

Chinese scientists announce the first complete sequencing of Mongolian genome

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Inner Mongolia Agricultural University (IMAU), Inner Mongolia University for the Nationalities (IMUN) and BGI, the world's largest genomics organization, jointly announced the first complete sequencing of Mongolian genome. This genomic study will help researchers to better understand the evolutionary process and migration of Mongolians and their ancestors from Africa to Asia, which also lays an important genomic foundation for further development of human genetic diseases research.

Nowadays, Mongol is a central Asian ethnic group mostly inhabited in Mongolia, Inner Mongolia in China and Buryatia in Russia with about ten millions ethnic mongol people. Tracing back to the 13th and 14th Century, the "Mongol Empire" was commonly referred as the "largest contiguous empire" in the world history, and it has stretched its territory from the Yellow Sea in eastern Asia to the borders of eastern Europe under the leadership of Genghis Khan and his descendants.

The vast empire had promoted exchange of new technology, commodities and culture, as well as trade and migration between different ethnic groups across Europe and Asia. The migration of Mongol in Eurasia Region including China, Middle East and Russia during the period of Mongol Empire has always been debated by scientists. The study of Monlogian genome will provide new insights to their potential impact on the [human evolution](#) at the [genetic level](#).

In this study, the DNA sample was from a male adult who belongs to the

Mongolian "Royal Family" and is the 34th generation descendant of Genghis Khan. "The sample is very valuable for the study with a full record of family pedigree and no background of intermarriage between other ethnic groups." said Professor Huanmin Zhou, Project Investigator and Director of Science and Technology at IMAU.

"With the completion of the first Mongolian genome, we believe that the genomics study of Mongolian will help us to explore the distinctive features of Mongolian and the [genetic differences](#) with other [ethnic groups](#), including the medical genetics and incidence of genetic diseases." stated by Ye Yin, Director of Research and Cooperation Division at BGI.

"We are currently planning to sequence and analyze more Mongolian samples, aiming to build genetic database of Mongolian for supporting research of Mongolian in medicine, migration, evolution, among others." said Professor Zhou, "We are also seeking more participants and helpful advices for the project to promote the research findings for bringing benefits to human." he added.

Provided by BGI Shenzhen

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