

Journal of Molecular Science

www.jmolecularsci.com

ISSN:1000-9035

Forensic Exploration Of Genetic Polymorphism In Autosomal Str Markers Among The Populations Of North India: A Review

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Article Information

Received: 06-06-2025

Revised: 15-06-2025

Accepted: 06-07-2025

Published: 24-07-2025

Keywords

DNA, PCR, Allele Frequency;
Power of Discrimination;
Polymorphism, STR Markers.

ABSTRACT

In forensic science, genetic polymorphism was studied to understand the different forensic parameters like allele frequency, power of discrimination, observed heterozygosity, power of exclusion etc. In DNA fingerprinting units in various forensic labs, research labs and universities in world wide. Genetic polymorphism study was studied of healthy individuals in different caste wise as well as random in human population in a particular area. In different research paper no of samples are different it is near about 150 -1000. DNA was isolated by using automate DNA extraction system, phenol chloroform method and extracted DNA was quantitated by using NanoDrop-1000 spectrophotometer generally. In Polymerase chain reaction DNA was amplified by using a thermal cyclor machine. PCR-amplified fragments were separated by using capillary electrophoresis on an ABI Prism 3500 Genetic Analyzer Applied Biosystems, USA, and data was analyzed by using the Gene Mapper ID-X software version 1.2. Autosomal STR genetic markers D3S1358, D1S1656, D2S441, D10S1248, D13S317, Penta E, D16S539, D18S51, D2S1338, CSF1PO, Penta D, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, FGA and D22S1045 was studied in population genetics for determining of forensic parameters and data was statistically analyzed by using Gen AlEx software version 6.5, Arlequin V3.5 Software, Power State and Microsoft Excel. The Hardy-Weinberg equilibrium analysis, allele frequencies at each locus, and mathematical computation of observed and expected heterozygosity.

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INTRODUCTION

The population of North India is characterized by its rich cultural heritage, linguistic diversity, and genetic heterogeneity. Understanding the genetic makeup of this region plays a crucial role in various fields, including population genetics, forensic investigations, and medical research. Autosomal short tandem repeats (STRs) have emerged as powerful genetic markers for studying genetic polymorphism and population structure.

Autosomal STRs are repetitive DNA sequences consisting of two to seven base pair units that are tandemly repeated throughout the genome. These regions exhibit high levels of variability, with the number of repeats varying among individuals. This inherent variability makes autosomal STRs highly informative for genetic studies.

In the field of population genetics, autosomal STR analysis provides valuable insights into the genetic diversity and evolutionary history of populations. By examining the distribution of alleles at multiple STR loci, researchers can unravel patterns of migration, admixture, and population differentiation. This knowledge is particularly important in a region like North India, where diverse ethnic groups, including Indo-Aryans, Dravidians, Tibeto-Burmans, and indigenous tribal populations, coexist.

Forensic genetics is another area where autosomal STR analysis has revolutionized human identification and crime investigations. The uniqueness of DNA profiles generated from multiple STR loci allows for accurate individual identification and exclusion. Furthermore, the comparison of DNA profiles with population-specific allele frequencies aids in assessing the rarity of a given profile within a particular population, strengthening the forensic utility of autosomal STR analysis.

Genetic polymorphism studies focusing on autosomal STR loci have been conducted in the population of North India to explore its genetic diversity, population structure, and forensic applications. These studies involve the collection of DNA samples from diverse individuals representing different ethnic groups within the region. The DNA is then extracted, and polymerase chain reaction (PCR) amplification is performed to target specific STR loci. Capillary electrophoresis is employed to separate and analyze the amplified fragments, allowing for the determination of allele sizes and frequencies.

We may acquire a thorough picture of the region's genetic landscape by reading the research that has already been published on genetic polymorphism studies of autosomal STR loci in North Indian populations. These investigations shed light on patterns of migration and mixing, population-specific allele frequencies, and the genetic relatedness of various ethnic groupings. The genetic diversity data generated from these studies contribute to our understanding of disease susceptibility, pharmacogenomics, and personalized medicine in the North Indian population.

