

Research team establishes family tree for cattle, other ruminants

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Jerry Taylor, MU professor of animal sciences, holds his “SNP” or “snip” chips. Using the technology, Taylor and a team of international researchers created a very accurate and widespread “family tree” for cows and other ruminants, going back as far as 29 million years. Credit: MU College of Agriculture

Pairing a new approach to prepare ancient DNA with a new scientific technique developed specifically to genotype a cow, an MU animal scientist, along with a team of international researchers, created a very accurate and widespread "family tree" for cows and other ruminants, going back as far as 29 million years.

This [genetic information](#) could allow scientists to understand the evolution of cattle, ruminants and other animals. This same technique also could be used to verify ancient relatives to humans, help farmers develop healthier and more efficient cattle, and assist scientists who are studying human diseases, according to the research, which is being published in this week's edition of the [Proceedings of the National Academy of Sciences](#) (PNAS).

"We studied 678 different animals, representing 61 different species, and using the new Illumina cow 'SNP chip,' or 'snip chip,' we were able to generate some very precise genetic data for which the chip was not designed," said Jerry Taylor, a professor of animal science in the MU College of Agriculture, Food and Natural Resource and lead author of the study. "Our SNP chips allow scientists to examine hundreds of thousands of points on an animal's genome simultaneously. When we applied this technique to 48 recognized breeds of cattle, we were able to construct a family tree and infer the history of cattle [domestication](#) and breed formation across the globe."

The research revealed the history of European cattle, with domesticated cattle moving sequentially through Turkey, the Balkans and Italy, then spreading through Central Europe and France, and ending in Britain. The scientists also found evidence supporting a second route of ancient cattle into Europe by way of the Iberian Peninsula.

The applications for this technology and information discovered in the research could help solve a number of problems and answer questions about evolution, including how humans are related to extinct hominids and how different plant species are related to each other, Taylor said.

Based on the findings, animal scientists can begin to study evolution of certain breeds. For example, if breeds of cattle with high amounts of intramuscular fat, which is known as marbling, are closely related to

each other, then they likely share the same gene variations to create the marbling, which is a trait some beef consumers prefer. On the other hand, if those same cattle are not closely related, different genetic variants might be at work. Understanding how different genetic variations allow high levels of marbling, feed efficiency and disease resistance in cattle could have a large economic impact for farmers who raise [cattle](#) throughout the world.

"This also provides us an opportunity to identify animal models for human disease since, for example, an excess amount of intramuscular fat in humans is associated with insulin resistance and type 2 diabetes," Taylor said. We're all interested in reconstructing our ancestry. This is essentially the same thing, except that we're able to zoom out by millions of years and include relatives who are long gone. The amazing thing about this technique is that it is very fast and extremely cheap. For relatively small amounts of money, we can generate the data that will allow us to recreate millions of years of evolutionary history."

Source: University of Missouri-Columbia ([news](#) : [web](#))

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