



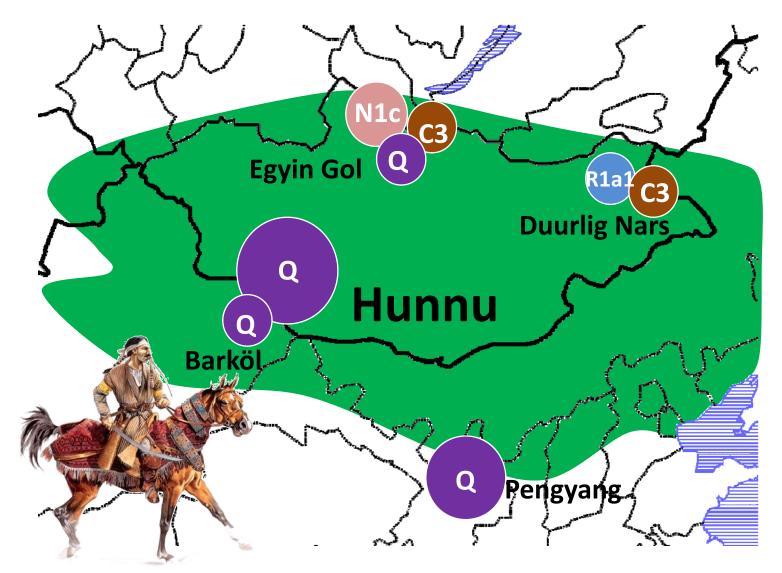
Evolutionary and Population Genetics, No. 2041F, Friday, Oct. 25, 10:30am-11:30am

Y chromosomes of ancient Hunnu people and its implication on the phylogeny of East Asian linguistic families



Key Laboratory of High Altitude Environment and Gene Related to Disease of Tibet Ministry of Education, Tibet University for Nationalities, Xianyang, Shaanxi, China.
MOE Key Laboratory of Contemporary Anthropology, School of Life Sciences, Fudan University, Shanghai, China.

The Hunnu (Xiongnu) people, also called Huns in Europe, were the largest ethnic group to the north of Han Chinese until the 5th century. The ethnolinguistic affiliation of the Hunnu is controversial among Yeniseian, Altaic, Uralic, and Indo-European. Ancient DNA analyses on the remains of the Hunnu people had shown some clues to this problem. Y chromosome haplogroups of Hunnu remains included Q-M242, N-Tat, C-M130, and R1a1. Recently, we analyzed three samples of Hunnu from Barköl, Xinjiang, China, and determined Q-M3 haplogroup. Therefore, most Y chromosomes of the Hunnu samples examined by multiple studies are belonging to the Q haplogroup. Q is mostly found in Yeniseian and American Indian peoples, suggesting that Hunnu should be in the Yeniseian family. The Y chromosome diversity is well associated with linguistic families in East Asia. According to the similarity in the Y chromosome profiles, there are four pairs of congenetic families, i.e., Austronesian and Tai-Kadai, Mon-Khmer and Hmong-Mien, Sino-Tibetan and Uralic, Yeniseian and Palaesiberian. Between 4,000-2,000 years before present, Tai-Kadai, **Hmong-Mien, Sino-Tibetan, and Yeniseian languages** into toned analytic transformed languages, becoming quite different from the rest four. Since Hunnu was in the Yeniseian family, all these four toned families were distributed in the inland of China during the transformations. There must be some social or biological factors induced the transformations at that time, which is worth doing more linguistic and genetic researches.