Genetic polymorphism studies of autosomal STR loci in the population of North India have significantly contributed to our knowledge of the region's genetic diversity, population structure, and forensic applications. By employing PCR techniques and analyzing STR loci, researchers have shed light on the unique genetic characteristics of North Indian populations. This literature review aims to summarize and highlight the key findings and implications of these studies, emphasizing the importance of autosomal STR analysis in unraveling the genetic landscape of North India.

DNA Isolation & Quantification:

Genomic DNA was isolated by using chelex method, automate DNA extraction unit applied Biosystems are generally used for forensic population data base research, phenol chloroform isolation method was also applied in some research paper after isolation of DNA, DNA quantification was done by using NanoDrop-1000 spectrophotometer generally.

PCR Amplification:

Approximately 1-2 ng of DNA was taken in this population data research paper; generally, pre-mixed prepared commercial kits were used to amplify the DNA. The generally used PCR kits are the Promega PowerPlex and the AmpFISTR SGM Plus PCR Amplification Kit applied by Biosystems. The PCR amplification reaction was carried out by using the Veriti thermal cycler applied by Biosystems USA. Thermal cycler parameters are set as per the protocol provided by the manufacturer in each of the samples.

STR Typing:

PCR amplified fragments were separated by using capillary electrophoresis on 3500 Genetic Analyzer (Applied Biosystems, USA) using POP-4 polymer and data was analyzed by using Gene Mapper ID-X software version 1.2 and latest version Gene Mapper ID-X software version 3.2.

Statistical Analysis:

Forensic parameters like allele frequencies, PD: Power of Discrimination, OH: Observed heterozygosity, and PE: Power of Exclusion were calculated using the STRAF, PowerStatsV1.2 software. Hardy-Weinberg equilibrium (HWE) and linkage disequilibrium, estimated through Arlequin v3.5.2 software, the exact test of population differentiation, GenAlEx version 6.5. A neighbor-joining phylogenetic tree was developed by using Poptree2 software. The most polymorphic marker was studied, and the results indicated that the STR markers revealed a high level of polymorphisms, which were suitable for personal identification and

parentage testing in forensic sciences.

Genetic Markers kits:

A genetic marker is a specific sequence of DNA that can be associated with a particular gene, these markers can be used to identify individuals or species, and they are typically found in non-coding regions of DNA but can also be associated with genes. Different types of commercial kits are available in worldwide applied Biosystems identifier, Y Filer, Minifiler, Globalfiler, Promega, USA. Sahajpal et al. (2019), studied the genetic diversity of the Rajput population of Himachal Pradesh, India, 20 autosomal Short Tandem Repeat (STR) loci included in the PowerPlex® 21 System (Promega, USA). The study included a total of 179 unrelated individuals from the Rajput population. The results of the study revealed that there were 227 alleles observed across the 20 STR loci, with an average of 11.35 ± 0.89 alleles per locus. Importantly, none of the loci deviated from the Hardy-Weinberg equilibrium (HWE), indicating genetic stability within the population. The locus Penta E was identified as the most polymorphic and discriminative among the studied loci. A phylogenetic tree analysis showed a high genetic affinity of the Rajput population of Himachal Pradesh with Rajput's of Madhya Pradesh and

Yadav of Bihar, suggesting shared genetic ancestry. Overall, the study concluded that the 20 autosomal STRs tested were polymorphic in the Rajput population and could be suitable for forensic casework and population genetic studies. Tania Hossain et al. (2016) used the PowerPlex Fusion System to perform a research on the genetic polymorphism of 22 autosomal STR loci in the Bangladeshi population. The goal of the study was to identify allele frequencies and forensic efficiency factors for kinship analysis and personal identification. The study involved 188 unrelated Bangladeshi Bengali people, and DNA samples from them were examined. With two exceptions, the loci all showed Hardy-Weinberg equilibrium. Penta E was shown to be the most informative locus, while TPOX was found to be the least informative. For each of the 22 loci, the combined power of exclusion (PE) and probability of match (PM) were determined. A neighbor-joining tree analysis indicated the genetic proximity of the Bangladeshi population to Japan, the Philippines, and East Timor. The findings contribute valuable population data for forensic applications and enhance our understanding of genetic diversity in the Bangladeshi population. A comparative chart in table-1

