

# MAMMOTH TRUMPET



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## Big Black Wolf

**A**N ARTICLE that appeared in the 6 March 2009 issue of *Science* puts the evolutionary history of North American gray wolves, coyotes, and domestic dogs under the microscope. The trait specifically scrutinized is coat color. Noting that black wolves are an almost exclusively New World manifestation, scientists set out to discover the gene responsible for the mysterious black fur. What they determined is that the black coat is a mutation that was passed not from wild canines to domesticated animals, but instead from domesticated dogs to native wolf and coyote populations of North America. The anthropologist's interest in this study lies in the role early Americans, who domesticated the dogs, had to play in this genetic puzzle. And this information may also shed light on New World migration—on the black-coated dogs that passed

on their trait, and on the humans they accompanied.

This look into the canid gene pool was originally meant to be a short-lived project of only a few months. “We simply wanted to find the gene that caused them [dogs, wolves and coyotes] to be black,” says the article’s lead author, Tovi Anderson, then a doctoral student at Stanford University. (Today she answers to Dr. Anderson.) They found the responsible gene, which in turn led their search beyond wolves and spilled over into neighboring species of coyotes and domestic dogs. What was meant to be a project spanning mere months stretched into four years.

### From fairy tale foe to Fido

Asked about the significance of her research on wolves, Anderson replies that “the work is important because it helps us

understand the nature of selection in natural populations and allows us to think about how introgression between closely related species can

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*A blast so catastrophic it incinerated entire species of megafauna, doomed a human culture, and triggered a drastic climate change? Jenn Marlon's team can't find proof in Clovis-age sediments of lake beds.*

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*A steppe bison, surfacing after being entombed for nearly 14,000 years, is ironclad proof for Yukon paleontologist Grant Zazula that retreating glaciers had cleared a Beringian passage prior to Clovis occupations.*

help or hurt native species." While this is of obvious interest to geneticists, anthropologists also are sitting up and taking notice, though for an entirely different reason. They see the process of dog domestication as a possible road map for exploring questions about ancient human life. Unfortunately, Anderson explains, the map isn't an easy one to read.

Dogs and wolves are essentially the same animal. That is, there are very few differences between DNA sequences found in wolves and dogs, which allows them to interbreed and produce viable offspring. The chief difference, which classifies one as *Canis lupus* (wolf) and the other as *Canis domesticus* (dog), is that dogs are domesticated and wolves roam wild. There's a very thin line between man's best friend and the big bad wolf ready to gobble up little pigs, sheep,

cult to narrow. *Where* domestication occurred, however, can be stated with a bit more certainty. Authorities pretty much agree on the continent of Asia, with China the most likely locality. Evidence of an Asian location exists in both the archaeological and historical record, and further genetic testimony appears in the analysis of DNA sequences from various breeds of dogs known to have originated in Asia. The DNA of Asian breeds such as chow chows, Lhasa apso, and Pekingese

shows they're older than breeds of dogs arising from other continents.

Just as there are numerous breeds of dogs, wolves also exist in an assortment of varieties, but it's the gray wolf that is believed to have been the puppy that first ate out of man's hand. Whether domestication was a onetime occurrence involving a handful of wolves that became ancestors to dogs, or whether wolves and humans bonded repeatedly throughout prehistory is unknown. Though the exact path of dog



Anderson, 2007.

and little girls who sport red capes. Even though what separates *lupus* from *domesticus* isn't chromosomal, it's still highly significant. Through the centuries humans have made it more so by encouraging certain traits in dogs, resulting in today's wide spectrum of breeds. No one who looks at a chihuahua and a gray wolf says they're the same animal.

Dog domestication is thought to have occurred somewhere between 15,000 and 40,000 years ago. Admittedly this is a wide window. Unfortunately, the similarity between the two species makes it diffi-



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Many years may pass between the time an important discovery is made and the acceptance of research results by the scientific community. To facilitate communication among all parties interested in staying abreast of breaking news in First Americans studies, the **Mammoth Trumpet**, a science news magazine, provides a forum for reporting and discussing new and potentially controversial information important to understanding the peopling of the Americas. We encourage submission of articles to the Managing Editor and letters to the Editor. Views published in the **Mammoth Trumpet** are the views of contributors, and do not reflect the views of the editor or **Center** personnel.

—Michael R. Waters, Director



domestication is murky, Anderson and her colleagues' research has answered a few questions. And, like all good science, has given rise to more.

### You! Out of the doggie gene pool!

It wasn't wolves in general that sparked Anderson's interest, but a subset of the species, black wolves. To understand her research we need to explore at the molecular level.

When looking into pigmentary diversity among numerous species of mammals, fish, and birds, mutations are generally found on the *Melanocortin 1 receptor* gene (*Mc1r*). It's here that the type and amount of pigment for the animal are determined through a process well understood by scientists. To make domesticated dogs black requires an additional component, found on the *K* locus, that encodes a beta-defense protein. Considering that domesticated dogs and wolves possess the same number of chromosomes, a probable link exists here.

Anderson's research benefited from the recent discovery of black wolves in Italy, the only location outside of North America where black wolves are known to exist.  $K^B$ , the allele (alternative form of a particular gene) responsible for black coats, is found in domesticated dogs across the globe. In Italy recent wolf hybridization with feral dogs has introduced black wolves into the Italian countryside. This phenomenon has been verified at the molecular level.

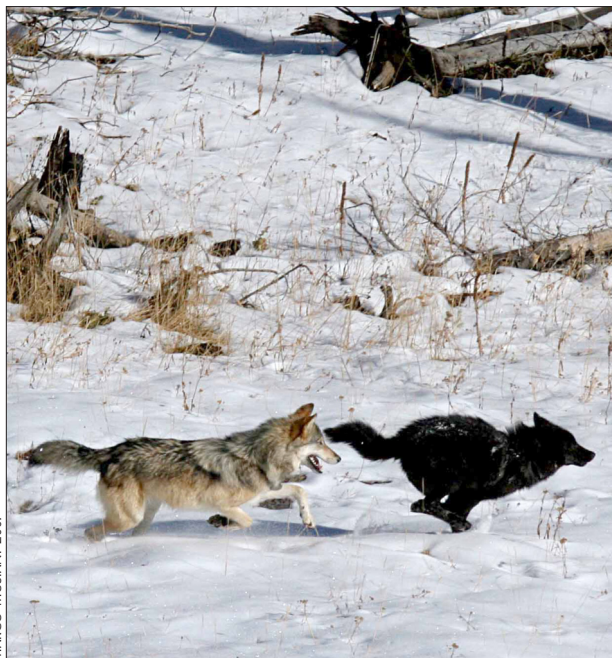
These new dark-coated wolves from Italy bolstered Anderson's project, which initially studied only a handful of individuals, but grew to more than 400 specimens throughout western North America. Of course, most individuals couldn't be tested genetically, but their coat color was documented by observing them in the wild. The phenotype (traits that are visible without sneaking a peek at DNA) can be difficult to distinguish; not only do wolves gray with age, those that are heterozygous for coat color (carrying alleles for both dominant black,  $K^B$ , and recessive gray,  $k^g$ ) are influenced by their environment. The black coat appears to have demonstrated positive selection; in locations where it is beneficial—in forested regions, for example, where a dark coat acts as a kind of camouflage—it becomes prominent with a selective sweep. Farther north on the snowy tundra, however, gray and white coats prevail. An alternative theory suggests that the protein that produces a black coat endows black wolves with a better immune system. "We do know that this defensin protein acts both to produce a black coat and is also active in some way in the immune system," Anderson explains.

### Reckoning the rate of canine mutation

Isolating a single trait in the maze of a species's genome is quite an accomplishment, but that's not the significance of Anderson and her team's research. Their triumph lies in the discovery that

$K^B$ , the allele responsible for black coats in dogs, is a mutation that occurred approximately 46,886 years ago. This estimated age has, according to Anderson, a 95 percent confidence limit ranging from 12,779 to 121,182 years. "We have a broad range because our age estimate is based on data collected from four dogs," Anderson explains. "If we had more data, say twenty dogs instead of four, we probably would have a more accurate estimate and a smaller confidence interval." This substantial uncertainty means scientists can't determine whether the black-coated mutation appeared before or after dog domestication. They were able, however, to isolate exactly what kind of mutation  $K^B$  is.