Thirteen ancient DNA samples of Hunnu from Barköl site have been typed for Y chromosome SNPs and STRs. All these samples fell into Y chromosome haplogroup Q. One of the samples showed the STR data as follows. DYS19 DYS391 DYS391 DYS393 DYS437 DYS439 DYS456 DYS458 DYS635 DYS385a 12 13 10 13 14 13 16 17 22 14 We inferred this sample to be Q-M3, however, the SNP typing of this sample was not read demonstrably. Haplogroups of the other samples included Q*, Q1a, and Q1b, indicating high

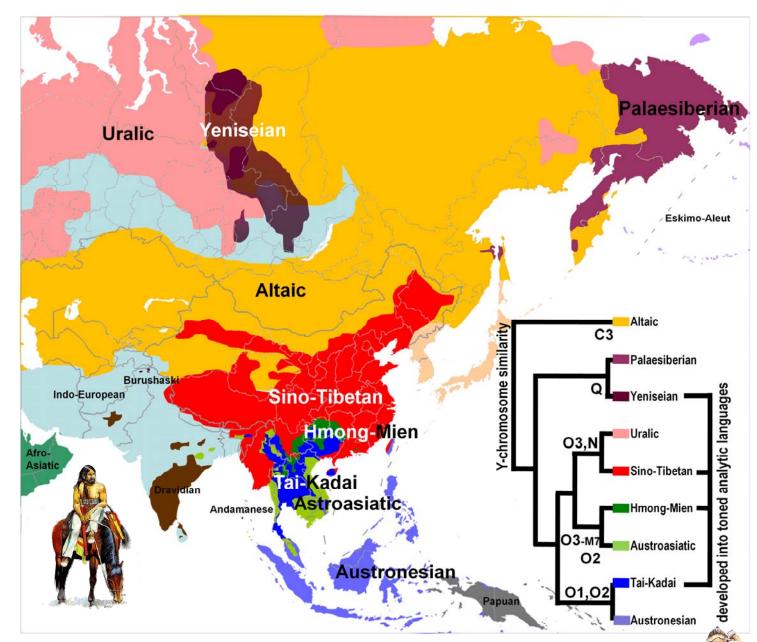
Q-M3 is the major haplogroup of all American Indians. The Barköl sample was most probably Q-M3, and had the STR pattern most similar to that of an aboriginal sample from Argentina. This similarity indicates that American Indians may have the same ancestor with the Hunnu people. Among the Asian ethnic groups, only Yeniseian people's dominant lineage is haplogroup Q. Therefore, we suggest that Hunnu people were most probably in the Yeniseian family. Moreover, the Hunnu and present Yeniseian languages share many words, such as "son" (kwatha), "horse"(kwetdeh), "stone" (kat), "milk" (mdong), etc. If Hunnu were Yeniseian people, the Yeniseian was then the largest family on the north to Sino-Tibetan in early history of China from around Neolithic Age to 5th century, and thus have been influenced by pre-Chinese culture intensively.



Hunnu writing: sun, moon, transform, work, their, way, great, impartial

This research was partly supported by grants from the National Science Foundation of China (30760097, 30890034, and 31071098), National Outstanding Youth Science Foundation of China (30625016), the Natural Science Foundation of Shanghai (10ZR1402200), Shanghai Commission of Education Research Innovation Key Project (11zz04), and the Genographic Project. L. Kang is supported by China Postdoctoral Science Foundation (200902208), the Key Project of Chinese Ministry of Education (208138), and National "Eleventh Five-Year" Technology Support Program (2007BA/25800); H. Li is supported by Shanghai professional development funding (2010001).

genetic diversity and long history of the Hunnu people. Previous studies of the Hunnu samples from Pengyang and Egyin Gol sites also found high frequencies of haplogroup Q. Only samples from the northern border of the Hunnu Kingdom were haplogroup C, N, or R. This diversity pattern indicated that Y chromosome haplogroup Q might be predominant in Hunnu people.



In the early history, the pre-Chinese culture influenced four groups of people, i.e., Sino-Tibetan, Hmong-Mien, Tai-Kadai, and Yeniseian people. Interestingly, only languages of these four groups had transformed into toned analytic languages, leaving their genetic relational populations to be different families. The contour tone systems can only be found in these four families among world languages. There might be some genetic factors contributed to these transformation.