



Haplotype data for 17 Y-STR loci in the population of Himachal Pradesh, India

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Abstract

We report here the data of Y chromosome haplotypes of 259 unrelated males from the population of Himachal Pradesh, India, using the Yfiler® multiplex kit. A total of 188 haplotypes were detected, out of which 148 were unique. Three samples showed bi-allelic pattern on locus DYS448. The observed genetic diversity and discrimination capacity were 0.996 and 0.73, respectively. In order to compare the genetic distance of the studied population with the published populations, multidimensional scaling (MDS) plot was constructed. The reported data is expected to be valuable for both forensic and population genetics.

Keywords Forensic · Y-Chromosomal STR · Haplotype · Genetic diversity

Y-STR DNA polymorphism based population genetic studies have documented large amount of genetic variation among studied Indian populations. The present status of Indian Y-STR haplotype population data is still insufficient and there is a need for creation and documentation of Y-STR based genetic studies from diverse Indian populations. We hereby present the population genetic analysis based on 17 Y-STR loci with the aim of augmenting the forensic database. All the samples belong to the population of northern Indian state Himachal Pradesh, a mountainous state which lies on the foothills of the Dhauladhar Range in the western Himalayas (Supplementary Fig. S1). Total population of Himachal Pradesh as per 2011 census is 6,864,602 of which males and females are 3,481,873 and 3,382,729 respectively [1]. Its total area is 55,673 km². We confirmed that these individuals were

not interrelated at least within three generations of the same family line. Samples ($n = 256$) were taken from routine case-work analysis of authors at the DNA Fingerprinting Unit, Central Forensic Science Laboratory, CBI, New Delhi, India. They were collected during the period from 2017 to 2018. All voluntary participants read and signed informed consent form in compliance with the Declaration of Helsinki [2]. There have been a few studies on the Y-STRs in which Y-STR haplotype diversity measured using current Y-STRs from different parts of India [3–8] has been studied. However, the population of Himachal Pradesh is still unexplored. This is the first report on the Y-STR polymorphism in population of Himachal Pradesh using 17 Y-STR markers. This manuscript follows the guidelines for the publication of data indicated by the journal [9, 10].

Genomic DNA was extracted using the Qiagen Kit (Germany) according to manufacturer's recommendations. PCR for 17 Y-STR loci was carried out using the Gene Amp® PCR System 9700 Thermal Cycler (Thermo/Applied Biosystems, USA) and Yfiler® PCR amplification kit (Thermo/Applied Biosystems, UK) according to the manufacturer's instructions except that half reaction volume was used in this study. PCR products were genotyped with capillary electrophoresis on the ABI 3500 Genetic Analyzer (Thermo/Applied Biosystems, USA). Fragment sizes were assigned using the Gene Mapper® ID-X (Applied Biosystems, USA). DNA typing and assignment of nomenclature was based on the ISFG recommendations [11]. A peak detection threshold of 50 RFUs was used for allele designation. All steps were

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performed according to the laboratory internal control standards and kit controls. Statistical evaluation of the data was done as described earlier [3–8]. Of the total 259 samples included in the analysis, three samples showed bi-allelic pattern (Supplementary Fig. S2) on locus DYS448; hence, they were not included in the haplotype analysis. Of the remaining 256 samples, a total of 188 different haplotypes were observed, out of which 148 were unique (Supplementary Table S1). Haplotype diversity and discriminating capacity were found to be 0.996 and 0.73, respectively. The genetic diversity value was observed to be highest (0.85) at single-copy locus DYS385b and lowest (0.39) on DYS391 (Supplementary Table S2, Supplementary Fig. S3).

The 17 Y-STR haplotype data included in this study have been submitted to YHRD (<http://www.yhrd.org>) with the accession number YA004551. The comparisons between the studied population and the previously reported populations on YHRD (yhrd.org.in) showed significant variation (P value < 0.05) in F_{st} value among all compared populations (Supplementary Table S3, S4). This finding is also supported by the clustering pattern observed in the MDS plot based on F_{st} values (Supplementary Fig. S4, S5).

Conclusion

The Y-STR genotyping data of the Himachal Pradesh population obtained from the Yfiler® kit have not been previously reported and therefore, it can serve as a valuable reference for future genetic research and forensic applications.

Quality control

The authors have passed the proficiency test of the YHRD (<https://yhrd.org/>), US Y-STRs (<https://www.usystrdatabase.org/>) and GITAD, Spain (<http://gitad.ugr.es/principal.htm>).

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Author contribution BKM, KC, and PS planned the study. BKM, KC, AS, and SD did the experiments. PS and KK did the analysis of data and PS wrote the manuscript. All the authors have read the manuscript.

Compliance with ethical standards

Conflict of interest The authors declare that they have no conflict of interest.

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