Mutations, permanent changes in the DNA sequence of a gene, are the fuel that powers the evolution engine. The DNA sequence consists of building blocks called nucleotide bases (labeled in shorthand A, C, G, and T), which appear in bewildering numbers and are arranged in a precise order. When base pairs are transcribed into RNA, each group of three base pairs codes a specific amino acid in a protein. In the case of a mutation, this process gets a bit dyslexic. A piece of the DNA sequence may be relocated, duplicated, or deleted, thus altering the entire sequence. Examining base pair sequences, Anderson's team of scientists found that the black-coat mutation resulted from a deletion. They then tracked the mutation back in time to identify the most recent common ancestor of black dogs and wolves by means of a complicated process that assumes mutations occur at an equal rate in both dogs and wolves. The result was startling. They conclude that



A gray wolf and a black wolf running free in the Canadian Arctic.

the  $K^B$  allele is older in domesticated dogs than in wolves, meaning that North American black wolves acquired their dark coats from dogs and not the other way around. Actually, two scenarios are possible. The gene may have originated in dogs. Or it may have originated in wolves before domestication and been passed to dogs, then became lost in wolf populations while surviving in dogs, who later reintroduced it to wolves. Nonetheless, either possibility has a profound effect on our knowledge of peopling of the Americas.

### Cave canem\*

The fact that black wolves only exist in North America (excluding the Italian aberration) is significant to anthropologists who study the oldest Americans. The black coat originated in domesticated dogs that had emigrated from Asia with their hu-

*continued on page 7*

\*Beware of the dog, in case you've forgotten your high school Latin.

# Fire Record Undercuts Clovis Comet Theory

This wildfire, the Erickson Creek fire at Yukon Flats in 2003, scorched 183 square miles of grass- and timberland. Another disaster documented by the Alaska Fire Service, the Grass River fire in 2006, destroyed 23 square miles. Lightning, not ET events, ignited both blazes.

P. HIGUERA

signature of an extraterrestrial impact with devastating consequences. The list of clues included magnetic grains with iridium, magnetic microspherules, charcoal, soot, carbon spherules, “glass-like carbon containing nanodiamonds,” and “fullerenes with ET helium.”

The key element in the theory, which explains how the impact caused the massive extinction event, is the extensive burning of forests and grasslands triggered by the blast. “Extreme wildfires” supposedly swept the continent destroying the food on which the giant mammals of the Pleistocene depended. The Clovis culture, which depended in turn on the herds of megafauna, also was obliterated, to be replaced by groups with a more generalized way of life.

**I**N A SERIES OF ARTICLES, beginning in 2008, the *Mammoth Trumpet* examined the evidence for the so-called Clovis Comet. According to this theory, 12,900 calendar years ago a comet blasted into North America with the explosive force of a 100-megaton bomb. The cataclysmic explosion ignited continent-wide forest fires that destroyed the food supply of the Pleistocene megafauna, driving them, and the Clovis hunters that depended upon them, into extinction, and initiated the Younger Dryas climate episode that plunged the Northern Hemisphere back into the Ice Age (**MT 23-1** through **-3**, “The Clovis Comet”). Now new research appears to undermine a key element of this theory: There was no continent-wide conflagration 12,900 years ago.

## The Clovis Comet theory

In 2001, Richard Firestone of the Lawrence Berkeley National Laboratory, along with numerous coauthors, presented the evidence for an extraordinary new theory to explain the extinction of the Ice Age megafauna and the simultaneous demise of the Clovis culture. The paper sent figurative shock waves through the paleontological and archaeological communities and caught the imagination of the general public. The popular public television program NOVA devoted an episode to the topic entitled the “Last Extinction.”

The evidence in support of the theory was

**Cathy Whitlock (left) and Marlon wrapping a long core from Beaver Lake, Oregon, 2005.**



MEGAN WALSH

found in a thin layer of sediment overlying Clovis-age sites across North America. Firestone and his co-researchers identified a suite of materials that together constituted a persuasive

## A continent aflame?

Jennifer Marlon, a doctoral student in the Department of Geography at the University of Oregon, along with an international team of 22 researchers from institutions in Canada, Denmark, France, Switzerland, the United Kingdom, and ten states of the United States, examined data from 35 lake-sediment records. Their goal was to study the relationship between the abrupt climate changes that occurred during the Last Glacial-Interglacial Transition (15,000–10,000 CALYBP) and changes in the frequency and magnitude of wildfires in North America throughout this same period. In their paper, published in *Proceedings of the National Academy of Sciences*, the team observed that the environmental changes in some regions at the beginning and the end of the Younger Dryas chronozone (12,900–11,700 CALYBP) “were larger than those at any subsequent

time.” And because both the magnitude and rate of change are similar to those that many climate scientists project for the future, these data provided an opportunity to study the effects changing environments will have on wildfires in decades to come.

Marlon and her co-researchers recognized that their data also afforded the opportunity to test the proposition that some catastrophic event

12,900 years ago had set the continent ablaze. If a continent-wide series of fires had scorched North America at any time



between 15,000 and 10,000 years ago, that event should show up clearly in every lake-sediment record studied by the team.

### Looking for the “smoking gun”

Marlon and her team studied every record with data relating to the time in question, including sediment cores from 35 lakes from Alaska to New Mexico and from California to Quebec. They examined changes in the abundance of charcoal particles that had been deposited along with the layers of sediment in these widely scattered lakes. These data gave them a record of biomass burned and fire frequency over time across North America.

They further studied 15 high-resolution charcoal records to refine their estimates of wildfire frequency and magnitude. They also recorded the changing abundances of tree pollen in the sediments to explore the relationships between fire frequency and available woody fuel levels. Finally, they compared the record of environmental change revealed in their sediment cores with the well-established and broad environmental changes documented in ice cores.

The team identified increasing levels of biomass burning at all sites from 15,000 CALYBP until the beginning of the Younger Dryas at about 12,900 CALYBP. Fire frequency and magnitude remained more or less constant through the Younger Dryas and, at around 11,700 CALYBP, fire frequency began to increase again.

Importantly, while these trends are clear and significant in the composite record of all 35 sites, there are differences apparent at particular sites that reflect variation at the regional or local scales.

### Climate change or catastrophe?

Factors that contribute to the occurrence of wildfires include weather patterns that produce either wet or dry conditions, with dry conditions favoring more fires, and the relative frequency of sources of ignition, such as lightning strikes. More storms mean more lightning strikes, which mean more fires.

Changes in vegetation composition, determined by factors such as temperature and precipitation, affect the magnitude of wildfires by changing the amount and quality of fuel available to burn.

Dramatic climate changes at the beginning of the Younger Dryas included changes in atmospheric circulation that affected temperature, rainfall patterns, and the severity and

tracks of storm systems. Although Firestone and his colleagues argue that these changes were the direct effects of the comet impact, an alternative and more commonly accepted theory for the cause of the Younger Dryas relates the climate changes to a unique combination of geographic and historical circumstances. As the Laurentide Glacier receded to the north beyond the St. Lawrence Valley, it opened an avenue for glacial Lake Agassiz to flush its massive volume of cold freshwater into

the North Atlantic instead of the South Atlantic by way of the Mississippi Valley. This disrupted ocean circulation patterns and plunged the Northern Hemisphere (at least) back into a relatively brief episode of glacial cold.

The question then becomes, How do we distin-



**Timberland ravaged by fire reflected in a small lake in the Charlton burn area, Oregon, 2003.**

guish between widespread fires caused by a catastrophic event, such as a comet impact, and fires caused by the indirect affects of more ordinary climate-change processes?

To test whether regional wildfires documented at the onset of the Younger Dryas were caused by rapid climate change or the proposed comet impact, Marlon and her team compared the record of fires at the beginning and the end of the Younger Dryas—both periods of rapid climate change. They reasoned that if fires were more common at 12,900 than at 11,700 CALYBP, then a special explanation, such as a comet impact,

might be necessary to explain the unusually high frequency. If, on the other hand, there was no difference, then the frequency of fires could be explained simply as a function of the rapidly changing climate regimes.

When Marlon's team examined the data, they found no evidence for increased burning associated with the time of the supposed comet impact at 12,900 CALYBP. In fact, there is no evi-



**Post-doc researcher Megan Walsh with a core sample from the bed of Pintlar Lake, Montana, 2006.**

dence for continent-wide fires at any time during the last 5,000 years of the Pleistocene Epoch. The observed trends in wildfire frequency and magnitude seem to be linked directly to periods of rapid climate change rather than to a singular and catastrophic event.

Firestone, in an interview with the BBC, argued that Marlon and her team's data did not undermine the comet theory of

Sites investigated by Marlon's team.

The timing of the peak charcoal layers varies from site to site across the continent with no clear pattern.