Table -1

Author	Title of research	No of Samples studies	No of Genetic markers studies	Name of Autosomal STR loci	Country	Source	Most Polymorphic marker	Findings
Tania Hossain et al. (2016).	Genetic Polymorphism studies on 22 autosomal STR loci of the PowerPlex Fusion System in Bangladeshi population.	188 (unrelated Bangladeshi Bengali individuals)	22 (Autosomal STR loci)	(D3S1358, D1S1656, D2S441, D10S1248, D13S317, Penta E, D16S539, D18S51, D2S1338, CSF1PO, Penta D, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, FGA and D22S1045)	Bangladesh	Legal Medicine	D2S441	The combined - PM & PE for all 22 STR loci were calculated to be 5.29×10^{-27} and 0.9999999945 respectively.
Sharif et al (2018)	Genetic Polymorphism of 16 Autosomal STRs Loci of the PowerPlex ESX 17 System in a Population Sample from Bangladesh	95 (randomly selected individuals from Bangladesh population)	16 (Autosomal STR loci)	D18S51, D21S11, TH01, D3S1358, D16S539, D2S1338, D1S1656, D10S1248, FGA, D8S1179, VWA, D22S1045, SE33, D19S433, D12S391 and D2S441	Bangladesh	Journal of forensic Medicine	SE33	The combined probability of match (PM) and combined power of exclusion (PE) was 1.31×10^{-20} and 0.999736
Hossain et al. (2014)	Population genetic data on 15 autosomal STR loci in Bangladeshi	595 (unrelated Bangladeshi Bengali individuals)	15 (Autosomal STR loci)	D21S11, D8S1179, D7S820, CSF1PO, TH01, D13S317, D16S539, D2S1338, D19S433, D3S1358, vWA, TPOX, D18S51, D5S818	Bangladesh	Forensic Science International: Genetics	D2S1338	The PE for all 15 loci tested 58 were calculated to be 0.9999992

	population.			and FGA				
Ahmad Ferdous et al. (2010)	Allele Frequencies of 10 Autosomal STR Loci from Chakma and Tripura Tribal Populations in Bangladesh	167 (Randomly selected 109 Chakma and 58 Tripura individuals)	10 (Autosomal STR loci)	D3S1358, vWA, D16S539, D2S1338, D8S1179, D21S11, D18S51, D19S433, TH01, and FGA	Bangladesh	Molecular Biology International	D18S51	Heterozygosity (H_o) of >0.7 and moderately polymorphic in Tripura population ($H_o > 0.6$).
Ahmad Ferdous et al. (2009)	Forensic evaluation of STR data for the PowerPlex TM 16 System loci in a Bangladeshi population	148 (Unrelated Bangladesh i individuals)	15 (Autosomal STR loci)	D3S1358 TH01 D21S11 D18S51 Penta E D5S818 D13S317 D7S820 D16S539 CSF1PO Penta D vWA D8S1179 TPOX FGA	Bangladesh	Legal Medicine	PENTA E	The combined PM and PE for all 15 STR loci tested were 2.05 _ 10_18 and 0.9999996, respectively
Sharif Akhteru zzaman et al. (2012)	Forensic evaluation of 11 non-standard STR loci in Bangladesh i population	102 (Unrelated Bangladesh i individuals)	11 non-standard autosomal STR loci	D21S1437, D22S683, D8S1110, D10S2325, D12S1090, D17S1294, D3S1744, D14S608, D20S470, D18S536 and D13S765	Bangladesh	Legal Medicine	D8S1110	The combined PD (1-PM) and MP was calculated to be 0.999999999999 7 and 2.23 1023, respectively
Hasan, M. M., Rahman, M. H., and Akhteru zzaman, S.(2021)	Genetic polymorphism and phylogenetic analysis of 15 autosomal STR markers in the Santal indigenous population of Bangladesh	132 (Unrelated Santal individuals of Bangladesh)	15 (Autosomal STR loci)	D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, and FGA	Bangladesh	Bioresearch Communication	FGA	The combined matching probability (MP), combined power of discrimination (PD) and combined power of exclusion (PE) for the 15 tested STR markers were 8.38 x 10-17, 0.999999998 and 0.0.999993866, respectively.
Carlo Wamaitha Chege (2019)	Allele Frequencies For 20 Autosomal Microsatellite Loci In The Kenyan Population	180 (Unrelated persons)	20 (Autosomal STR loci)	D3S1358, D13S317, PentaE, D16S539,D18S51, D2S1338, CSF1PO, Penta D, TH01, vWA, D21S11, D7S820, TPOX, D8S1179, FGA, D2S1338, D5S818, D6S1043, D12S391, and D19S433	Kenya	Research Square.	D3S1358	PIC values and heterozygosity of 0.799 and 0.831 respectively across the 20 loci.
Maria Elena Ghiani (2021)	Estimating population genetics and forensic efficiency of the GlobalFiler PCR amplification kit in the population of Sardinia	500 (Unrelated individuals)	21 (Autosomal STR Loci) + 03 Sex determining Loci	D3S1358, vWA, D8S1179, D16S539, CSF1PO, TPOX, D19S433, TH01, FGA, D21S11, D18S51, D2S441, D22S1045, D5S818, D10S1248, D1S1656, D13S317, D7S820, SE33, D12S391,	Italy	Gene , Elsevier	SE33	Marker SE33 showed the highest degree of polymorphism, whereas TPOX was the least informative locus.

