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Letter to the Editor

Allele frequencies of 12 Y-chromosomal STRs in Chinese Tuvans in the Altay region

Dear editor,

Tuvans were traditionally nomadic people who spread into Central and Northern Asia (Siberia, Mongolia and Northwest China). Majority of Tuvans are now living in the Republic of Tuva (or called Tuva Republic or Tyva Republic), a federal subject of Russia (which in history was part of the Tannu Uriankhai district of Chinese Qing Dynasty). And a small population is living in the city of Altai of the Northwest China [1]. The phylogenetic origin of the Tuvans in China remains controversial. These people were classified as Mongolians in the early 1950s by the National Ethnic Affairs Commission of China, but they recognized themselves of an independent origin. The main aim of the this study was to determine the genetic structure of the Chinese Tuvans in the Altay region using 12 Y chromosome short tandem repeats (STR) loci (DYS19, DYS385a/b, DYS389I/II, DYS390, DYS391, DYS392, DYS393, DYS437, DYS438 and DYS439).

150 randomly selected males from the city of Altai of Xinjiang Uygur Autonomous Region were sampled and typed using the PowerPlex® Y System (Promega, Wisconsin, USA). The sample collection in this study was permitted by the Ethical Committee of Medical Faculty of Zhongshan Medical College of Sun-Yat Sen University and all participants signed the informed consent. The laboratory passed a quality control (Y Chromosomal Haplotype Reference Database, YHRD, http://www.yhrd.org/index.html) test, and quality assurance standards as stipulated by the Scientific Working Group on DNA Analysis Methods (SWGDAM) were followed. Genomic DNA was extracted using the AxyPrep™ Blood Genomic DNA Miniprep Kit (Axygen Biosciences, California, USA) following the manufacturer's protocol. Multiplex-PCR was performed with the PowerPlex® Y System kit (Promega) according to the manufacturer's instructions. Detection and genotyping of all PCR products were accomplished on ABI PRISM 3100 Genetic Analyzer (Applied Biosystems, California, USA) using the protocol recommended by the PowerPlex® Y System (Promega) and the profiles were determined using the GeneMapper® ID v3.5 Software (Applied Biosystems). Haplotype and allele frequencies were estimated by gene counting. The gene or haplotype diversity (GD) was calculated as $GD = n(1 - \Sigma x^2)/(n - 1)$, where n was the number of individuals and x was the allele frequency in the given population sample [2]. To compare our data to other populations, analysis of molecular variance (AMOVA) was assessed with pairwise ΦST values, and the distance was visualized in two multi-dimensional scaling (MDS) using YHRD online tools (www.yhrd.org) [3].

Allelic frequencies of the analysis markers and the whole genotype set are presented in Supplementary Tables S1 and S2. A total of 60 different haplotypes were observed and 32 were unique in the analyzed Chinese Tuvan population. A number of 3–5 alleles were observed at 3 loci at the same time, 6 and a relatively high level of polymorphism (over 20 alleles) was observed at only 1 loci (DYS389II and DYS385a/b, respectively). The overall haplotype diversity was 0.9708. Gene diversity value of all 12 Y-STR loci ranged from a minimum of 0.1767 for DYS393 locus to a maximum of 0.9035 for the DYS385a/b loci.

Allele frequencies of Chinese Tuvans were compared to available data submitted to the YHRD database (http://www.yhrd.org/index.html) for the same markers in nine other populations, namely Central Mongolia (Khalkh), Northern Mongolia (Khalkh, Darkhad, Uriankhai), Western Mongolia (Khalkh, Durvud, Bayad, Uriankhai, Khazak, Torguud, Uuld, Zakhchin), East Kazakhstan (Kazakh), South Kazakhstan (Kazakh), Buryat [4], Han, Yakut [5] and Tibetan [6]. Fig. 1 shows a multi-dimensional scaling (MDS) plot based on pairwise ΦST values (see Supplementary data Table S3). A compact cluster of populations of Mongolia can be observed in the plot, meanwhile the Kazakh, Han Constitute another loose cluster. Chinese Tuvans show an intermediate position between these groups, in accordance with the geographical regions of these populations. The population of Chinese Tuvans is closer to Han and Kazakh of East Kazakhstan, reveal that these populations may have gene exchange between their ancestors. In our study, there was significant difference between Chinese Tuvans and populations of Mongolia, despite a lack of admixture proportions data. This finding based on Y-STRs is consistent with previous phylogenetic

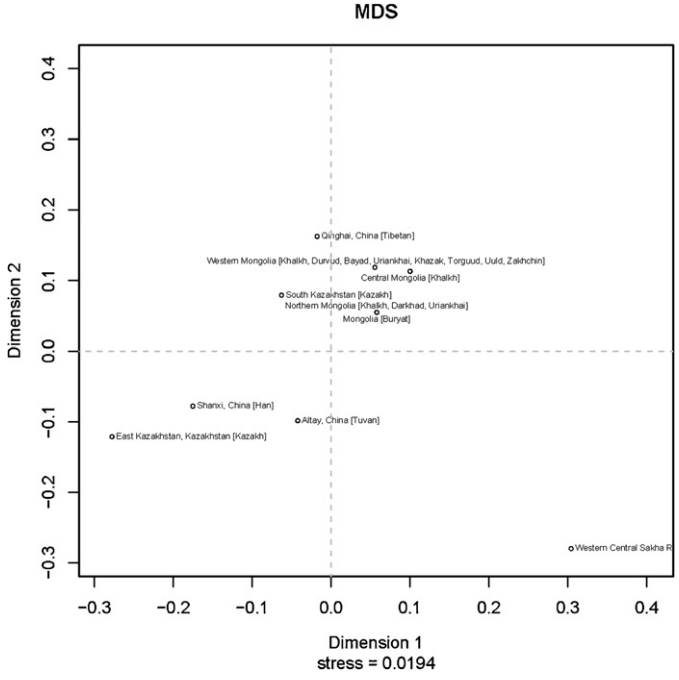

Fig. 1. MDS plot based on pairwise ΦST values.

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studies in our study population, indicating an independent origin of Chinese Tuvans [7].

In conclusion, this is the first study for Chinese Tuvans based on the 12 Y-STRs loci. These data can contribute to the development of a suitable STR database for forensic sciences and anthropology in the populations of this region.

This paper follows the guidelines for publication of population data requested by the journal [8] and the ISFG recommendations [9].

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Appendix A. Supplementary data

Supplementary data associated with this article can be found, in the online version, at http://dx.doi.org/10.1016/j.fsigen.2012.10.008.

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