If the Clovis comet caused a pan-continental wildfire, you'd expect all the sites to show a peak at 12.9 ka.

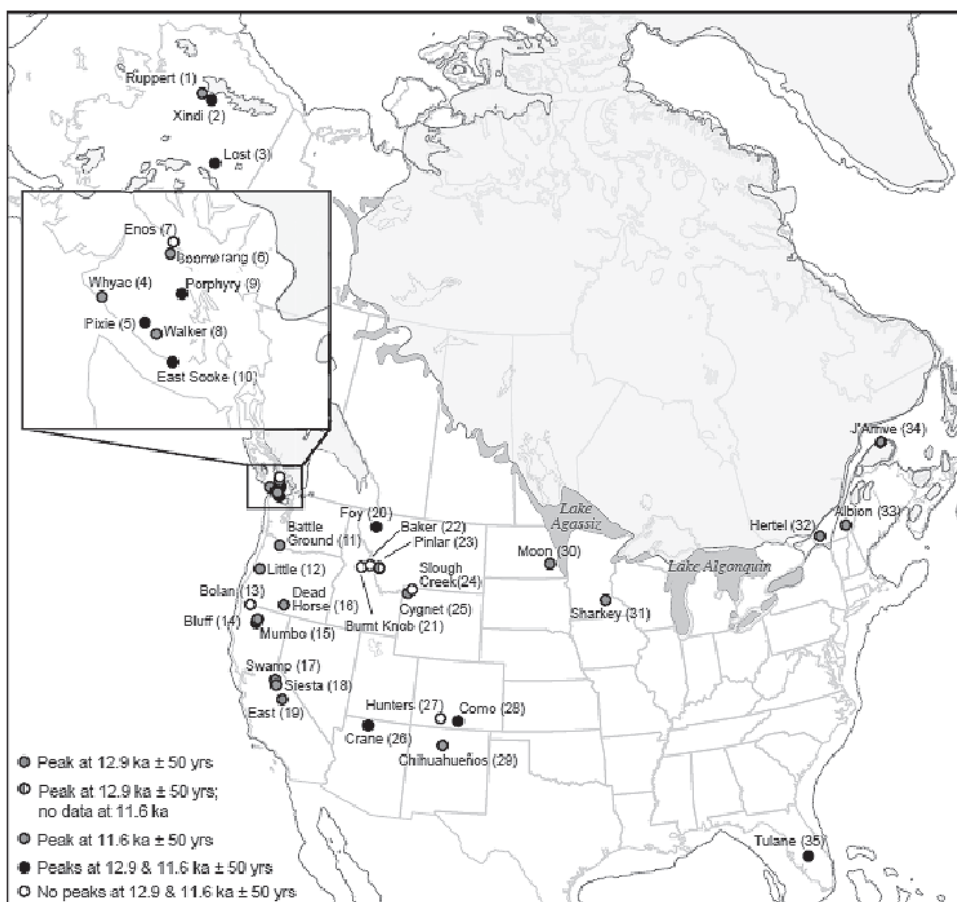
megafaunal extinction: "The paper merely shows that fire increased near the onset of the Younger Dryas and continued for some time. Their results are in complete agreement with what we observed." In the same BBC news story, however, Wallace Broecker of the Lamont-Doherty Earth Observatory at Columbia University stated flatly that the new results hit "right at the heart" of Firestone and his team's argument.

### An earlier and bigger increase in wildfires?

Marlon and her team did observe a "particularly steep increase in charcoal influx" at 13,200 CALYBP, which they characterize as "the largest and most rapid change in biomass burning during deglaciation." It was "widespread," but even this big increase in wildfires was not "continent wide." Since this widespread episode of burning is 300 years too early to attribute to the comet impact, it's not directly relevant to testing the Clovis Comet hypothesis. What makes this increase so interesting, however, is that it coincides with the arrival of the Clovis culture in North America.

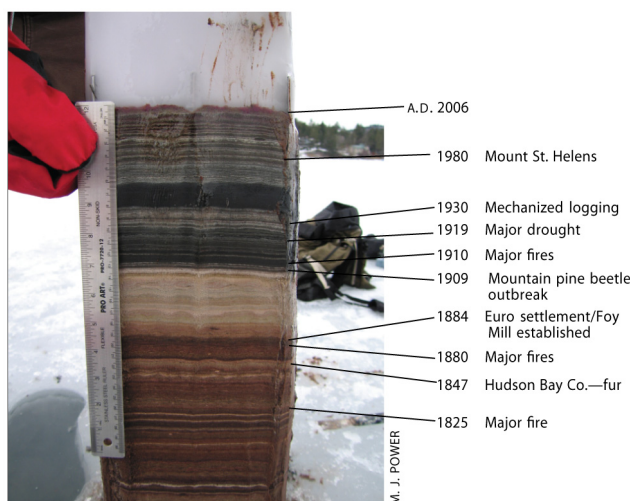
Marlon and her coauthors offer multiple working hypotheses to explain the correlation of increased burning with the appearance of the Clovis culture. First, the increase in burning may be due to an abrupt climate change, its apparent association with Clovis only coincidental. Second, Clovis hunters may have set fires intentionally either to drive game or to increase the productivity of the environment for game animals. Third, Clovis hunters may have indirectly caused the increase in fires by hunting the megafauna. Reduced numbers

**Laminated sediment core from Foy Lake, Montana, which establishes a timeline for historic events in the watershed. Similar cores revealed the incidence of wildfires during the late Pleistocene.**



FROM JENNIFER MARLON

America. This more or less simultaneous appearance of evidence for increased fires across the continent isn't consistent with the expectations of the time-transgressive movement of people across the continent. In other words, if Clovis hunter-gatherers were directly responsible for the increased fires, then the peaks in burning should occur earliest in those regions in which they first appeared and later in regions subsequently occupied by the migrating wave of colonization. Therefore, the single "fire peak," rather than a succession of peaks following the movement of Clovis colonists, is more simply explained by a change in climate only coincidentally related to the appearance of the Clovis culture and the departure of the megafauna. An additional fact that argues against Clovis hunter-gatherers as the agent responsible for increased fires is that many of the lakes from which Marlon's team obtained their samples are remote, and many lie at high elevations in rugged terrain where travel by foot is extremely difficult.



of large game animals would mean fewer plants were being eaten, so there would be more vegetation available for burning.


Marlon and her team observed the "fire peak" at 13,200 CALYBP at several sites widely dispersed across North

America. This more or less simultaneous appearance of evidence for increased fires across the continent isn't consistent with the expectations of the time-transgressive movement of people across the continent. In other words, if Clovis hunter-gatherers were directly responsible for the increased fires, then the peaks in burning should occur earliest in those regions in which they first appeared and later in regions subsequently occupied by the migrating wave of colonization. Therefore, the single "fire peak," rather than a succession of peaks following the movement of Clovis colonists, is more simply explained by a change in climate only coincidentally related to the appearance of the Clovis culture and the departure of the megafauna. An additional fact that argues against Clovis hunter-gatherers as the agent responsible for increased fires is that many of the lakes from which Marlon's team obtained their samples are remote, and many lie at high elevations in rugged terrain where travel by foot is extremely difficult.



## Clovis Comet fizzles

Marlon and her team found “no evidence of synchronous continent-wide biomass burning at any time” during the period under study. And, while their data do not address the question of whether or not a comet or other extraterrestrial body smashed into, or exploded over, North America during the late Pleistocene, they do demonstrate unequivocally that even if there was such an impact, it did not result in a pan-continental firestorm. Marlon is quoted in a University of Oregon press release as saying, “We had the data to look for widespread fires if they had occurred, but what we saw instead was a general increase in biomass burning whenever the climate warmed.” Therefore, there is no smoking gun, or smoldering forest, to

prove that a comet strike had anything to do with the extinction of the Pleistocene megafauna—except, of course, for any luckless individuals that happened to be in the immediate blast zone of an incoming extraterrestrial body. 

—Bradley Lepper

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## Big Black Wolf

*continued from page 3*

man companions. Therefore the entry of human populations into the New World dates back as far as the appearance of the  $K^B$  allele in North American gray wolves, possibly earlier. Now, if research proved the allele has only been present in wolves for, say, 500 years or less, this wouldn't shed any anthropological light on the subject. It would merely suggest the allele came over with Europeans. But what if we could prove that the presence of  $K^B$  in wolves was 15,000 years old? Or 16,000? Precisely dating the age of the  $K^B$  allele in wolves could push back in time our estimate of when the first human colonizers arrived in the Americas.

