



Correspondence

Haplotype structure of 27 Yfiler® Plus loci in Chinese Dongxiang ethnic group and its genetic relationships with other populations



Dear Editor,

The Dongxiang are one of China's official minority groups. They were called "Dongxiang Hui", "Dongxiang Mongolian" prior to 1949, when their name was changed to the Dongxiang (East District) people. Most of the Dongxiang live in the Linxia Hui Autonomous Prefecture and surrounding areas of Gansu Province in northwestern China. According to the 2010 census, their population numbers 621,500. Dongxiang people communicate with Dongxiang language which belongs to the Mongolian Language of the Altaic family. Many of their vocabularies are borrowed from Chinese, and some are from Turkic, Arabian and Farsi, without their own writing form. Historians are divided in their views about the ethno-origin of the Dongxiang ethnic minority. Some hold that the Dongxiangs were descendants of Mongolian troops posted in the Hezhou area by Genghis Khan (1162–1227) during his western conquest. Other historians believe that they were a mixed population consisting of Muslims, Mongolians and Han Chinese. Moreover, the Dongxiang group claimed to be Sarta (a similar word Sartrefers to the Arab traders and Turkic-speaking city dwellers in Central Asia), suggesting another possibility of western Asian origin (<http://www.chinatrans.com/facts/dongxiang-ethnic-minority.htm>). Thus, regarding the issue of the ethno-origin of the Dongxiang group, previous studies with limited genetic markers and small sample size have been unable to provide a clear answer [1–3]. Yao et al. recently analysed 15 autosomal STRs in 372 individuals from Dongxiang and Hui in Linxia, Gansu province and determined their population affinity with 45 populations (13,793 individuals) all around the world. Both genetic distance and Bayesian-clustering methods showed significant genetic homogeneity between the two Muslim populations and East Asian populations, suggesting a common genetic ancestry [4].

Y-specific short tandem repeats (Y-STRs) are informative markers used in investigations of sexual assault, paternity and genealogical tests, and evolutionary studies, since they are inherited paternally and their haplotype distribution may be distinct from other populations of different geographic regions or with different ethnic backgrounds [5–7]. To have a better understanding of the Dongxiang genetic background and inter-population relationships, we investigated haplotypes of 27 Y-STR loci in 526 Chinese Dongxiang male individuals using a commercially available STRtyper-27Y system [8]. Further, we used the overlapped 17 Yfiler loci haplotypes to compare the Dongxiang group with other neighboring and/or linguistically close populations.

Blood samples were collected with informed consent from 526 unrelated Dongxiang male individuals. All samples were collected after receiving informed consent, and individuals were considered autochthonous if their ancestors lived in the Linxia Dongxiang Autonomous Region, Gansu Province for at least three generations. The study was under the approval of the Ethics Committee of Biological Research at Fudan University, People's Republic of China. Genomic DNA was extracted from blood samples using the Chelex-100 protocol as described by Walsh et al. [9]. Amplification was carried out in GeneAmp® PCR system 9700 (Thermo Fisher Scientific, Waltham, MA, USA), using an STRTyper 27Y kit ((HEALTH Gene Technology Ltd., Ningbo, China) according to the manufacturer's recommendations. Electrophoresis and Y-STR genotyping were performed in an upgrade ABI 3130 Genetic Analyzer (Thermo Fisher Scientific, Waltham, MA, USA). Allele nomenclature followed the recommendations of the International Society for Forensic Genetics [10].

Experiments were performed in the Key Laboratory of Evidence Science (China University of Political Science and Law), which is accredited according to the ISO 17025 standard and passed the YHRD Quality Control Exercise in 2009. Data were submitted to the YHRD (Y-chromosomal haplotype reference database, <https://yhrd.org> [11]) following the guidelines of Forensic Science International Genetics and received the accession number YA004178. The geographical locations and YHRD accession numbers of the Dongxiang people and 15 reference populations are presented in Fig. S1 and Table S1.

