

## The Story of the Horse

**At the CANA Foundation we are committed to saving the wild horses of the American West through advocacy and education. In this section we outline how our scientists are studying the evolutionary history of the horse using fossil and modern evidence.**

**Background:** The earliest identifiable members of the horse family, known as Equidae, arose some 13 million years after the demise of the dinosaurs 66 million years ago. That places them among the oldest families of mammals that have survived into modern times. Equids have lived in North America for 53 million years, in an unbroken stretch from the early Eocene until the end of the Pleistocene 11,500 years ago. Fossil records indicate that at the end of this interval *Equus* populations were living not only throughout North America, from Alaska to Central America, from California to the Atlantic coast, but also in South America, from the llanos of Venezuela to the pampas of Argentina. Much earlier they had entered Eurasia over the Bering landbridge. Everywhere horses went, they prospered.

But then something happened. In one of the greatest natural history mysteries of all time, horses, along with dozens of other large (or megafaunal) species, died out in the Americas 10,000-11,000 years ago. For most of them, this was the end of their evolutionary road. In a few cases, species that had migrated during their evolutionary history managed to carry on elsewhere. In even fewer cases, the immigrants came back home to the places in which they originated. The horse is such a one.

**Beringia, the intercontinental land bridge, and the *Equus* diaspora.** Long before equids disappeared in the New World, they repeatedly dispersed over the Beringian landbridge, which links northeastern Asia with Alaska. Unlike the Panamanian land bridge, which formed comparatively recently, the Beringian land bridge has been up and down multiple times over the

past 66 million years. It was not only North American equids that used the bridge as a faunal highway---over this long period of time dozens of different groups passed east to west, or west to east, adding to the diversity on both sides. Equids found new lands and opportunities in Eurasia and Africa. Various lineages eventually differentiated into some of the species we know today, including asses, kiangs, zebras, and others. Thanks to their ability to successfully disperse, the horses we have today are among these survivors, despite the fact they completely died out in their original homeland, North America.

Or did they? According to various Native American oral traditions, not all horses died out at the end of the Pleistocene. Some survived; later on, their descendants were domesticated by Indians long before the Spanish showed up—with domesticated European horses--in the early 16<sup>th</sup> century. Whether these traditions have a factual basis is currently difficult to determine from a scientific perspective, as there are no horse fossils from the New World which confirmably fall within the critical interval between roughly 10,000 and 500 years ago. Obviously, until and unless specimens are found that unquestionably document late survival, this will have to remain an intriguing but unverified possibility.

**What does domestication mean biologically?** We are all familiar with domesticated mammal species, especially companion animals like dogs and cats. The process of domestication is multifaceted, involving not only changes in physical characteristics, but also modifications in behavior. But such changes are due to *artificial selection*, that is, breeding for characteristics determined by humans, not nature. There are many obvious examples. In the case of horses, think of the differences between a Belgian (bred for great size and strength) and a Shetland (bred for small size and behavioral docility). Yet despite their physical differences these breeds share a very recent common ancestry. Their joint ancestors lived just a few centuries ago.

How can such massive changes, normally taking hundreds of thousands to millions of years, be explained? Artificial selection works on a faster time scale than natural selection,

because humans are usually interested in enhancing only a limited range of traits in their domesticants. By restricting breeding to animals that express acceptable versions of such traits, within a few generations so-called “pure-breeding lines” can be created, ones that express the features desired and are capable of passing them on to their progeny.

But note that there is nothing pure about pure-breeding lines. If you ignore the traits that define a particular breed and focus instead on features that were not subjected to artificial selection, you'll see that they often vary freely, just as they would in natural populations. For an overwhelming number of traits, horse breeds do not significantly differ from one another (for example, non-conformational characteristics, facial features, organ size).

**How did domestication occur?** According to the archeological record, efforts at horse domestication began at least 6000 years ago in Central Asia, on several different occasions. One of the first things that humans probably did as part of the domestication process was to select for behavioral characteristics like docility and responsiveness to human commands. Ancient horse breeders realized that one key to successful domestication was to select for animals that could be trained to accept human dominance. They probably did that by observing the roles of dominant mares in herd organization. Interestingly, although there were efforts in the 19<sup>th</sup> century to domesticate zebras, they were unsuccessful in part because zebras aren't like our horses. Dominant females do not play an overarching role in zebra herd structure; no domination, no effective domestication.

