International Journal of Legal Medicine (2021) 135:1771–1772
https://doi.org/10.1007/s00414-021-02545-8

POPULATION DATA

Genomic insight into Y-STR diversity in the population of Odisha, India

Subhasish Sahoo[1] · Rashmita Samal[1] · Suchismeeta Behera[1] · Sumit Biswas[2] · Shivani Dixit[3] · R. K. Kumawat[4] · Gyaneshwer Chaubey[5] · Varsha Bhasney[3] · Pankaj Shrivastava[3]

Received: 21 December 2020 / Accepted: 15 February 2021 / Published online: 9 March 2021

Abstract

This study evaluated the haplotype diversity of 17 Y chromosomal genetic markers among 202 unrelated males who were randomly selected in the population of Odisha, India. Out of total 196 haplotypes observed in this study, 190 were unique haplotypes. Forensic relevant parameters, viz., gene diversity (GD) and discrimination capacity (DC), were calculated as 0.999999998 and 0.970 respectively, for the studied population. The highest genetic diversity was observed at the locus DYS385a/b (0.9541) and lowest at the locus DYS437 (0.3326) among all the studied Y chromosomal loci. The polymorphic information content (PIC), power of discrimination (PD), and matching probability (PM) was found to be 0.999999965, 0.999999998, and 1.6×10^{-9} for the tested Y STR loci. The genetic data observed in this study would enrich the existing Y STR data of the Indian population and would also be useful for forensic application.

Keywords Y-STR · Gene diversity · Forensic · Odisha · Discrimination

Introduction

Odisha is the 9th largest geographical province in terms of the geographical area and is located in the eastern part of the country along with the Bay of Bengal (Fig. S1). According to census 2011, the total population of Odisha was 41,974,218 (21,212,136 male and 20,762,082 female) which contributed to 3.47% of total population of the country [1]. Population of Odisha constitutes of diverse socio-cultural groups with unique religious events like Ratha Yatra and the spoken language belongs to Indo-Aryan linguistic groups [2]. Due to its geographical location, this state was relatively unaffected by external invasion which resulted in a conserved demographic structure. However, migration and interstate marriage system influenced the genetic structure of this population. The population of Odisha is sub-structured into various castes and tribal populations [3]. The present study was undertaken to explore the haplotype diversity and forensic characterization of 17 Y STR markers in the Odia population. This is the first ever global report on 17 Y-STR markers in the population of Odisha to the best of our knowledge.

In the present study, 202 unrelated male individuals were randomly selected from routine casework of DNA Profiling Unit, State Forensic Science Laboratory, Rasulgarh, Bhubaneswar, Odisha, India, during the period from 2018 to 2020. The sample collection followed the ethical recommendations and the Declaration of Helsinki [4]. Written informed consent was taken from the donors. All the donors self-declared that they were residing in the state for more than three generations. This study was approved by the Institutional Ethics Committee of Banaras Hindu University, Varanasi, India (Ref. No. - I.Sc./ECM-XII/2018-19/06).

Subhasish Sahoo, R. K. Kumawat and Pankaj Shrivastava have equal credential.

✉ Pankaj Shrivastava
pankaj.shrivastava@rediffmail.com

[1] DNA Profiling Unit, State Forensic Science Laboratory, Rasulgarh, Bhubaneswar, Odisha 751010, India

[2] Department of Biological Sciences, Birla Institute Of Technology & Sciences, Pilani, K.K. Birla Goa Campus, NH 17B, Bypass Road, Zuarinagar, Sancoale, Goa 403726, India

[3] DNA Fingerprinting Unit, State Forensic Science Laboratory, Department of Home (Police), Govt. of MP, Sagar 470001, India

[4] DNA Division, State Forensic Science Laboratory, Jaipur, Rajasthan 302016, India

[5] Cytogenetics Lab, Department of Zoology, Banaras Hindu University, Banaras, India

The selected samples were processed for 17 Y-STR genotyping as per the manufacturer's recommendations and statistical evaluation of haplotypic data was performed as per previously published studies [5] using GenAlEx 6.5 software [6], STRAF [7], YHRD [8], and PAST 3.02a software [9].

