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Short Communication

Haplotype Diversity of 17 Y Chromosomal STRs in Jat Population of Pakistan

Abida Shehzadi*, Muhammad Shafique and Ahmad Ali Shahid

Forensic DNA Typing Research Laboratory, Centre of Excellence in Molecular Biology, University of the Punjab Lahore Pakistan-53700.

ABSTRACT

This population data relates to Y chromosomal short tandem repeat (Y-STR) haplotype diversity analysis of 143 healthy unrelated male individuals from Jat population of Pakistan. Seventeen Y-STR loci were simultaneously amplified through AmpFISTR®Yfiler™ PCR amplification kit. Evaluation of statistical parameters for forensic importance revealed in recognition of 124 unique haplotypes with diversity value of 0.996. Locus DYS385a/b demonstrated highest power of discrimination, polymorphism information content and gene diversity as 0.907, 0.854 and 0.807 respectively. Analysis of Molecular Variance (AMOVA) and multidimensional scaling plot (MDS) were also generated by using online tools at YHRD database. The data from this study could have significant importance in forensic applications, population studies and in strengthening the Y-STR database.

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Authors' Contribution
AS and MS designed the study anddrafted the manuscript. AS conducted the research. MS performed statistical analysis. AAS critically reviewed the manuscript.

Key words
Genetic diversity, Y chromosome, Jat population, Haplotype diversity

Pakistan is a land with strong historical and cultural background. It dwells multiple ethnic groups with their specific genetic and linguistic affinities. Jat population is among the major caste in Pakistan and is diversely populated in Punjab and Sindh region of Pakistan. Muslim Jats are followers of Islam and are considered to be descendants of Jat people from Northern Areas of Indian Subcontinent (Mahal and Matsoukas, 2017).

Materials and methods

To explore the genetic portrait of Pakistani Jat population, a total of 143 blood samples from healthy unrelated male individuals were collected from Punjab Pakistan, with their informed consent. The genomic DNA extraction was carried out by organic extraction procedure (Signer *et al*., 1988) followed by DNA quantification on ABI7500 Real-Time PCR using Quantifiler Kit (Barbisin *et al*., 2009) and amplification through AmpFISTR®Yfiler™PCR kit. The amplified PCR product was run for capillary electrophoresis on ABI Genetic Analyzer 3730xl and the genotype data was analyzed on Gene Mapper ID software v3.2. Allele frequencies, power of discrimination and match probability were calculated through PowerStat software v1.2 (Tereba, 1999). Powermarker v3.25 was used for estimation of haplotype frequency, polymorphism information content and gene diversity (Liu and Muse, 2005). Pairwise Rst p-values for Y-STR haplotypes and MDS of Jat population with 22 reference populations were generated through AMOVA tool available at YHRD database (Willuweit *et al*., 2007), whereas haplogroups were determined through online tool at Haplogroup Predictor (http://www.hprg.com/hapest5/).

Results and discussion

Among 143 unrelated male individuals, a total of 131 haplotypes were found with 124 unique haplotypes while seven haplotypes were repeated more than once. The highest haplotype diversity value obtained was 0.996 as given in Supplementary Table I. Among seventeen Y-STR loci, highest power of discrimination, polymorphism information content and gene diversity were observed as 0.907, 0.854 and 0.807, respectively at locus DYS385a/b (Table I). The allele 15 was found most frequent at locus DYS456 with frequency value of 0.699. MDS plot clearly depicts that Jat population is clustered in close proximity to Haryana India, Pakistani Sheikh, Gujjar, Sindhi, Karnataka India and Andhra Pradesh population while Urdu Punjabi (Christians), Arain Pakistani and Turkish also shared the same quadrant. However, rest of the populations were scattered in different quadrants as shown in Figure 1. The most common haplogroup observed in studied population

* Corresponding author: abida@cemb.edu.pk
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was R1a (42%) likewise to previous study reporting R1a as major haplogroup in Eurasia and Indian geographic regions (Singh *et al*., 2018). The population data of Jat Punjab, Pakistan was submitted to YHRD (www.yhrd.org) with accession number YA004734. The data generated through this study would be very helpful in population genetics, forensic applications and the Y-STR database development.

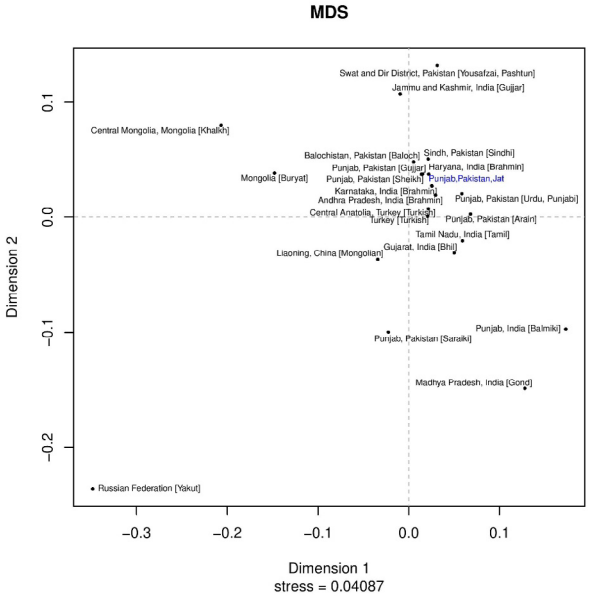

Fig. 1. Multidimensional scaling plot (MDS) generated at online YHRD AMOVA tool for Jat population of Pakistan, compared with 22 other populations of the world.

Table I. Forensic efficiency and statistical parameters for 17 Y-STRs in Jat population, Pakistan.

STRs	MP	PD	PIC	GD
DYS456	0.518	0.482	0.454	0.482
DYS389I	0.382	0.618	0.557	0.618
DYS390	0.225	0.775	0.738	0.775
DYS389II	0.257	0.743	0.703	0.743
DYS458	0.253	0.747	0.711	0.747
DYS19	0.316	0.684	0.625	0.684
DYS385a/b	0.093	0.907	0.854	0.807
DYS393	0.381	0.619	0.559	0.619
DYS391	0.514	0.486	0.397	0.486
DYS439	0.314	0.686	0.627	0.686
DYS635	0.212	0.788	0.761	0.788
DYS392	0.439	0.561	0.532	0.561
GATA_H4	0.339	0.661	0.596	0.661
DYS437	0.488	0.512	0.461	0.512
DYS438	0.386	0.614	0.558	0.614
DYS448	0.356	0.644	0.586	0.644

MP, matching probability; PD, power of discrimination; PIC, polymorphism information content; GD, gene diversity; STRs, short tandem repeats.

Supplementary material

There is supplementary material associated with this article. Access the material online at: https://dx.doi.org/10.17582/journal.pjz/20210805110806

Statement of conflict of interest

All authors have declared no conflict of interest.

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