Of course, it's impossible to determine exactly when—either during human migration, or at an indeterminate time after arriving—domestic dogs passed their genes to wolves. Although wolves and dogs can interbreed, they don't usually do so. If they did, black-coated wolves would be prevalent throughout the world. According to Anderson, dogs and wolves will only mate when two conditions are met. First, either the local dog or wolf population must be depleted, with the result that a mate of the same species cannot be found. Second, they must share a common environment, making it possible for them to interact. These two conditions must have been met in North America at some time after the arrival of dogs.

Unfortunately there isn't a concrete genetic date to specify when North American gray wolves first acquired their black

coat. Anderson's team suspects that it could have happened anywhere from 500 to 15,000 years ago, either with the introduction of European dogs, or soon after the arrival of American's first human migrants and their pooches, or somewhere in between.

Nevertheless, obtaining a precise genetic date may be possible. Anderson says it would require “different molecular techniques” and considerably more genetic samples of wolves. Such a complex procedure would be a formidable undertaking all its own, but one with the potential to yield answers many anthropologists are eager to learn.

### Whose best friend?

Anderson and her team didn't expect to find that the  $K^B$  allele, which causes a black coat in canines, is a recent mutation. On researching this mutation's history by identifying the most common recent ancestor of black dogs and wolves, whoever would have expected to find that the younger species passed on traits to its ancestor species? Not only have these traits survived in wolves, they have helped them flourish. With climatic change, the snowy tundra is diminishing and thick forests are pushing northward. This will make a black coat an even more valuable asset for wolves.

Perhaps the hand of man played a part in producing black-coated wolves. Although natural selection is largely responsible for the prominence of the  $K^B$  allele in wolves, ancient humans may have coaxed along this trait in dogs when it was new. Anderson doesn't dismiss the possibility out of hand. “People would have found a new coat color novel and interesting,” she

concedes. "I would imagine people back then wanted to breed dogs for specific traits that were cosmetically appealing, as they do today."

Anderson's research does, in fact, point to probable human influence in the genetic composition of North American wolves, for they carry within their genomes a little piece of DNA (the  $K^B$  allele and the region surrounding it) that likely came from Native American dogs. "We know that Native Americans brought dogs over from Asia," she explains, "and genetic analysis shows Native American dogs do not exist today." (All dogs in North America today come from dogs more recently domesticated in Europe or Asia. See "Suggested Readings," Leonard et al.) "So the  $K^B$  allele in North American wolves," she concludes, "may be a remaining remnant of the now 'extinct' Native American dogs."

### Disproving the theory of an eminent scientist

An unintended casualty of Anderson's research and the work of other canine geneticists is the theory on the origin of domesticated dogs proposed by Konrad Z.

**Polar opposites in the Canadian Arctic: black and white wolves scuffle.**



MARCO MUSIANI 2007


Lorenz, the famed Austrian naturalist, behavioral scientist, medical doctor (he served as a Wehrmacht battle surgeon in World War II), and Nobel Prize winner. Best known for *On Aggression*, his seminal study of the killer instinct in animals and man, Lorenz in 1952 wrote a charming personal recollection of his lifelong companionship with animals titled *King Solomon's Ring*. In the chapter dealing with man's best friend, Lorenz sets forth his theory on the *dual* domestication of wild canines, the wolf and the jackal, *Canis aureus*. It was the jackal, Lorenz states unequivocally, that was first domesticated by man. "The northern wolf (*Canis lupus*) only figures in the ancestry of our present dog breeds," he declares, "through having been crossed with already domesticated Aureus dogs." He argues convincingly that the jackal or wolf ancestry of a dog today is evident in its physical and temperamental characteristics.

Brilliant scholar though he was, Lorenz unfortunately predated genome research and DNA analysis. Anderson isn't aware of any instances in which jackals were domesticated to produce dogs, although she concedes that she "cannot say with certainty that this never occurred." Nevertheless, she continues, "I am able to say with absolute certainty that of the hundreds of breeds of dogs that exist around the world today, none have jackal ancestry and all are entirely descended from the gray wolf." Dogs of all different breeds have been analyzed at the genetic level, she explains, and are seen to be nearly indistinguishable from wolves. She insists that "if there were any traces

of jackal DNA in domestic dogs it would be quite obvious." Although she allows the possibility that jackals may have been domesticated in isolated instances, she notes that "there are no known breeds that result from hybridization with canines like coyotes, foxes, or jackals." She supposes that when Lorenz wrote *King Solomon's Ring* "there was much speculation about where dogs came from because nobody could yet look at their genetic sequences. It probably seemed likely that very small dogs must have come from some canine other than the larger wolf."

### What North American wolves can tell us

It isn't the coat color, however, or even how it came about that's of interest to anthropologists. Instead, it's *when* it came about, and then only if it's near the time that current research suggests humans first arrived in the Americas. The potential to fix the age of the  $K^B$  allele in North American gray wolves is out there.

If dog genes in wolves ultimately prove that the first migrants to the New World made their trip before the suspected date of 15,000 years ago, those dogs might become not just man's, but also the anthropologist's best friend. 

—K. Hill

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### Suggested Readings

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**DNA** IS THE ALPHABET OF HEREDITY. Therefore the DNA nestled within your cells, both the DNA in the cell's nucleus and the distinctive DNA contained in the mitochondria, comprises a kind of genealogical history that can be decoded to reveal insights into the sources, routes, and timing of the migrations made by your ancestors. Ugo Perego and Alessandro Achilli, both of the University of

along with its mtDNA, is derived from the mitochondria in the cytoplasm of your mother's egg cell—and thereby imprints a record of your ancestry along the maternal line. Occasional mutations in the mtDNA are clues geneticists use to track the movements of our grandmothers across the generations and around the world.

Mitochondrial haplogroups are lineages that can trace their



MARCELLO PEREGO—MILKIT.ORG

Pavia in Italy, along with 14 colleagues representing other Italian universities as well as scholars from China, Germany, Spain, and the U.S., have studied the mitochondrial DNA of 69 populations from China through North and South America in order to “shed light on the origin of Paleo-Indians.” They conclude that Paleoindians followed two routes into the Americas—a Pacific coastal route and a route through the Ice-free Corridor into the interior of North America.

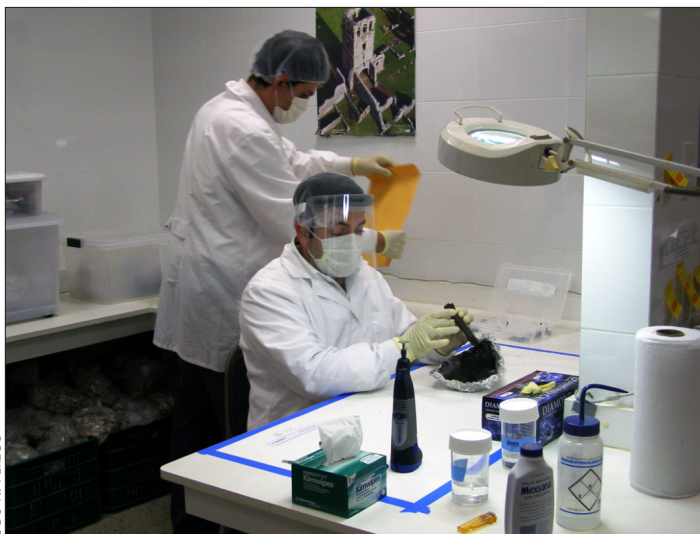
### Aboriginal American mtDNA

Mitochondria are organelles within the cell that have their own DNA. When writing about mitochondrial DNA scientists add the prefix “mt” to DNA so that it's clear they're not referring to the nuclear DNA, which is the genetic blueprint for each of us. We get our mitochondria from our mothers, because it's only the nuclear DNA of the sperm cell that makes it into the egg cell during fertilization. As a result, the mitochondria in your cells,

origin to a common maternal ancestor that first possessed a particular mutation. There are four common mtDNA haplogroups represented in Native Americans and a fifth that, while rare, has received a degree of notoriety that has exaggerated its importance. By convention, haplogroups are designated by letters of the alphabet.

Haplogroup A is most commonly found in northern North America, especially among the Inuit, Aleuts, and the Na-Dene (or Athapascans). It occurs in decreasing frequencies to the south. Haplogroup B, on the other hand, is virtually absent in northern North America and is present at the highest frequencies in the southwestern U.S. and in the Andean region of South America.

**Ugo Perego (seated) and Alessandro Achilli collecting ancient DNA samples in Panama.**



Haplogroups C and D are most abundant in South America, with decreasing frequencies to the north.

