Which takes us full circle. It had become evident to physical anthropologists of the early 20th century that the scenario that José de Acosta had originally proposed on the basis of biblically inspired logic in the 16th century was, in fact, supported by multiple lines of biological evidence. Hrdlička himself believed that Native Americans arrived in North America via a land bridge that stretched from Siberia to North America. He conducted a great deal of fieldwork in Alaska trying to test this idea.

The Genetic Puzzle

Long before techniques were invented that allowed scientists to amplify and sequence DNA and "read" variation directly from genes, human genetic differences had to be inferred by looking at "classical" genetic markers such as blood groups and variants of other proteins (called polymorphisms). The frequencies of these markers were variable in different populations. This variation was easy to detect, and it gave geneticists an idea of the underlying genetic variation in different populations (42).

Data from these classical genetic markers were collected by the first generation of anthropological geneticists from many populations across the Americas, including from North Americans belonging to 53 tribes (43). By this point, although their approaches to informed consent were somewhat mixed, many of the first generation of anthropological geneticists sought consent for conducting their research from both individuals and communities as a whole. We will discuss the history of research ethics more in chapter 9.

Together, their studies revealed that Native Americans had

genetic variants that were unique to the Americas and widely shared across North, Central, and South America. These variants must have been present in a shared ancestral population. The studies also showed that Native American populations were genetically most similar to Siberian and East Asian groups.

Classical genetic markers were like the edge pieces of a complicated puzzle; they allowed for the rough outlines of the history of Native American peoples to be assembled but still gave only hints about what the picture contained. Archaeological and linguistic evidence also linked Native Americans to Northeast Asia sometime in the distant past.

Beginning in the late 1980s and early 1990s, anthropological geneticists imported tools from molecular biology that filled in a few more pieces of the puzzle. In chapter 5, I will walk you through the process of retrieving and sequencing DNA order to characterize a person's mitochondrial DNA lineage or haplogroup. Before these processes were invented, researchers were able to identify what haplogroup someone belonged to in a cruder way: by digesting extracted mitochondrial and Y chromosome DNA with enzymes that cut the molecules at different spots depending on a person's DNA sequence. The resulting fragments would appear in specific patterns when run out on an agarose gel. This method, known as restriction fragment length polymorphism analysis (RFLP), was performed on DNA sampled from Native Americans across North, Central, and South American populations. Later, when more refined techniques for amplifying and directly sequencing DNA were imported from molecular biology, large sections of the puzzle began to be filled in.

MITOCHONDRIAL AND Y LINEAGES IN THE AMERICAS

Think of maternally inherited mitochondria and paternally inherited Y chromosomes as similar to a family tree: Individual lineages are related to each other because of descent from a common ancestor (a "grandparent"). Geneticists classify groups of closely related lineages—families—into haplogroups. Several mitochondrial and Y chromosome haplogroups arose on the American continents that are seen only in people of Native American descent. Just as members of a family may resemble one another in physical features, lineages belonging to a single haplogroup have the same set of "mutations" (DNA variants called single nucleotide polymorphisms, or SNPs) at certain spots in their sequence—these are used to classify lineages into haplogroups. And just as you are not identical to your grandmother, lineages within a haplogroup may have additional variation beyond the haplogroup-defining mutations; DNA bases change over generations.

Before European contact, all the Indigenous peoples in the Americas could trace their mitochondrial and Y chromosome lineages inherited along maternal and paternal lines, respectively, back to several founding haplogroups. (Today Native Americans are genetically quite diverse and may carry mitochondrial and Y lineages commonly found in other parts of the world as well.)

The founder haplogroups are direct descendants of ones present in Siberia, with additional variation that arose

during the founding population's isolation and after population dispersal throughout the continents. The distribution of mitochondrial and Y lineages across the continents is not random; it reflects population history and has been used to identify events such as migration and gene flow or long-term continuity within a region. The so-called "Pan-American" mitochondrial haplogroups (A2, B2, C1b, C1c, C1d, C1d1, D1, D4h3a) are thought to have been present in the initial founding groups as they dispersed across North and South America. D4h3a (found primarily along the Pacific coast of the continents) and X2a (found only in North America) have been suggested to be markers of two migration routes, coastal and interior.

Mitochondrial haplogroups present in pre-contact First Peoples include the following:

South of the Arctic: A2
B2
X2a, possibly X2g
C1b, C1c, C1d, C1d1, C4c
D1, D4h3a
In circum-Arctic peoples: A2a, A2b, D2a, D4b1a2a1a

Geneticists sometimes use "A, B, C, D, X" as a shorthand for these haplogroups, reflecting a period of time when approaches for determining haplogroups could not distinguish between sub-haplogroups like A2a and A2b. All mitochondrial lineages commonly found in populations below the Arctic Circle share common ancestors between about

18,400 and 15,000 years ago. This close agreement suggests that they were all present in the initial founder population(s). Mitochondrial lineages within Siberian and Native American populations show that their ancestral populations became isolated from each other between about 25,000 and 18,400 years ago. From this genetic diversity, one can estimate the effective female population size of the founding population to be approximately 2,000. This is not the actual population size, but rather an estimate of breeding individuals (in this case, females). The actual population size would have been larger than that, but the total is hard to estimate. Arctic lineages show a much more recent expansion consistent with the Paleo-Inuit and Neo-Inuit migrations (see chapter 8).