Domestication comes at a price—for the animals concerned. Controlling breeding for features that might appeal to humans, but have no useful role otherwise, may result in creating lineages that are, in adaptational terms, total disasters. Such lineages are only kept from rapidly dying out because we can make it so. Particularly common in many breeds of domestic animals is the high frequency of recessive traits that would normally be edited out if natural selection were in

full force. No surprise: we know that the same thing happens in human groups where excessive inbreeding is allowed. In short, domestication is not and never was a natural process, whatever its perceived benefits to ourselves.

### **What is the biological status of domesticated lineages compared to their wild ancestors?**

Although there is disagreement among scientists as to how such lineages should be classified, at CANA we take a position that is grounded in evolutionary biology. All such lineages should be regarded as populations that are derived from, and therefore remain as members of, the wild species in question. Consider dogs. No biologist questions whether the lineages of these companion animals ultimately converge in wolf ancestors, perhaps as much as 30,000 years ago or more. Yet over this vast expanse of time, wolves and domestic dogs have hardly diverged in one critical way: wolf-dog crosses still result in viable, fertile offspring. Nowadays biologists do not regard domestic dogs and wolves as different species, grouping everything from chihuahuas to great danes along with their wild relatives in one species, *Canis lupus*. That's not to say we can't recognize different groupings for other reasons. Obviously, female chihuahuas and male great danes are not likely to successfully produce offspring just because the sheer difference in the size of fetuses would make normal delivery out of the question. But that does not make them different *species* on any reasonable biological ground. Their genetic endowments are overwhelmingly the same, apart from changes forced by controlled breeding.

The hallmark of any good natural species is that breeding between normal adults regularly results in viable, fertile offspring. The fundamental reason for this is close correspondence in parental genomes, so that all of the biological processes set in motion after fertilization almost always result in successful development. Over time, populations will tend to diverge because they are subjected to different selective forces, but this does not happen on a rigid schedule. Even after what seems like very lengthy separations in space and time, populations may not have diverged to the extent that production of fertile, viable offspring is no longer possible.

Divergence should be thought of as a spectrum, not as an absolute. Horses and donkeys can still be successfully mated, but chromosomal differences between these two species are now too great to result in fully successful outcomes. Mules are certainly viable---even desirable from the human standpoint because of their compact size and great strength---but they are almost never fertile. In evolutionary terms, they are dead ends.

**The Myth behind the BLM's Myth #12.** If you go to the Bureau of Land Management (BLM) website, you'll encounter a page which lists a series of so-called myths about wild horses (<https://www.blm.gov/programs/wild-horse-and-burro/about-the-program/myths-and-facts>). Myth #12, *Wild horses are native to the United States*, quoted below, makes a number of assertions.

This claim is false. The disappearance of the horse from the Western Hemisphere for 10,000 years supports the position that today's American wild horses should not be considered "native." American wild horses are descended from domestic horses, some of which were brought over by European explorers in the late 15th and 16th centuries, plus others that were released or escaped captivity in modern times. Over this 500-year period, these horses (and burros) have adapted successfully to the Western range. Regardless of the debate over whether these animals are native or non-native, the BLM manages horses and burros on public lands according to the provisions of the 1971 Wild Free-Roaming Horses and Burros Act, which describes the animals as "wild" rather than feral.

Of particular interest is the statement that the domestication of horses 6,000 years ago in Central Asia would have changed them into something else entirely. This implies that domestication remodelled or reconstituted them, somehow erasing their biological history. In this version of the facts, the horses brought to the Americas by early European settlers were not returnees but invaders, members of a new, invasive species with no ties to this land and thus no right to be here. Can such a claim be tested, and if so, how? And if it turns out to be false, are there better, more scientifically grounded interpretations that can tell the story of *Equus caballus* more accurately?