Haplotype and allelic frequencies were estimated by direct gene-counting. Gene and haplotype diversities were calculated according to the formula by Nei [12]. The discrimination capacity was calculated as the proportion of different haplotypes in the sample. The pairwise *R*_{st} between the Dongxiang ethnic and 15 reference populations from which data for the 17 Yfiler loci were available in the YHRD or published [13–20] were calculated by AMOVA online tool (YHRD). A multidimensional scaling (MDS) plot was built utilizing the SPSS 20.0 program [21] to illustrate the relationship between the populations based on pairwise *R*_{st}.

The allele frequencies and gene diversity values (GD) of the 23 single-copy Y-STR loci and 2 multi-copy Y-STRs (DYS385a/b and DYS387S1a/b) for the 526 unrelated Dongxiang male individuals are summarized in Table S2. Deletions were detected at locus DYS448 in 4 individuals and confirmed as still displaying the null type by the Yfiler® Plus kit. Nine different microvariants were detected and confirmed by repeating the amplification process using the Yfiler® Plus Kit (namely, at marker DYS481 the alleles 24.1, 25.1, 26.1 and 27.1, DYS448 the allele 19.2, DYS458 the allele 18.2, DYS627 the allele 13.1, and DYS518 the alleles 36.2 and 40.2). Distinctive tri-allelic patterns were observed at DYS385a/b:11-13-18 (n = 1) and at DYS387S1a/b:37-38-39 (n = 7), 36-39-40 (n = 1), 37-38-40 (n = 1), 37-38-42 (n = 1).

Y-STR haplotypes found in the Dongxiang group at the 27 Y-STR loci level and 17 Y-filer loci level are shown in Table S3. The changes in haplotype resolution with four different combinations of Y-STR loci are shown in Table S4. Using 17 Yfiler loci, only 256 haplotypes (73.99%) were

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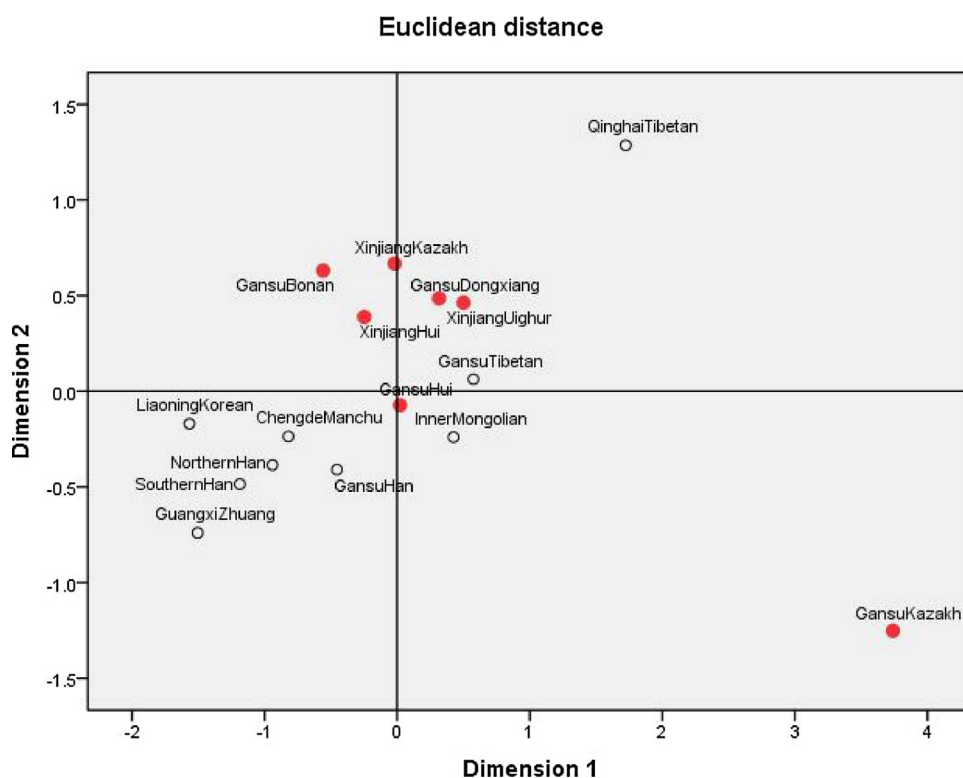