Haplogroups A, B, C, and D are all common in Siberia and southern Asia, which supports the established view that the

original Native Americans came to this New World from Asia by way of Beringia—whether over the Bering Land Bridge or across the Bering Sea in boats. The fifth haplogroup, referred to as X, occurs at low frequencies in only a few North American tribes, including the Ojibwa, Nuu-Chah-Nulth (or Nootka), Sioux, Yakima, and Navajo, but originally it wasn't known to occur in eastern Asia. It was only known in western Asia and Europe, which led some geneticists to propose the radical hypothesis that some early Americans had come to this hemisphere across the Atlantic Ocean from Europe. Subsequently, however, X was found among the Altai of Siberia, which makes its appearance in America less of a mystery.

### Digging deeper

Perego, Achilli, and their colleagues decided that looking at the most common, virtually pan-American mtDNA haplogroups would provide

tific literature: 2 extra examples of D4h3, 11 cases of X2a, and one of X2g. These 69 genomes were incorporated in a phylogenetic analysis, which essentially means that Perego, Achilli, and colleagues constructed a family tree showing the relationships among the groups from whom these mtDNA sequences were obtained.

### Timing of the initial migration

Slight differences in the mtDNA sequences for the X2a and D4h3 genomes provide a measure for approximating the time when these lineages diverged from their ancestral populations. The analyses undertaken by Perego, Achilli and their colleagues indicate that both the X2a and D4h3 lineages diverged at about the same time from “either the same Beringian source population or different yet related Beringian sources.”

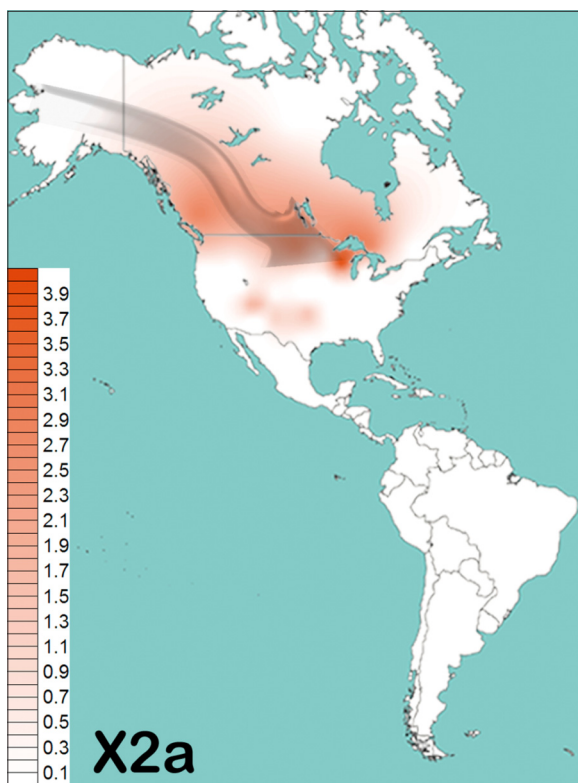
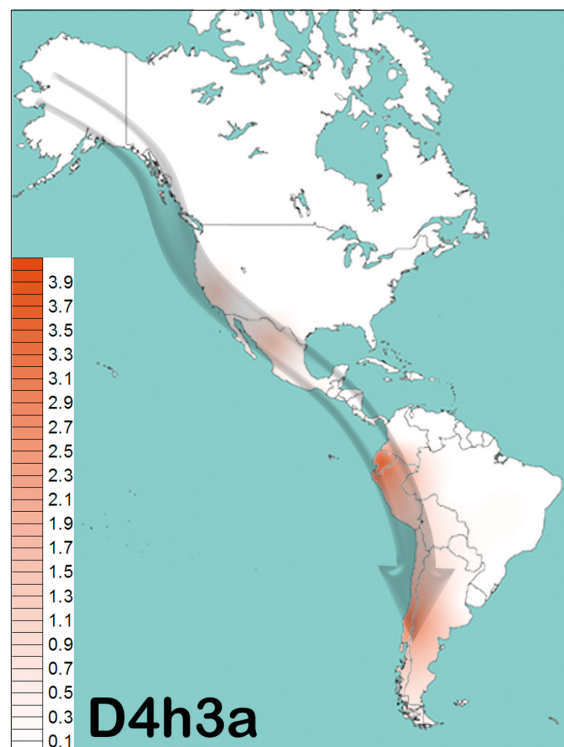
To obtain a meaningful estimate of the date of the human migration into the Americas, Perego, Achilli and their co-researchers incorporated 276 “complete coding-region sequences belonging to A2, B2, C1b, C1c, and D1” into the family tree. Using two estimates of how fast mutations occur and accumulate in mtDNA sequences, Perego, Achilli, and their team determined that the average age of the Native American lineages was about

The coastal migration route in the Americas suggested by the distribution of D4h3a, a recently discovered mtDNA haplogroup. The scale indicates the percentage of the haplogroup in the sample of Native Americans tested.

The interior migration route suggested by the distribution of X2a, a rare mtDNA haplogroup. ►

only a general view of Paleoindian migration history. For insight into more specific and possibly more diverse migration histories of distinctive groups within the broad movement of people out of Asia, they focused instead on two rare variants, or sub-haplogroups, of the five more inclusive haplogroups: X2a, a variant form of X, and D4h3, a variant of D.

They identified a total of 54 “unrelated mtDNAs, from either Native American populations or American populations of mixed origin” that most likely represented either sub-haplogroup X2a or D4h3. In addition, they included one mtDNA sequence from eastern China (D4h3). These mtDNAs were completely sequenced and analyzed resulting in a total of 44 examples of D4h3 and 11 of X2a. To these the researchers added 14 additional complete mtDNA sequences available in the scien-



16,000 years CALYBP. This doesn't necessarily imply that people were in America at this early date, but it's strong evidence that a distinctive source population had developed in Beringia by this time; and it was from this population that the ancestors of modern Native American would be drawn.

### Two migration routes

The most interesting pattern to emerge from the data studied by Perego, Achilli, and their colleagues is the divergent spatial distributions of variant sub-haplogroups D4h3 and X2a. D4h3 was “detected at low frequencies in modern and ancient population samples of both North and South America, with an overall higher frequency and peaks along the

Pacific coast and the western side of the Andes.” In contrast, X2a was detected only in North America and predominantly east of the Rocky Mountains.



The estimated divergence times indicate that D4h3 and X2a began to spread into North America at about the same time, but D4h3 appears to have dispersed rapidly along the Pacific coast. The distribution of D4h3 sequences “is restricted to near-coastal areas in the west” of both North and South America, and its deep antiquity in this region is evidenced by its presence in the human remains from On Your Knees Cave in Alaska, dated to 10,300 years CALYBP (**MT 23-3**, “Early-Holocene Caveman Sinks His Teeth into Genetics”). According to Perego, Achilli and their coauthors, these data fully support the hypothesis that “the Pacific coast was the major entry and diffusion route for the early Paleo-Indians.”

The spatial distribution of X2a was quite different. In spite of a similar time of expansion, X2a “is restricted to northern North

Achilli, and their coauthors is that groups possessing the X2a sub-haplogroup left Beringia following the Ice-free Corridor between the Cordilleran and Laurentide glacial ice sheets into the interior of North America, while the pan-American haplogroups, including D4h3, followed the coastal route. Perego, Achilli, and coauthors assert that this scenario “is in complete agreement with both the extent of diversity and distribution of X2a observed in modern Native American populations.” Moreover, they suggest that “the two inferred dispersal events were responsible for the emergence of the two major Paleo-Indian traditions of North America—fluted-point industries in eastern U.S. and stemmed-point industries in western U.S.” They concede, however, that further studies of ancient DNA from across North America will be needed before it can be

determined whether these distinctive artifact traditions actually correspond to populations with distinctive mtDNA profiles.

One problem with the two-migration-route scenario is that D4h3 is “very rare in North America and mainly found in South America with deep variation.” Perego, Achilli, and their team speculate that while the initial wave of migration along the west coast included all or most of the pan-continental mtDNA haplogroups, there may have

**The research team studying the genetic footprints of Paleoindian migrations across the Americas. Front row (l-r): Baharak Hooshkar Kashani, Maria Pala, Anna Olivieri. Back row (l-r): Matteo Accetturo, Antonio Torroni, Ugo Perego, Alessandro Achilli.**



UGO A. PEREGO

America, with a focus in the Great Lakes and the Great Plains regions.” The “frequency peak” is in the Great Lakes area.