A total of 202 male individuals were genotyped for 17 Y-STR markers. As a result, 190 unique haplotypes were observed, while 6 haplotypes were found twice (Table S1). The allele 14 of locus DYS437 was observed as the most frequent allele among all the studied loci in the population of Odisha (Table S2). The gene diversity (GD) and discrimination capacity (DC) were observed to be 0.999999998 and 0.970, respectively, for the studied population. The lowest gene diversity was observed at locus DYS437 with a value of 0.3073 and highest at the locus DYS385a/b with a value of 0.9541, among all the studied Y chromosomal loci. The combined polymorphic information content (coPIC), power of discrimination (coPD), and matching probability (coPM) was found to be 0.999999965, 0.999999998, and 1.6×10^{-9}. The forensically important parameters, viz., gene diversity, matching probability, polymorphic information content, and power of discrimination, are shown in Table S3. The haplotype data of this study was submitted to the YHRD (http://www.yhrd.org) and accession number assigned was **YA004706**. Analysis of molecular variance (AMOVA), pairwise distances based on Rst values between the studied population and selected populations from the YHRD database was analyzed using the YHRD online tool (Table S4). MDS plot was drawn between the studied population and when compared with other population revealed a close cluster with the population of Andhra Pradesh and Tharu population of Uttar Pradesh. The geographically distinct population's included Beijing, China (Han); Punjab, India (Balmiki); and Balochistan, Pakistan (Hazara) (Fig. S2). The genetic distance matrix was plotted in the neighbor-joining (NJ) tree (Fig. S3) using PAST software and was found to be consistent with the MDS plot.

Overall, the haplotype data of this study was found to have a high degree of forensic relevance and haplotype diversity. In population differentiation evaluation, the studied population showed a close genetic affinity with Indian population and was genetically distant from the population of China and Pakistan. This study would be useful for forensic applications and enrichment of the existing Indian Y-STR database.

Supplementary Information The online version contains supplementary material available at https://doi.org/10.1007/s00414-021-02545-8.

Declarations

Ethical statement The study was conducted in compliance with ethical standards and approved by the ethics committee of Banaras Hindu University, Varanasi, India (Ref. No. - I.Sc./ECM-XII/2018-19/06).

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

References

1. Chandramouli C, General R (2011) Census of India 2011. Provisional Popul Total New Delhi Gov India
2. Bhottada (2014) SCSTRTI, Government of Odisha, Bhubaneswar, Odisha
3. Sahoo S, Samal R, Behera S, et al (2020) Genomic portrait of Odisha, India drawn by using 21 autosomal STR markers. Int J Legal Med 1–3
4. Rickham PP (1964) Human experimentation. Code of ethics of the world medical association. Declaration of Helsinki. Br Med J 2:177
5. Kumawat RK, Shrivastava P, Shrivastava D, Mathur GK (2020) Molecular diversity of 23 Y-STR genetic markers in the population of Rajasthan, India. Meta Gene 100694
6. Peakall ROD, Smouse PE (2006) GENALEX 6: genetic analysis in Excel. Population genetic software for teaching and research. Mol Ecol Notes 6:288–295
7. Gouy A, Zieger M (2017) STRAF—a convenient online tool for STR data evaluation in forensic genetics. Forensic Sci Int Genet 30:148–151
8. Willuweit S, Roewer L, Group IFYCU (2007) Y chromosome haplotype reference database (YHRD): update. Forensic Sci Int Genet 1: 83–87
9. Hammer Ø, Harper DAT, Ryan PD (2001) PAST: Paleontological Statistics Software Package for Education and Data Analysis Palaeontol. Electronica 4:1–9