Y chromosome founder haplogroups in Native Americans include Q-M3 (and its sub-haplogroups, including Q-CTS1780), and C3-MPB373 (potentially C-P39/Z30536). Other haplogroups found Native American populations, like R1b, were likely the result of post-European contact admixture (44).

The picture that genetic data revealed was incomplete and lacking many details, but it was enough to unequivocally answer the question posed at the beginning of this chapter and confirm the growing body of archaeological and linguistic evidence showing connections with northeast Asian populations. Many Native Americans possessed mitochondrial (A, B, C, D, X) and Y chromosome haplogroups (C and Q), clearly sharing common ancestry with haplogroups from Asia. These lineages also had

additional genetic variation that arose after their separation from Asian lineages.

Together, mitochondrial and Y chromosome DNA from contemporary Native American populations gave a clear signal that they *were* the descendants of a population that had split from a larger group in northeast Asia and then had been isolated from other peoples for many thousands of years.

Ancient DNA researchers confirmed this model by finding the same lineages within ancient Native Americans. They found no evidence for ancestry from any other source in populations predating European contact. This finding effectively refuted the long-standing (though by now fringe) theories about the ancient Mound Builders (see "European Influences on Ancient North America?" sidebar). It confirmed the reconstructions based on dental and some skeletal traits linking the ancestors of Native Americans to Siberian ancestors.

EUROPEAN INFLUENCES ON ANCIENT NORTH AMERICA?

Alongside mainstream archaeological models for how people got to the Americas lie alternative ideas for their origins. These theories are bizarre, diverse, and fanciful, encompassing everything from the notion that the first peoples in the Americas were ancient astronauts to the absurd idea that Smithsonian curators are secretly hiding the skeletons of giants in their vaults. (I've been in these facilities and can assure you that there are no giant skeletons or hidden secrets.) While fringe theories about the past often pretend to be scientific, they

history at the site, and there are even oral traditions among both Native Americans and Norse about this meeting. The Solutrean-Clovis connection rests upon a similarity in one kind of tool, without any other cultural connections, and a bunch of conjectures about what "could have happened." But science isn't built on "could haves" and "maybes." Models must be built based on evidence you have, not evidence you wish you had. The Solutrean hypothesis is lacking sufficient evidence to be considered a serious explanation for the origins of Clovis by the vast majority of archaeologists and—I'm going to be bold here—literally every credible geneticist who studies Native American history.

Some proponents of the Solutrean Hypothesis suggest that mitochondrial haplogroup X2a, found in some ancient and contemporary Native Americans from North America, might be a marker of European ancestry. Today, lineages of haplogroup X are found widely dispersed throughout Europe, Asia, North Africa, and North America. We can reconstruct their evolutionary relationships—much like you can reconstruct a family tree. Lineages present in the Americas (X2a and X2g) are not descended from the lineages (X2b, X2d, and X2c) found in Europe. Instead, they share a very ancient common ancestor from Eurasia (X2). X2a is of a comparable age to other indigenous American haplogroups (A, B, C, D), which would not be true if it were derived from a separate migration from Europe. Finally, the oldest lineage of X2a found in the Americas was recovered from the Ancient One (also known as Kennewick Man), an ancient individual dating to about 9,000 years ago and from the West Coast

(not the East Coast as would be predicted from the Solutrean hypothesis). His entire genome has been sequenced and shows that he has no ancestry from European sources. There is no conceivable scenario under which Kennewick Man could have inherited just his mitochondrial genome from Solutreans but the rest of his genome from Beringians. Thus, without additional evidence, there is nothing to justify the assumption that X2a must have evolved in Europe (51).

No Europeans need to be invoked as the intellectual forces behind Indigenous technologies or cultural achievements. The true histories, evident in genetics, oral traditions, and archaeology, are exciting enough.

But even mitochondrial and Y chromosome sequences gave only a limited glimpse of history. It took the genomic revolution to start filling in the missing pieces, and we're still only partway there. With the ability to obtain whole genomes from ancient individuals, geneticists could confirm what was already pretty certain: There was a clear ancestor-descendant relationship between the ancient peoples of the Americas and contemporary Native Americans. And their line of ancestry stretched back thousands and thousands of years, eventually connecting during the Paleolithic, with cousin lineages stretching from present-day East Asians and Siberians. But before we can delve into that story, we must first understand what the archaeological record tells us about the earliest peoples in the Americas. We'll begin this exploration in the next chapter.