Perego, Achilli, and their colleagues propose two alternative explanations for these distributions. First, the sub-haplogroup X2a was represented in the founding population of Paleoindians along with the main haplogroups, including the D4h3 variant. For one reason or another, however, X2a “disappeared from the wave front of the expanding population at a very early stage” and so became isolated in a coastal enclave “from where it expanded toward the east after the complete retreat of the Cordilleran ice sheet.”

The main problem with this scenario is that it’s difficult to imagine the circumstances in which a genetic variant would be lost during a period when the population was rapidly growing and expanding into large and previously unpopulated regions. Perego, Achilli and their colleagues assert that in such circumstances the risk of “the loss of a lineage due to genetic drift is minimized.”

The alternative, preferred hypothesis advanced by Perego,

been “back wave[s]” of migration of some groups “with a slightly shifted haplogroup composition” in which D4h3 occurred at much lower frequencies, or was lost entirely. This explanation, however, appears to suffer from the same problem as the postulated disappearance of X2a during a period when the effects of genetic drift should have been minimized.

### Phylogeography of Native America

Perego, Achilli, and their colleagues conclude that the phylogeography (the mapping of mtDNA family trees across the landscape) of sub-haplogroups D4h3 and X2a, “when evaluated at the level of complete mitochondrial genomes,” shows that Paleoindians followed at least two routes of entry from Beringia into the Americas: a coastal route, and an interior route following the Ice-free Corridor. The source population for the First Americans was a “dynamic Beringian gene pool” that was “continuously reshaped” by the forces of gene flow and genetic drift. Within a span of time as short as 2,000 years

*continued on page 20*



# decoding the woolly mammoth part I

An in situ mammoth skull at the pre-Clovis level of the Lamb Spring site in Colorado, now curated at the Denver Museum of Nature & Science. (Inset) a Clovis point from Blackwater Draw, New Mexico.



TONMY FULGHAM

**C**ONVENTIONAL THINKING says that when a creature becomes extinct, it's gone forever. Well, maybe . . . but in the face of modern technology, conventional thinking sometimes goes out the window. Advances in the biosciences, spurred by the human ability to think around corners, have transmuted unconventional ideas into reality—from bacteria that manufacture human insulin, to glowing transgenic mice. We've even managed to map the human genome, and more recently we extended our new-found abilities not just to other living species, but to a few that succumbed entirely to the ravages of time and environment. A prime example is the woolly mammoth, the icon of the late-Pleistocene epoch.

With the exception of a few holdouts like bison, caribou, and elk, most of the large animals (megafauna) native to North America died out during the chaotic transition from Ice Age to interglacial about 10,000–13,000 CALYBP. Some, like the horse, were rendered regionally extinct, but survived elsewhere; others, like the woolly mammoth, disappeared completely—not

just in North America, but everywhere in the world. Mammoths didn't disappear overnight; we now know that small populations persisted for thousands of years in isolated locales. But by 4,000 years ago, even those were gone . . . though possibly not forever.

## Woolly Mammoths 101

*Mammuthus primigenius*, better known as the woolly mammoth, was one of about a half-dozen species of mammoths that roamed the Pleistocene world. A close cousin of modern elephants and a contemporary of the mastodon, now also extinct, mammoths first appeared about 5 million years ago in Africa, Asia, and Europe. Mammoths and living elephants as a group, referred to in biological circles as the “elephantine elephantids,” are most closely related to the stegodontines, an extinct group of proboscideans with which they shared a common ancestor in the late Miocene. Elephantids in general are



related to a primitive mastodon-like stock called gomphotheres.

The woolly mammoth, the final and smallest species in the mammoth line, first shows up in the fossil record more than 200,000 years ago as a descendant species of the Eurasian steppe mammoth, *M. trogontherii*. In this case, small is a relative term: adult woolly mammoths were about 9 ft tall and massed about 10 tons. That is, they were a bit shorter but more heavily built than Asian elephants and quite a bit smaller than African elephants, our largest living terrestrial mammal. Woolly mammoths were characterized by a high, peaked head and tiny ears. Elaborately curved tusks up to 16 ft long were presumably used to root in the snow or loose soil for food. The hair of their shaggy coats, which grew as long as 3 ft, varied in color from light to dark. Some may have been blond, others brown or reddish brown. Like all its *Mammuthus* cousins (and unlike the mastodons, which browsed on trees), woolly mammoths were primarily grazers, subsisting on a diet of sedges, grasses, and rushes, with a small admixture of cacti and bushes like water birch and blue spruce. The average adult required up to 600 pounds of food a day. Woolly mammoths were presumably herd animals, although males probably left the herd when they reached puberty at about 12 years old.

Woolly mammoths probably ventured into North America at least 200,000 years ago. Here they joined three other mammoth species already present: the huge Imperial mammoth (*M. imperator*), the Columbian mammoth (*M. columbi*), and the Jeffersonian mammoth (*M. jeffersonii*). These species tended to live side-by-side, ranging from Canada as far south as Nicaragua and Honduras; it's possible, in fact, they were actually a single widely variable species. But *M. primigenius*, the star of this article, was definitely a distinct species. How can we be certain? Because woolly mammoths stuck pretty much to the tundra of the far north, the environment to which they were physically adapted, and that frigid environment has preserved hundreds of specimens for us to examine.

### The woolly mammoth's fate

The end of the Pleistocene saw a drastic reduction in the number of large terrestrial animals all over the world. For North America, geochronologist Tom Stafford and geoscientist

Russell Graham have documented a two-pulse megafaunal extinction, the events occurring about 11,200 and 10,850 RCYBP (MT 21-4, "Earlier Than You Think: The Timing Of Megafaunal Extinctions In North America"). Interestingly, the North American proboscideans survived the first great pulse of extinction, when horses, camels, ground sloths, giant bison, and musk ox exited the continental stage. But both mammoths and mastodons succumbed to the second pulse; populations dwindled rapidly, and within a century they were all but gone, with the exception of tiny woolly mammoth populations that hung on for a few millennia in isolated refuges.

It's hard to say exactly what did the mammoths in; many

theories have been postulated about their extinction, some verifiable, some not. The quickly changing climatic conditions may have played a role, particularly when they caused wide-ranging shifts in vegetation regimes. Research by R. Dale Guthrie of the University of Alaska, for example, suggests that this was in fact the case for the already declining mammoth populations of Alaska and Yukon (MT 22-3, "Megafaunal Extinctions Revisited"). Local conditions favored a rapid shift from a short, grass-sedge-sage steppe vegetation regime, which the mammoths thrived on, to taiga-tundra vegetation including species that were either toxic to mammoths, such as dwarf birch, or



Poinar (in mask) and MacPhee collecting a sample from a mammoth bone at the Zoological Institute in St. Petersburg, Russia.

couldn't support as large a biomass.

On the other hand, the arrival of a new competitive species, *Homo sapiens*, is considered by many to have contributed to (if not actively precipitated) the mammoth extinction. This is the basic assumption of the overkill theory proposed by geologist Paul S. Martin, who pointed out that massive extinctions have coincided with the spread of humanity for the past 50,000 years. Not every large animal genus has died out congruent with the expansion of modern humans; but so many have, on every new continent that modern humanity has set foot on, that it's hard not to come to the conclusion that we're at fault. Ross MacPhee, a specialist in extinct mammals at the American Museum of Natural History, makes no bones about the connection: "It seems there's an aspect of singularity related to human presence as they entered specific continents." He points out, for

example, that there's only one Paleo-Eskimo site on Wrangel Island, one of the woolly mammoth's last havens—and it's roughly coeval with the last of the mammoths, at about 4,000 RCYBP. "That's generally consistent with Paul Martin's argument," Dr. MacPhee concludes. "Humans come, and animals go."

A decade ago, MacPhee expanded on the concept that humans were directly associated with Pleistocene extinctions by offering an alternate mechanism: hyperdisease. According to the hyperdisease theory, humans didn't kill off the megafauna directly; they introduced pathogens that ravaged the megafauna populations, which were already overstressed by climatic changes—and yes, by over-hunting (**MT 14-1**, "Explaining Pleistocene Extinctions: Hyperdisease"; **MT 18-4**, "Tuberculosis Found in Mastodon Makes the Case for Hyperdisease in Megafauna"). The resulting

the extinctions were driven by the impactor hitting North America, the size of the effect would have been equal to what happened at the KT [Cretaceous/Tertiary] boundary. This did not happen." MacPhee believes the Clovis Comet theory is structurally inadequate for what it's being asked to bear—but so are hyperdisease and over-hunting, he says. "At the end of

MacPhee (left) and Poinar collecting a sample at the St. Petersburg facility. ►

Poinar with Dima, the baby mammoth, at the Museum of Zoology, St. Petersburg. ▼



BOTH: DEBI POINAR



the day that's not very scientific," he muses, "but it may be all that we can do at this stage."

