departure, the prehistoric populations of this region were without a ceramic tradition. Yet, for a brief period, a group of people with a cultural need for multiple types of ceramics occupied the area. The round or oval houses of the ceramic makers were replaced by the square or rectangular houses of later populations (Stenger, 1992). The large knives and projectile points associated with the ceramic makers were replaced with smaller tools, made from different materials. The few fragments of ceramics that are observed in the more recent occupation areas evidence radical secondary modification, such as needle sharpening scars on items that were once figurines.

An additional question remains. Did any animal and human population replacements occur at the same time? If the paleontological and archaeological data indicate

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<sup>23</sup> See statements by Owsley, quoted in Time Magazine (2006:5), and Schneider (2007:19). Also Davis (1989) for the results of analysis of hair follicles and blood types of contemporary Tribal people.

simultaneous changes, then climate change should be considered as a factor. As climate shifts would alter the populations of flora and thus fauna, the movement of hunter-gatherers would also be indicated (Bryson and Frison, 2003). The continuation of a single occupying population throughout time is not justifiable for most of the world. Interestingly, we do not question the historic record when we read of replacement populations in Europe, or when we see history mirrored in the artifacts or features that we have excavated. Yet, in the field of North American prehistory many people balk at the concept of replacement populations, despite a lack of evidence to support their position.

### Genetic identifiers

Genetics will undoubtedly prove integral to future findings. When considering all of the above issues, genetics will prove to be a significant part of unraveling fact from fiction. The obvious questions that we hope to have answered by genetic studies include the defining of biological relationships between populations. Who was related to whom? Who seems unrelated? When did one population arrive, and another modify its genetic profile? Further, how accurate is the clock for genetic drift? Whether the research is considering the entry of a specific bear species into a new region, or the arrival of a human population from another land, these questions are important to consider.

Skeletal attributes, especially those defined by craniofacial morphometrics, have proven valid over and over again. These studies strongly indicate that the earliest Americans had very different ancestors from those of more recent times. In one specific study, the measurements of ancient skulls were compared with corresponding data that included nine American Indian groups from western North America. The craniofacial morphology of the ancient specimens fell "...outside the range of variation of all modern groups, especially that of the American Indian." (Owsley and Jantz, 2005:289-294).

When viewed by geographic region, the craniofacial measurements of specimens that are immediately post-Archaic tend to be a population apart from the ancient and the very recent groups. Importantly, there are quantifiable differences within each cluster of individuals, when grouped by their geographic area and by their antiquity (Nelson 2005:277-288; Owsley and Jantz, 2005:289-294). This allows for a range of variability to be established for each population group, while more clearly identifying individuals who do not correspond to them morphologically.

Molecular biology validates these observations. Multiple migrations over time are indicated.<sup>24</sup> In a continuing effort to address the issue of origins, haplogroups have been defined for primary and secondary populations. Modern Tribes are associated with haplogroups A, B, C, D or X. However, relationship models based upon DNA data are still problematic, at least for New World populations. As pointed out recently by researchers, if an ancient individual is identified as having a haplogroup associated with a modern American Indian group, this does not prove that the ancient individual is ancestral to any contemporary Tribal people. The data only suggest that both the ancient and the modern group descended from people who once resided in Asia, where these haplogroups originated and still exist (Schneider, 2007:20).

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<sup>24</sup> See Shurr's discussion in Time, in "The Untold Saga of Early Man in America" (2006:8).

Inhabitants of the ancient and the modern world are being categorized by haplotype. Thus far, the largest database focuses upon mtDNA, the maternal lineage. However, as the traveling populations may have been predominately male, Y-chromosomal studies may prove to be more significant as these data increase. More, and improved, methods of testing are becoming available. Further, additional laboratories are employing scientists capable of properly analyzing samples. This allows for testing of specimens by more than one laboratory, which has obvious importance when samples are limited. This is especially true with Ancient human remains, where so few specimens are actually available for study.

Importantly, analysis is ongoing for many species of plants and animals. When these findings are combined with the results of precise specimen dating, an accurate profile of changes over time can be defined. Then, when changes in multiple plant and animal populations are well delineated, the replacement of human groups will be more clearly explained. While this type of work is in its relative infancy, results thus far support the archaeological and anthropological findings.

The results of molecular studies suggest that the answers are not currently as absolute as most people assume (Gilbert, 2007). What can we realistically expect to learn from fields such as molecular biology? At this stage, what questions can not be answered? What should we be asking? One exciting aspect of recent molecular studies is that the line of questioning may be vastly expanded beyond what was feasible even a decade ago. This expansion in thought and methods, however, can facilitate an inaccurate interpretation of the data. For this reason, the multiple lines of evidence that result from a multidisciplinary approach become the safeguard that is needed.

### Closing

The end of this conference will hopefully be the start of a new way of thinking for most of us. How did animals, and then people, travel in the Pleistocene—and before? How important was the Bering Land Bridge? Were pathogens the primary cause of the major extinction events? Who were the ancient people?

One of the most important issues is how best to challenge the theories that we learned in school. So much of what we were taught, and that is still being taught, is erroneous and needs to be eliminated. As scientific findings increase, textbooks become even more obsolete. Further, as the agendas of special interest groups often appear to outweigh the rights of scientists, it may only be a matter of time before our right of inquiry is severely limited or possibly eliminated.

The right to study, by legal standards, is supposed to be based upon multiple lines of evidence. These include relevance, expert evidence, accepted scientific technologies, evidence that is not emotionally skewed, external standards, and findings that are acceptable within the scientific community (Barran, 2007). Those standards were demonstrated during this week's meetings, and through this publication.

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- [www.friendsofpast.org](http://www.friendsofpast.org) see distribution map of ancient human remains, and data on each.
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