



Molecular characterization of 23 Y chromosomal STR markers in the Gurjar population of National Capital Region (NCR), India

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Abstract

In the present study, DNA samples of 202 unrelated male individuals of Gurjar population were evaluated for the molecular diversity at 23 Y chromosomal Y-STR markers. Out of selected individuals, results showed 143 unique haplotypes. Highest degree of gene diversity (GD), polymorphic information content (PIC), and power of discrimination (PD) was observed as 0.7941, 0.7590, and 0.7902, respectively, for the locus DYS385a/b. Haplotype diversity (HD), gene diversity (GD), polymorphic information content (PIC), and power of discrimination (PD) was found to be 0.7079, 0.999999999989, 0.9999999996, and 0.99999999986, respectively, for the studied 23 Y-STR markers. Allele 11 of locus DYS392 was found to be the most frequent allele with the frequency of 0.762. In inter-population relationship, studied population showed genetic relatedness with the population of Jammu and Kashmir, India, and Ladakh, India. The haplotype data of the present study will not only enrich the existing Indian Y-STR data but will also be useful for forensic DNA application.

Keywords Y-STRs · Haplotype diversity · Forensic DNA · Gurjar · NCR

Introduction

Gurjars also known as Gujjars inhabit the northwestern region of the Indian subcontinent. In India, the Gurjar population is estimated to be around 1.6 crores. It is a

heterogeneous group of populations ranging from the Gurjar-Parihara rulers of north India to the Gujjar and Bakarwal nomads of Jammu and Kashmir Valley (today's Sunni Muslims) [1–3]. The Gurjar population shows linguistic and religious diversity as they follow different religions such as Hinduism, Islam, and Sikhism, and is internally differentiated on the basis of religion, occupation, and socioeconomic status [4]. Hindu Gurjars inhabit Indian states namely Uttar Pradesh, Rajasthan, Haryana, Punjab, and Maharashtra. Muslim Gurjars are settled in Pakistan, Afganistan, and the Indian Himalayan region viz. Jammu and Kashmir, Himachal Pradesh, and Garhwal/Kumaun region of Uttarakhand. The word Gurjar is derived from a Sanskrit word “Gurjara” which means “Destroyer of enemy” [5, 6]. According to one view, Gurjars were pastoral nomads of Central Asia and originated from a foreign origin. During the fifth or sixth century A.D., they came to India from Central Asia via Georgia from the Caspian sea. Gurjars have also been associated with white Huns who invaded India in the fifth century A.D. [6]. Cunningham (1871) identified them as Yuchi or Tochari, the tribe of Indo-Scythians [5]. Puri [1] and Warikoo and Som [6] reported that Gurjars originated from Aryans, who were inhabitants of mount Abu (ancient

Kapil Dev, R. K. Kumawat, and Pankaj Shrivastava have equal credentials

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Arbuda mountain) region of present-day Rajasthan and later moved to Delhi and northward into Punjab, Uttar Pradesh, neighboring hills, and the Himalayan region. Hindu Gujjars showed common ethnic origin with Jats and Rajputs and showed divergence with the Ahir population, based on serogenetic markers [7]. Muslim Gujjars and the Hindu Gujjars showed significant differentiation which may be attributed to their geographical dispersal in diverse habitats. This could also be attributed to the inflow of genes from Islamic invaders as well as non-Islamic surrounding populations, the inbreeding effect, and the comparative breeding isolation [1, 6, 7]. These interesting historical facts have drawn our attention to explore the genomic diversity and inter-population relationship in the present study. Two hundred two unrelated healthy male individuals of the Gurjar population residing in the National Capital Region (NCR), India, were randomly selected for the study (Fig. S1). The blood samples of the selected individuals were collected following the declaration of Helsinki and ethical guidelines. Prior written informed consent was obtained from the volunteer donors. No minor was included in the present study. The samples were directly amplified for 23 Y chromosomal STR markers in the PowerPlex® Y 23 system (Promega). Genotyping and statistical evaluation were conducted as described in our previous study [8]. The Y chromosomal STR data of the present study was submitted to Y-STR Haplotype Reference Database (YHRD) (<http://www.yhrd.org>), and the accession number YA004719 was assigned. Out of the 202 haplotypes, 143 unique haplotypes were observed (Table S1). Haplotype diversity (HD) was found to be 0.7079. Allele frequency of haplotype data has been presented in Table S2. Allele 11 of locus DYS392 was found to be the most frequent allele with the frequency of 0.762. Forensic relevant parameters viz. gene diversity (GD), power of discrimination (PD), and polymorphic information content (PIC) were found to be 0.999999999989, 0.999999999986, and 0.99999999996, respectively, for the studied Y-STR loci (Table S3). The locus DYS385 was found to be the most useful marker, as it has the highest value of gene diversity, polymorphic information content, and power of discrimination viz. 0.7941, 0.7590, and 0.7902, respectively, among all the studied Y-STR loci.

To explore the inter-population relationship, the studied population was compared with the Y-STR haplotype data of the other Indian populations viz. Odisha, India [Bhotra], Andhra Pradesh, India [Indian], Himachal Pradesh, India [Indian], Jammu and Kashmir, India [Indian], Jharkhand, India [Indian], Karnataka, India [Indian], Madhya Pradesh, India [Indian], Maharashtra, India [Indian], Rajasthan, India [Indian], Tamil Nadu, India [Indian], Uttar Pradesh, India [Indian], Uttarakhand, India [Indian], West Bengal, India [Indian], and Ladakhi, India. Formal statistical AMOVA test

based on the Rst and P value distances between the studied and compared population was performed using Y-STR Haplotype Reference Database (YHRD) online software (<http://www.yhrd.org>) (Table S4). The pairwise genetic distance was plotted using PAST software for Principal Coordinate Analysis (PCoA) (Fig. S2). Neighbor-joining tree (Fig. S3) and heat map (Fig. S4) were also plotted which revealed that the studied population has genetic relatedness with Jammu and Kashmir, and Ladakhi population.

Conclusively, the present study offered interesting Y-STR marker data for the Gurjar population, and to the best of our knowledge, it is the first global report on Y chromosomal data for the Gurjar population of NCR, India. The data of this study will be very useful for forensic DNA application and population genetic studies and also enrich the existing Y-STR data of the Indian population.

Supplementary Information The online version contains supplementary material available at <https://doi.org/10.1007/s00414-021-02623-x>.

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Declarations

Ethical approval The study was approved by the Institute Ethics Committee (Human Studies) of Maharani Laxmi Bai Medical College, Jhansi, UP, India, vide letter no. 4648 dated 05.09.2020.

Conflict of interest The authors declare no competing interests.

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