Some researchers have proposed that a combination of all the aforementioned factors, and possibly others, drove mammoths into extinction. That seems realistic to many; after all, Mother Nature rarely hands us a solution wrapped up in a simple, neat package. But MacPhee cautions against such arguments: "Multicausal arguments are fine, as long as you can factor in each of the causes that contributed to the effect. If you can't, it's spreading the veil of obscurity further. You have to find evidence of each before it deserves a place at the table of argument."

plague would have finished off most of the mammoths, leaving only the small populations previously noted.

It's also possible that a cometary impact in eastern Canada about 13,000 years ago was the final blow that rendered the proboscideans locally extinct (**MT 23-1**, "The Clovis Comet: Evidence for a Cosmic Collision 12,900 Years Ago"). The evidence marshaled for this theory is both extensive and fascinating, as we chronicled in our recent four-part series on the subject, and the researchers involved are still presenting evidence supporting the impact. The problem with that theory, says MacPhee, is that it's specific to North America. "It pays no attention to the fact that there are basically coeval disappearances in Asia and South America," he explains. "If

### CSI: The Pleistocene

The woolly mammoth is long extinct, but that doesn't mean we can't probe its genome, and maybe even learn how to build one someday. But the question is, Why mammoths? Wouldn't saber-toothed tigers or dire wolves be, well, sexier than big, hairy elephants?

You might think so, but woolly mammoths have a few advantages over other extinct megafauna. For one thing, they're pretty popular. "There's no magic in mammoths," MacPhee admits, "but because of all the studies going on and interest groups involved, we get a lot more mileage out of mammoths than we would out of any other extinct species. They're totally iconic for the Pleistocene." Hendrik Poinar, Director of the

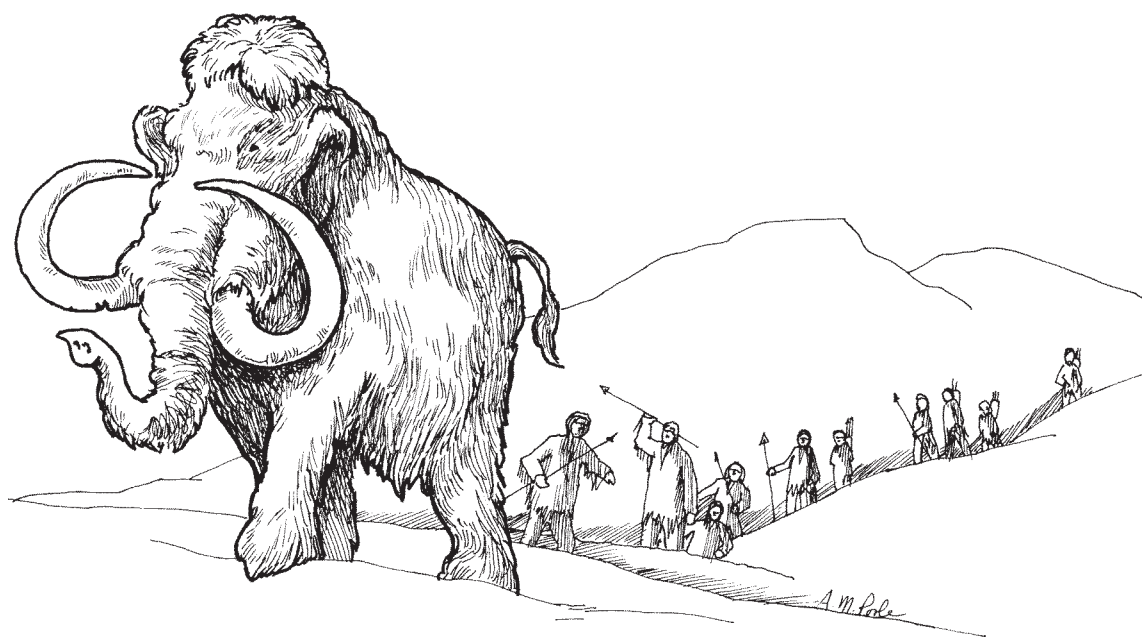


Ancient DNA Centre at Ontario's McMaster University (**MT 20-1**, "Ancient DNA: A Tough Nut to Crack"), agrees; in fact, the term "iconic" often comes up during mammoth discussions. "Another thing," Dr. Poinar adds, "is that they have living relatives, some of the most fascinating animals still alive—kind of modern surrogates that give us an idea of what they would have looked like."

And then there's the fact that mammoth remains are common. As science writer Henry Gee laconically put it in a *Nature* article back in February 2006, "The permafrost environment seems to favour the preservation of ancient DNA in quantity." That's a bit of an understatement: people have been finding preserved mammoths, both whole and partial, in the permanent icebox of the Arctic for hundreds (perhaps thousands) of

nuclear DNA of 160 mammoths from across the Arctic. This study—which both MacPhee and Poinar participated in—suggests that toward the end, North American woolly mammoth populations moved into Siberia and displaced their Eurasian cousins.


It's now believed that mammoths and African elephants split into divergent lineages about 6 million years ago, with Asian elephants diverging about half a million years later—and that all of them descend from an earlier mastodon ancestor. The DNA studies mentioned here may eventually provide detailed information on the form and appearance of mammoths, as well as common diseases associated with the genus—and if we dare, they may lead us to recreate the woolly mammoth on our own.



years, sometimes complete with hair and soft tissues. Bones are even more common. Not surprisingly, permafrost specimens offer the greatest potential for advancing mammoth studies; moreover, our ability to extract useful information from bone and even sediments is advancing rapidly, promising exciting discoveries in the future.

Since the initial isolation of mammoth DNA in 1984 and the determination of an initial base sequence in 1994, at least three research groups have published the complete mtDNA sequence of a woolly mammoth. Meanwhile, nuclear DNA hasn't been ignored; but given the immensity of the task, results have been slower in coming in. However, in the 20 November 2008 issue of *Nature*, a team led by Webb Miller and Daniela Drautz of Pennsylvania State University's Center for Comparative Genomics and Bioinformatics published a study expanding the nuclear genome of the woolly mammoth to at least 3.3 billion base-pairs. They confirmed previous estimates that the mammoth genome contains more than 4 billion base-pairs, about a billion more than ours.

In another recent study, which appeared in the 9 September 2008 issue of *Current Biology*, a large team examined the

In Part II of this article we'll take a more detailed look at what these DNA studies reveal about the evolution of woolly mammoths and their closest relatives. 

—Floyd Largent

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**A** MUMMIFIED CARCASS, big and hairy and stinking to high heaven, surfaced following a permafrost landslide in August 2007 outside the town of Tsiigehtchic, Northwest Territories. The thawing remains unavoidably caught the attention of resident Shane Van Loon, who, for reasons we can only imagine, labored for a week to remove them from the river bank and stuff them into his freezer.

The scientific community owes a giant debt of gratitude to Van Loon for his heroic feat, for what he saved from destruction is the first Ice Age megafauna carcass found in this previously glaciated area. The soft tissues hold many times more information about the animal's health and its place on the evolutionary scale than could be gleaned from bones alone. Its mere presence in this section of Beringia, rendered uninhabitable during much of the terminal Pleistocene by the Laurentide ice sheet, has enlarged our knowledge of the Ice-free Corridor.

### Enter the experts

The scientist that Van Loon first notified of his find was Glen Mackay, an archaeologist with the Department of Education, Culture and Employment at the Prince of Wales Northern Heritage Center, Northwest Territories, who enlisted the help of Grant D. Zazula, a paleontologist for the Yukon Paleontology Program at the Yukon Department of Tourism & Culture. Together Mackay and Dr. Zazula first stopped at the collection site, which lies at the confluence of the Arctic Red and Mackenzie rivers. There they examined sediment structure and stratigraphy and, according to Zazula, experienced firsthand the rotten stench that still clung to the earth where the remains had been removed less than two weeks earlier.

The scientists identified the remains as steppe bison, *Bison priscus*, a megaherbivore. For 700,000 years it dominated the cool grasslands that during the Pleistocene extended from England across northern Eurasia and into North America. The steppe bison eventually crossed the Bering Land Bridge probably sometime during the last 125,000 years of the Pleistocene. Its image can be found in Paleolithic cave paintings in France and Spain. In our own time, well-preserved remains have been found in the Yukon, Alaska, and Siberia. Probably the best-known instance is "Blue Babe," an adult male steppe bison that

had been killed and partially eaten by American lions about 36,000 years ago. (The nickname, borrowed from Paul Bunyan's mythical ox, was applied to this remarkably intact carcass because a bright blue mineral, vivianite, an iron phosphate, coated its hide.)

