

DNA Analysis of the Neolithic Human Bones from the Jiangjialiang Site

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matrilineage society

Three kinds of valuable information can be obtained from a phylogenetic analysis of ancient biological remains, and they are morphological information, chemical information (chemical molecular and metabolism product of creature) and genetic information (biological macromolecular which preserved primary structure). Under certain preservative conditions, ancient biological remains still have some DNA fragments. In recent years, DNA sequences have successfully abstracted from ancient biological remains by using molecular biological techniques, which provide the valuable genetic information to some unsolvable archaeological issues such as the origin, evolution, migration, syncretism and wane of the ancient or modern population.

The Jiangjialiang (JL) 姜家梁 grave site is located in Yangyuan 阳原 county, Hebei 河北 province. The analysis of cultural remains indicates that this site demonstrates some unique local characteristics and should be dated to the late Yangshao 仰韶 Culture or to the transitional period from the Yangshao Culture to the Longshan 龙山 Culture. Because its special time period (5000–6000 BP), the social attribute of the JL people becomes an issue, i. e., whether the JL people were in a patrilineal society or a matrilineal society. Our study focused on this issue by using the molecular biological method, and tried to provide a new perspective and method for the similar archaeological problems in the same time.

The samples for the DNA analysis were collected from the JL population remains, including 10 individuals excavated from 4 joint burials. We extracted DNA from the samples using the routine methods of ancient DNA study, and then determined nucleotide sequences of their mitochondrial

D-loop regions through PCR amplification. As the results, ancient DNA sequences were successfully obtained from all these samples. There are 9 haplotypes, 15 polymorphic positions at which the JL sequences differ from the reference sequence deriving from Anderson and others. These changes were all transitions, 12 were pyrimidines transitions and 3 were purine transitions and no transversion was found between the pyrimidine and purine. The biggest obstacle in the DNA study is the contamination problem. Since primers of PCR are specially designed for human mitochondria, the contamination coming from microorganism is not a serious problem. However, the contamination coming from modern human is the problem. We established the blank and PCR control as negative comparison to assure no contamination in the experimental process, and maintain no nucleotides lab environment at the same time. We carried through the experiment in different places twice for all the samples, and got the same result. Consequently, we are confident that the sequences we have obtained from the JL samples are authentic.

We constructed a phylogenetic tree from the sequences by the Maximum Likelihood Method using the Puzzle program. From the tree, we can see that the sequences of the JL population are divided into 4 groups, and each group corresponds to a joint burial. All groups show a high bootstrapping value. This suggests that the tree reflects a phylogenetic relationship among these 10 individuals. In our experiments, the study object is mitochondrial DNA, yet the mtDNA is transmitted only by the maternal lineage. According to the traditional theory of ethnology, the matrilineal clan has an important characteristic that all members of the same clan live to

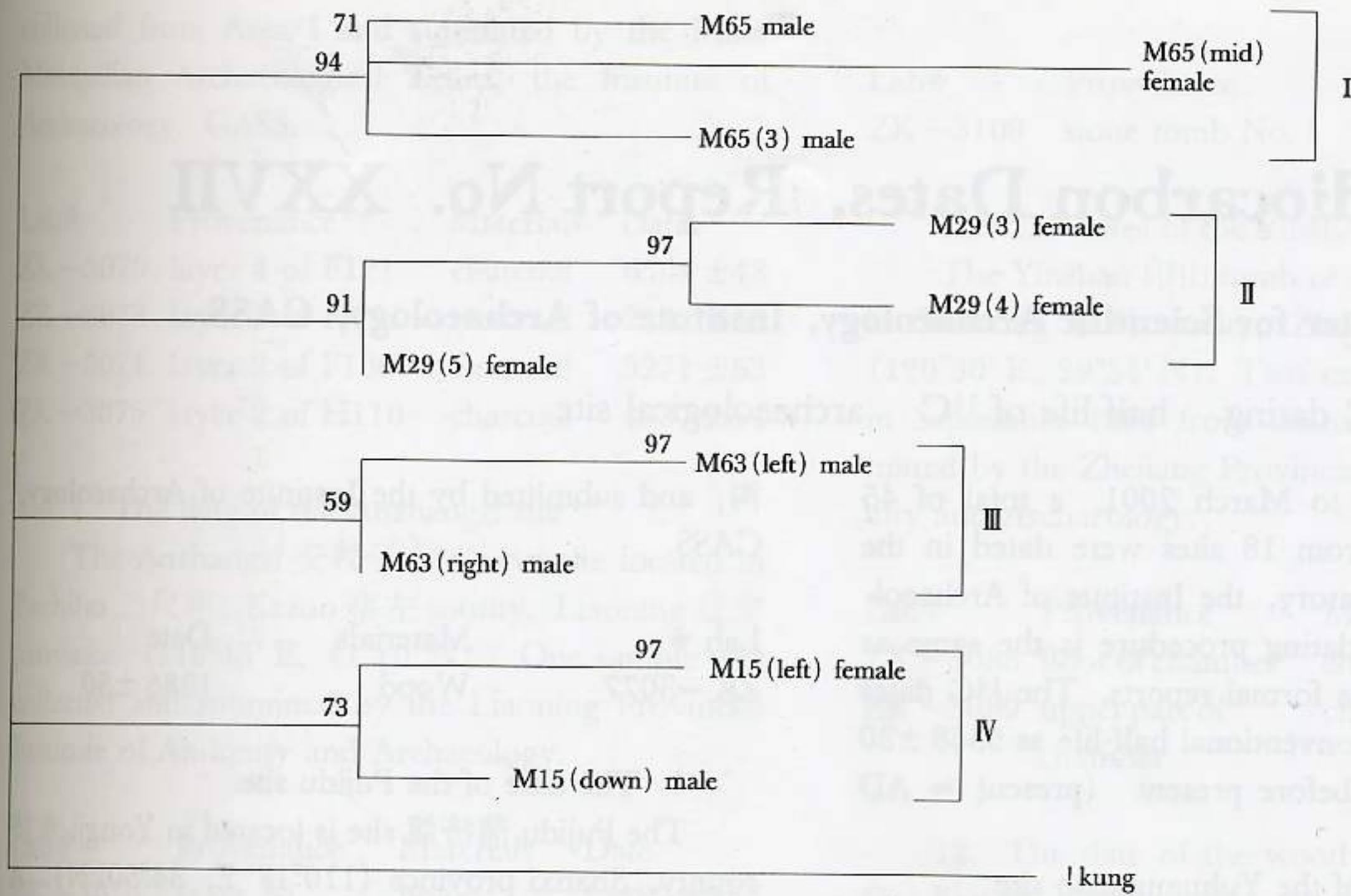


Fig. 1 Phylogenetic tree by the Maximum Likelihood Method using the Puzzle program

!Kung is an African mtDNA sequence as outgroup reference

gether, and they were buried in the joint burial when they died. If the JYL population was a matrilineal clan, the members of a same joint burial should belong to a matrilineage, and therefore they should have the same DNA haplotype. But, the results we have obtained show a different pattern with the above hypothesis. Therefore, the social attribute of the JYL population in the Neolithic period should not be judged as a matriarchal society.

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