### **The Back Home Project (BHP)**

To tackle some of these questions, the CANA Foundation created the Back Home Project in 2020. Among the research objectives the Back Home Project has recently supported

are efforts to establish, using ancient DNA techniques, whether prehistoric horse populations on opposite sides of the Bering landbridge maintained genetic continuity (ability to successfully interbreed) right up to the time of the New World extinctions 11-12,000 years ago. Scientists working on this problem, with support from various organizations, are seeking to establish whether these prehistoric horse populations share certain unique genetic markers (“fingerprints”) with modern domestic horses. Sharing would imply that all could be a single species, *Equus caballus*, making an objective case for the argument that horses ought to be considered part of the native fauna of North America.

To undertake this work, they use what are known as **ancient DNA techniques**. Under certain circumstances, genetic material may be preserved in a fossil well enough for scientists to substantially recover the organism’s actual DNA code. The results can then be compared to codes from related populations or other species, including living ones. In this way DNA similarities and differences can be catalogued in great detail, so that we gain a full idea of the genetic makeup of the organisms under study. A further step, called **phylogenetic reconstruction**, involves using this information to create very detailed family trees, which allow investigators to establish how specimens from different populations are related to one another, and when they last shared a common ancestor.

We have seen that “genetic continuity” is one of the tests for a population’s membership in a species: if members of the target population can successfully breed with members of other such populations, and produce viable, fertile offspring, then according to the biological species concept all should be grouped in the same species. This definition applies across the board to most multicellular organisms that reproduce sexually. By establishing the degree of genetic similarity among and between ancient and modern horse populations, paleogeneticists have already made a number of important discoveries that bear on the problem of continuity. Their results will be fully documented in peer-reviewed scientific papers.

## ***Glossary***

**Different people may legitimately understand different things about the same word. At CANA we utilize meanings to describe the horse and its evolutionary descent that are in general use by biologists and other scientists.**

**Equidae.** This is a formal taxonomic family, which today includes “the horse” (see below) as well as donkeys, asses, zebras and kiangs. All living members of Equidae are regarded as comprising species of a single genus, *Equus*. In the distant past there were many more genera and species.

**The Horse.** When we refer to “the horse”, we mean the species *Equus caballus*. This species, which includes all living horses and all of the descendants of their joint last common ancestor, was named by the famous Swedish taxonomist Carolus Linnaeus in 1758. He knew only of the domestic horse, and thus defined *Equus caballus* on this basis. Some biologists think that it would be better practice to confine Linnaeus’ name to domesticated varieties, and to refer to the non-domesticated ancestors of the horse by a different name, *Equus ferus*. This may be convenient for some purposes but use of two terms for what is biologically the same thing inevitably obscures the clear, continuous connection between horses from the distant past and those that exist today.

**Biological species definition.** Although you might think that it is comparatively easy to distinguish one species from another, there are actually a lot of decisions that need to be made

along the way. Some of the decisions may be easy—does A look like exactly B, or is it very different?—but others are quite difficult and rely on the taxonomist’s informed judgement. In determining species limits taxonomists may use a wide range of indicators, such as aspects of morphology, behavior, geographic location, and, increasingly, genetic information, to define species in ways that helps to distinguish one from another.

Ultimately, there is no infallible test of “specieshood”, one size fits all. However, one biologically-centered test is often cited as the standard. This is the “biological species concept”, which holds that **if individuals (or individuals within the same group) are capable of producing viable, fertile offspring by mating with other individuals of opposite sex, then they are considered to represent one and the same species.** Although the biological species concept works for most practical purposes, it only becomes a true test when the results of breeding can actually be observed. This is not possible to do with living organisms in many cases, and is out of the question with extinct ones. This is where genomics is especially relevant, because it is possible nowadays to come up with very precise determinations of the degree of genetic resemblance between populations and species. Thanks to advances in ancient DNA, it is also possible to treat fossil DNA in much the same way. Although we cannot utilize the biological species concept as such in paleontological contexts, the requirement that successful breeding always requires very high genetic similarity between partners can be indirectly tested.