	(Italy)			D2S1338); one Y-STR locus (DYS391) and one Y indel.				
Jilani, Nadeem, Tahir, and Rasool (2016)	Genetic analysis of the Saraiki population living in Pakistan	150 (unrelated individuals of the Saraiki population)	15 (Autosomal STR loci)	D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA	Pakistan	Canadian Society Of Forensic Science Journal	D2S1338	The average heterozygosity and polymorphism information content (PIC) at all loci were 0.77 and 0.766, respectively
Abban, Edward Kofi, and colleagues (2020)	Population dataset for 21 simple tandem repeat loci in the Akan population of Ghana	109 (unrelated healthy individuals)	21 (Autosomal STR loci)	D21S11, TPOX, D1S1656, D12S391, SE33, D10S1248, D3S1358, D22S1045, vWA, D19S433, D8S1179, D2S1338, D2S441, D18S51, FGA, D16S539, CSF1PO, D13S317, D5S818, D7S820, TH01	Ghana	Data in Brief, Elsevier	SE33	The combined match probability, combined power of exclusion and combined power discrimination were 1 in 4.07×10^{-25} , 0.999999999 and 1, respectively
Hashom Mohd Hakim (2020)	Dataset on 21 autosomal and two sex determining short tandem repeat loci in the Kedayan population in Borneo, Malaysia	200 (Blood samples consisting of 128 male and 72 female)	21 (Autosomal STR Loci) + 02 sex determining STR loci	D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, VWA, TPOX, D18S51, D5S818, FGA, D12S391, D1S1656, D2S441, D10S1248, D22S1045, SE33, Amelogenin and DYS391	Malaysia	Data in Brief, Elsevier	D1S1656	This p-value < 0.002 was obtained by dividing the standard p-value (0.05) with total number of tested loci (i.e. 21 locus). Similarly, standard significant level for deviation from LD between pair of STR loci (< 0.05) was also adjusted to $p < 0.002$ (0.05/231, where 231 is the total combinations of STR loci)
Alicia Borosky and colleagues (2021)	Allele frequency data for 23 aSTR for different ethnic groups from Republic of Zimbabwe	478 (Individuals from 19 different ethnic groups)	23 (Autosomal STR Loci)	CSF1PO, FGA, TH01, vWA, D1S1656, D2S1338, D2S441, D3S1358, D18S51, D19S433, D5S818, D7S820, D8S1179, D13S317, D16S539, D10S1248, D12S391, D21S11, Penta D, Penta E, D22S1045, TPOX, and SE33.	Zimbabwe	International Journal of Legal Medicine	SE33	The most polymorphic system was SE33 (GD = 0.9336) Whereas the less one was D13S317 (GD = 0.7084). The DP ranged from 0.9891 (SE33) to 0.8567 (D13S317) with PE values spanning from 0.8683 (SE33) to 0.4571 (D3S1358)
Asmer Aliyeva and colleagues (2021)	Population genetic data for 21 autosomal STR loci in the Azerbaijani population	467 (Individuals from Baku.)	21 autosomal loci from the Globalfiler™ kit	Globalfiler™ kit	Azerbaijan	International Journal of Legal Medicine	TPOX	Expected Heterozygosity HE were seen, with a minimum of 0.637 for TPOX and a maximum of

