

The complete sequencing of genomes of 4 important representative species in Inner Mongolia, China

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Inner Mongolia Agricultural University (IMAU) and BGI, the world's largest genomics organization, jointly announced the complete sequencing of genomes of four important representative species in Inner Mongolia Autonomous Region of China. They are Mongolian sheep, Alxa Bactrian Camel, Mongolian horse, and Mongolian cattle.

The [genome](#) projects are highly valuable for the studies on genetic analysis of important economic traits in Mongolian characteristic species, such as fast breeding and reproduction, strong [disease resistance](#), superior meat quality, among others. The complete genomes also lay the important genomic foundation for further development in livestock breeding.

Inner Mongolia lies in the north of China and is one of the most important bases for agriculture and [livestock production](#), with over 100 million head of livestock in 2011. Currently the worldwide market for Mongolian livestock production totals more than 33 billion USD in annual revenue from a broad range of products, including dairy foods, leather goods, wool or camel hair products and meat products. The four main species - Mongolian sheep, Alxa Bactrian camel, Mongolian horse and Mongolian cattle, are the most productive domestic livestock in Inner Mongolia. They are widely distributed throughout Inner Mongolia, characterized by tolerance to cold and drought, resistance to the unfavourable ecological conditions and poor vegetation.

"Recognizing the importance of the four Mongolian livestock, we partner with BGI to initiate this project one year ago." said Professor Huanmin Zhou, PI of this project and Director of Science and Technology at IMAU, "The whole genome sequences are the basic gene resources for the further study on Mongolian species and also provide a critical foundation for the better understanding of their [genetic traits](#) and protecting the important germplasm resources in China." he added.

In this project, utilizing whole genome shotgun (WGS) sequencing strategy and next generation sequencing technology, libraries of different insert sizes including 170 bp, 500 bp, 800 bp, 2 kb, 5 kb, 10 kb and 20 kb were sequenced by pair-end. The genome sizes of the four Mongolian species - Mongolian sheep, Alxa Bactrian Camel, Mongolian horse, and Mongolian cattle – are about 3 Gb, 2.4 Gb, 2.8 Gb, 2.8 Gb, respectively. "We will perform further comparative genomics and evolution analysis in order to find more scientific evidence to reveal the evolution process, geographical migration and ecological value of Mongolian species." said Zhou.

The genome project of Mongolian [species](#) is part of BGI's '1000 Plant and Animal Reference Genomes Project'. Ye Yin, PI of '1000 Plant and Animal Reference Genomes Project' and Director of Research & Cooperation Division at BGI, congratulated the breakthrough in Mongolian species' genomes research. He said, "Based on next-generation high-throughput sequencing technology and powerful bioinformatics platforms, BGI will do more work in this field and continue to promote the applications of genomics in agriculture."

Provided by Beijing Genomics Institute

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