Fig. 1. Euclidean representation of Reynold's genetic distances; stress value 0.02748; the solid circles indicated the Chinese Muslim communities.

observed once, and the most frequent haplotype was shared by 9 individuals. By adding 10 additional Y-STRs (DYS449, DHS460, DHS481, DHS518, DHS533, DHS570, DHS576, DHS627 and DHSF387S1a/b) to the Yfiler loci, 423 haplotypes were observed once, which accounted for 89.81% of the total observed haplotypes. The most frequent haplotype was shared by 4 individuals, and their unrelatedness was confirmed by the analysis of autosomal STRs (data not shown). In addition, the discriminatory capacity (DC) of the 17 Yfiler loci was 0.6578 with 346 different haplotypes. With the addition of 10 Y-STRs to the 17 Yfiler loci, an improved discrimination capacity was obtained as a DC of 0.8954 from 471 observed haplotypes in 526 Dongxiang samples. However, the discrimination power of 27 Y-STR haplotypes less than 0.9000 in the Dongxiang population is comparably low for forensic and kinship casework. An extended genotyping and analysis of more Y-STRs are needed for forensic practice.

Population pairwise genetic distances (R_{st}) computed by 17 Yfiler haplotypes of 16 populations ($n = 9974$) with statistical significance are presented in Table S5. Pairwise analysis showed no significant differences ($P > 0.05$) between Dongxiang and Uighur ($R_{st} = 0.0012$). Although significant, low R_{st} values between Dongxiang and Xinjiang Hui, Gansu Hui, Bonan, and Mongolian populations were obtained (0.0073–0.0299). In comparison, highly significant distances were observed (0.0458–0.2973, $P = 0.0000$) between Dongxiang and Han Chinese origin populations and the remaining minority populations. The Gansu Kazakh drastically differed statistically from all other populations (0.2325–0.4958), which might be attributed to the cultural customs (such as descent lines, marriage and patrilocal residence patterns) and pastoral economies.

Uighur, Dongxiang, Hui, Bonan, and Kazakh are typical of contemporary Chinese Muslim communities. The multidimensional scale (MDS) plot based on Euclidean distance is shown in Fig. 1. The Dongxiang group displayed affinity to the Xinjiang Uighur, Xinjiang Hui, Gansu Bonan, Gansu Hui and Xinjiang Kazakh populations, indicating that the genetic differences among these Chinese Muslim populations are relatively small. However, the Gansu Kazakh group, who share the same ethnolinguistic and religion background and is close in geographic distance, did not show a genetic similarity as expected. It is also noted that Gansu Kazakh did not map closer to the Xinjiang Kazakh. For the other populations, Northern Han, Southern Han, Gansu Han, Chengde Manchu, Liaoning Korean, and Guangxi Zhuang clustered together in the left lower quadrant. Additionally, Qinghai Tibetan and Gansu Kazakh minority groups demonstrated significant population heterogeneities from all the other populations included, in this case may attributable to the founder effects, genetic isolation and endogamy among these populations [22]. Uighur has already been proven to be a typical admixture of East Asian and European via genome-wide scans [23]. The Dongxiang group showed significant genetic homogeneity with Uighur group, which can be supports a viewpoint that they might retain a genetic imprint from their Central Asian and West Eurasian ancestry taking phylogenetic results and historic evidence into account. However, it is important to consider that other genetic markers with more samples would be helpful to further elucidate the population history of the Dongxiangs.

In conclusion, these data in Chinese Dongxiang ethnic group could be potentially useful for the regional specific and prerequisite reference to the forensic, genealogical, and evolutionary purposes. The work presented here is in compliance with the update of the guidelines and recommendations on forensic analysis using Y-chromosome STRs [24]. This paper follows the guidelines for publication of population data proposed by the journal [25].

Conflicts of interest

The authors state that they have no conflicts of interest.

Acknowledgments

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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.2017.12.014>.

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