

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Sequence polymorphism data of the hypervariable regions of mitochondrial DNA in the Yadav population of Haryana

Kapil Verma^a, Sapna Sharma^{a,*}, Arun Sharma^b, Jyoti Dalal^a, Tapeshwar Bhardwaj^a

^a Department of Genetics, Maharshi Dayanand University, Rohtak, Haryana 124001, India ^b Govt. of Himachal Pradesh, Junga, Himachal Pradesh 173216, India

ARTICLE INFO

Article history: Received 23 January 2018 Received in revised form 9 February 2018 Accepted 1 March 2018 Available online 8 March 2018

Keywords: Genetic variation Hypervariable regions mtDNA Forensic Yadav

ABSTRACT

Genetic variations among humans occur both within and among populations and range from single nucleotide changes to multiplenucleotide variants. These multiple-nucleotide variants are useful for studying the relationships among individuals or various population groups. The study of human genetic variations can help scientists understand how different population groups are biologically related to one another. Sequence analysis of hypervariable regions of human mitochondrial DNA (mtDNA) has been successfully used for the genetic characterization of different population groups for forensic purposes. It is well established that different ethnic or population groups differ significantly in their mtDNA distributions. In the last decade, very little research has been conducted on mtDNA variations in the Indian population, although such data would be useful for elucidating the history of human population expansion across the world. Moreover, forensic studies on mtDNA variations in the Indian subcontinent are also scarce, particularly in the northern part of India. In this report, variations in the hypervariable regions of mtDNA were analyzed in the Yadav population of Haryana. Different molecular diversity indices were computed. Further, the obtained haplotypes were classified into

* Corresponding author.

E-mail address: sapforsci@gmail.com (S. Sharma).

https://doi.org/10.1016/j.dib.2018.03.004

2352-3409/© 2018 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (http://creativecommons.org/licenses/by/4.0/).

different haplogroups and the phylogenetic relationship between different haplogroups was inferred.

© 2018 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license

(http://creativecommons.org/licenses/by/4.0/).

Specifications Table

Subject area More specific subject area Type of data How data was acquired	Forensic Science Forensic Genetics Tables and Figure Data was acquired by extracting, amplifying, sequencing and analys- ing the target region of mtDNA from the blood samples by using SureCycler 8800 (Agilent Technologies, USA), Gel Documentation System (Alpha Innotech, USA) DNA sequencer (Applied Biosystems by Life Technologies, CA, USA) Arlequin software version 3.5 (Computa- tional and Molecular Population Genetics Lab, Zoological Institute, Switzerland), HaploGrep 2 software (Medical University of Innsbruck, Austria)
Data format	Analysed
Experimental factors	Blood sample collection, DNA Extraction, PCR Amplification, Sequencing and Interpretation of Data
Experimental features	During the experiments of extraction and amplification, the con- tamination is eliminated by using the filtered pipette tips, gloves, masks, lab coats, autoclaving of stock chemicals/tubes and separation of pre and post amplification areas in the laboratory
Data source location	Haryana (A northern state of India) Latitude: 29.0588°N Longitude: 76.0856°E
Data accessibility	The data is available with this article

Value of the data

- The present data is highly useful for the identification of individuals hypervariable involved in mass disasters, missing person cases and criminal cases in the Yadav population of Haryana.
- This data will help assess matches in mtDNA sequences in forensic casework in Haryana, and will be useful for population analyses based on specific sequence polymorphisms in the Yadav population of Haryana.
- The data report will provide baseline information for genetic studies based on the control region of mtDNA for tracking families related to the Yadav population of Haryana.
- This report is important for anthropological and evolutionary research, as well as for phylogenetic studies on the Yadav population of Haryana.
- This report could also be used by evolutionary biologists to study genetic variations in order to understand the possible relationships of the Yadav population with other populations.
- The data presented here can be used as reference material for future genetic studies on the Yadav population of Haryana.
- The mtDNA haplogroups generated in this data report can be used for tracing the migration and ancestry of the Yadav population of Haryana.
- The present data will contribute to the DNA database for the Yadav population of Haryana, which can be used for calculating the probability of matches based on mtDNA.

Download English Version:

https://daneshyari.com/en/article/6596767

Download Persian Version:

https://daneshyari.com/article/6596767

Daneshyari.com