### Radiocarbon testing and the Ice-free Corridor

Blue Babe, however, was found near Fairbanks, Alaska, and apparently lived during a relatively warm phase (interstadial) of the last glaciation that occurred from about 50,000 to 25,000 years ago. The Tsiigehtchic steppe bison was found in an area that had been occupied by the Laurentide ice sheet, a part of Beringia that had never surrendered megafauna remains dating to the Ice Age. As a check, Zazula ordered radiocarbon

# Bison Carcass Dates the Ice-free Corridor



Skull of the Tsiigehtchic steppe bison.

ALL PHOTOS: GRANT D. ZAZULA, YUKON GOVERNMENT

dating of the remains. Dr. Fiona Brock of the Oxford Radiocarbon Accelerator Unit at the University of Oxford performed an AMS (accelerator mass spectrometry) analysis on a sample from the bison's right metacarpal (foot bone). Zazula expected the results would reveal an age of about 30,000 RCYBP, a time that predated glaciers in that part of Beringia. To his surprise, the bison yielded a radiocarbon age of  $11,830 \pm 45$  RCYBP.





### DNA testing and local extinction

The specimen found at Tsiigehtchic had a few surprises for geneticists who analyzed its DNA. The steppe bison species was an intermediate step in the evolutionary continuum of bison. Before becoming extinct, *Bison priscus* gave rise in Europe to *B. bonasus*, the wisent, in North America to *B. bison*, the American buffalo. DNA tests performed by Dr. Beth Shapiro and Brandon Letts of Pennsylvania State University Department of Biology, however, show the Tsiigehtchic specimen is a member of a completely distinct clade (species subset) of bison not

**The site where the steppe bison carcass was found. In the background is the town of Tsiigehtchic, in the foreground the Arctic Red River.**

The reeking carcass that Shane Van Loon rescued from a slumping river bank thus confirms that the Laurentide ice sheet must have receded from the lower Mackenzie River valley by about 13,700 CALYBP, less than 500 years before the oldest Clovis occupation. This establishes a known date when the lower valley was ice free and therefore open for business for travelers, human and animal. Although the lower valley has always been a proposed corridor linking Beringia with the continental U.S. to the south, the absence of sites in the Mackenzie River valley with firm radiocarbon dates had previously made it difficult to state with confidence when the ice sheet receded from the valley. Consequently, scientists constructing models of migratory routes through Beringia have had to substitute dates from other areas to the east and south.

The steppe bison carcass doesn't change the existing postglacial models for the region; on the contrary, Zazula emphasizes that it confirms them. "The find gives real weight to the established models," he says, "which is nice because sometimes these models are based on a lot of problematic ages or pieces of data. It is nice to have something to hang your hat on in terms of a real date. Sometimes those are hard to come by in this sort of work."

related to the mtDNA lineage that gave rise to modern bison—in other words, it's an evolutionary dead end. "The Tsiigehtchic specimen is from one of the last remaining steppe bison from Beringia," says Zazula, "extinct a few hundred years later."

Scientists believe that groups of steppe bison living in Beringia during the late Pleistocene must have been isolated from populations of steppe bison living south of the ice sheet, progenitors of modern *B. Bison*. Based on mtDNA samples from assorted fossil specimens, they concluded that steppe bison in Beringia (present-day Alaska and the Yukon Territory) became extinct at the end of the Ice Age. Data gathered from the Tsiigehtchic carcass don't contradict that theory. Zazula believes that after Beringian steppe bison became extinct, probably because of an inability to survive the quickly changing climate, the area may have become recolonized with bison from the south, members of the evolutionary mainstream.



**Zazula at a recent archaeological survey in the mountains of the Yukon.**

### Extinction, the penalty for failing to adapt

Though the reason for the steppe bison's local extinction isn't known for certain, one possibility is that the rapidly changing environment overwhelmed the bison herds of Beringia. "The





transition from steppe tundra, grassland-type environment to present-day tundra and boreal forest occurred in just a couple of thousand years,” Zazula explains. Fossil-pollen records obtained from lake cores confirm that wet meadows, marshes, and ponds took over the landscape. Steppe bison, able to subsist on more diverse forage than the mammoth or horse, survived roughly 2,000–3,000 years as the sole Beringian megaherbivore before their own local extinction. In comparison, environmental changes occurring in the Great Plains south of the continental ice sheets weren’t as dramatic. Either the behavior of bison to the south was more plastic, he reckons, enabling them to adapt more readily to a changing environment, or change there was so gradual that individuals unable to adapt were weeded out while the species survived.

#### **Soft tissue remains—a first**

Because the Tsiigehtchic remains date to a time when the Beringian steppe bison population was declining, the soft tissues give scientists a window into a crucial time for these megafauna.

Rapid burial probably accounts for the excellent preservation of the Tsiigehtchic steppe bison carcass. Outwash plains in front of glaciers often contain quicksand, and it’s possible the bison, traveling near the foot of the glacier, was swallowed by the slurry, which became an oxygen-depleted grave. Zazula, grateful for his good fortune, remarks that “to find mummified tissue in an area that was glaciated is completely new to research up here.” The soft tissues include muscle, hair, stomach, and intestines. What’s most amazing for Zazula is the hide.






bison carcass dates to 11,800 RCYBP, it's reasonable to assume there may be archaeological sites of that age awaiting discovery in the Mackenzie River valley. For Zazula, such a find would be "mind-blowing because most of the archeological record in the Northwest Territory doesn't begin until about 10,000 years ago, well after people had been established in the late Pleistocene on the American continent." He hopes that someday a method will be devised to systematically scan the area for terminal-Pleistocene archaeological and paleontological sites. But even if that day never comes, he's happy to continue relying on fate—which, he believes, sometimes "works in our favor when stuff like this pops out of the ground."

### A boost for civic pride

The roughly 200 people in the village of Tsiigehtchic have taken a great interest in the find: the first mummified carcass of an Ice Age mammal ever found in an area previously covered by the Laurentide ice sheet in Canada, and the first radiocarbon-dated Pleistocene mammal excavated from the Mackenzie River valley. The townspeople have agreed to watch for anything else that might melt out of the permafrost there.

Today the Tsiigehtchic specimen is keeping many scientists

occupied examining and conserving it. Zazula has no doubt that the information gleaned will be put to good use. "There are still so many outstanding questions about why mammals go extinct at the end of the Ice Age," he reasons. "To find a specimen that dates to within that time interval, and of such amazing condition and such quality may possibly help us work out some answers to those questions."

It's a pleasure to report a satisfying end to a project with such an unsavory beginning. A playwright with a fine appreciation for irony might call this another instance of the sweet smell of success. 

—Dale Graham

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## Paleoindian Migration Routes


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during the late-Pleistocene epoch, a succession of migrations flowing back and forth along these two main routes resulted in the patterns of genetic variability that can be traced in the varying mtDNA of modern Native Americans.

### Issues with the study of mtDNA

Cecil Lewis, a molecular anthropologist at the University of Oklahoma (MT 23-2, "Largest-ever Survey of Native American Genes Sheds Light on First Americans"), points out an important limitation of studies that rely upon mitochondrial data to test hypotheses about human migrations: "The mitochondrial genome evolves like a single genetic locus. Inferences about population history from a single genetic locus can be confounded by stochastic events more easily than inferences from multiple, independently evolving, genetic loci." In other words, frequencies of mitochondrial DNA haplogroups, particularly if they are rare in a population, may be so vulnerable to the slings and arrows of random events that the disappearance of variants, such as X2a or D4h3, from different segments of a colonizing population may not be especially surprising or as significant as it might at first appear. Although Albert Einstein famously quipped that God does not play dice, molecular evolution does in fact involve a substantial component of dice-throwing. And small, random events can have large consequences for evolution.

Dr. Lewis thinks the importance of studies like the one

conducted by Perego, Achilli, and their colleagues lies in their demonstrating that "the population dynamics that occurred during the peopling of the Americas were not simple." He suggests that future studies foster collaborations with more Native American communities to obtain a more representative geographic sampling of genetic variability in the Americas; focus increasingly on collecting data on "multiple, independently evolving, genetic markers"; and apply more and more robust analytical methods to their analysis "to further tease out the relevant patterns in these data." 

—Bradley Lepper

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## Suggested Readings

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