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ONLINE NEWS

Horse Genome Map Complete

by: Erin Ryder, Staff Writer

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The first genome map of a horse is complete, providing scientists with a new set of tools for investigating equine disease, scientists at the Broad Institute, a part of the Massachusetts Institute of Technology, and the National Human Genome Research Institute (NHGRI) announced Wednesday (Feb. 7). To read the release click [here](#).

According to Ernie Bailey, PhD, geneticist and professor of veterinary science at the University of Kentucky's Gluck Equine Research Center, the finished map will allow researchers to identify genetic variation between horses and better understand how our equine management practices affect horses' genetic expression.

Sequencing of the domestic horse genome began in 2006, and was built upon the 10-year collaborative effort of the Horse Genome Project (www.uky.edu/Ag/Horsemap), an International group of scientists hoping to use genomics to address important equine health issues. Scientists at the Broad Institute completed sequencing the horse last year, but the sequence was not organized. In effect, they found all the puzzle pieces but had not arranged them to create a picture. This week, the picture was completed.

"It's just basically been a collection of 30,763,255 random DNA sequences in a database," Bailey said. "They determined the relationships among the sequences and ordered them along the 32 pairs of horse chromosomes.

The completed gene map is currently available for researchers through the Broad Institute's Web site, and will be placed on online browsers for easier access within the next couple of weeks.

Now that the completed map is available, Bailey said the information can be applied to studies of genetic expression as well as hereditary variation, leading to a new level of understanding of equine diseases. For example, researchers can study the DNA of laminitic horses and compare it to the DNA of horses that have not had laminitis to find what differences might exist on a genetic level, and therefore identify risk factors for particular horses.

"The nice thing is that prior to this we always needed to have families in order to do studies, and we would follow inheritance patterns through families," Bailey said. "Right now we don't need that because we have so many genetic markers. We can compare genetic markers in randomly-selected horses to horses selected on the basis of the characteristics of interest. These experiments are comprehensive but costly. The Morris Animal Foundation is working to provide the tools necessary to conduct these experiments."

As well as the original horse sequenced (a Thoroughbred mare named Twilight), researchers used DNA from seven different horse breeds to provide information on genetic variation.

According to Bailey, the goal behind the project has always been rooted in its practical applications for horse health.

"The 125 or so scientists that have been involved in this for the last 10 years came to this not because they were DNA scientists or molecular biologists, but because they were interested in particular diseases," Bailey said. "We recognized 10 years ago that we needed this kind of a tool to make progress.

"This is going to be a tool that is like radiographs, vaccination and antibiotics," Bailey said. "The impact of this is going to be equivalent to those."

Readers are cautioned to seek the advice of a qualified veterinarian before proceeding with any diagnosis, treatment, or therapy.



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