	using the Globalfiler™ kit							0.949 for SE33.
Gasana Paul and colleagues (2021)	Genetic Polymorphism of 24 Autosomal STR in the Population of Rwanda	505 (Unrelated individuals)	24 (Autosomal STR loci)	D3S1358, D13S317, D7S820, D16S539, SE33, D10S1248, D5S818, D21S11, TPOX, D1S1656, D6S1043, D19S433, D22S1045, D8S1179, Penta E, D2S441, D12S391, D2S1338, vWA, Penta D, TH01, D18S51, CSF1PO and FGA.	Rwanda	Biochemical Genetics	SE33	SE33 presented the highest polymorphism (PIC=0.921) among these 24 loci, whereas D13S317 presented the lowest one (PIC=0.671).
Amine Abdelia and Traki Benhassine et al (2019)	Genetic diversity of 15 autosomal STRs in a sample of berbers from Aurès region in the Northeast of Algeria and genetic relationships with other neighbouring samples	308 Individuals.	15 Autosomal STR loci	Amelogenin, D3S1358, D19S433, D2S1338, D22S1045, D16S539, D18S51, D1S1656, D10S1248, D2S441, TH01, VWA, D21S11, D12S391, D8S1179 and FGA.	Algeria	Annals of Human Biology	FGA	All loci were highly polymorphic and no significant deviation from HWE was detected.
Apolina Ekka et al (2020)	Genetic Polymorphism of 15 autosomal STR Loci in population of Chhattisgarh, India.	445 unrelated healthy individuals	15 Autosomal STR loci	D8S1179, D21S11, D7S820, CSF1PO, D3S1358, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA	India	Gene Reports Elsevier	“FGA”	The paternity index and cumulative matching probability for the examined loci were found to be 3.7×10^5 and 3.8×10^{-18} respectively. The Power of discrimination and exclusion were detected to be 1 and 0.99999764 respectively.
Jian Liu and colleagues (2013)	Genetic analysis of 15 STR loci from a Xibe population in Liaoning, Northeast of China	150 unrelated Xibe individuals	15 STR loci	D8S1179, D21S11, D7S820, CSF1PO, D3S1385, TH01, D13S317, D16S539, D2S1338, D19S433, vWA, TPOX, D18S51, D5S818, FGA	China	Annals of Human Biology	D18S51	Allele frequencies ranging from 0.001 to 0.507. D18S51 had the highest polymorphism (PIC:0.840) among all 15 STR loci, whereas TPOX had the lowest (PIC:0.590).
Xiaolong Han and Anna Shen and their colleagues (2020)	Genetic diversity of 17 autosomal STR loci in Meizhou Hakka population	638 unrelated healthy individuals	17 Autosomal STR loci.	D2S1338, D19S433, Penta E, Penta D, D5S818, D8S1179, D3S1358, TH01D21S11, D18S51, D7S820, vWA, D13S317, D16S539, CSF1PO,	China	International Journal of Legal Medicine	Penta E	Penta E showed the highest values of polymorphism information content (0.9073), expected heterozygosity (0.9147), and

				TPOX, and FGA				observed heterozygosity (0.9373), whereas TPOX showed the lowest (0.5373, 0.6035, and 0.6082)
Xue Wu and colleagues(2020)	Genetic polymorphisms of 20 autosomal STR loci in the Han population of Zhangzhou City, Southeastern China	1555 Unrelated Han individuals	20 Autosomal STR loci	D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX, FGA, D19S433, D12S391, D6S1043, D2S1338, D1S1656	China	Legal Medicine	Penta E	A total of 262 alleles were observed with the highest allele frequency (0.5521) in TPOX locus.
Lalita and colleagues (2020)	Genetic variation of 20 Autosomal STRs in "JATS" belonging to Delhi, India.	120 JATS Individuals	20 Autosomal STR loci	D3S1358, TH01, D21S11, D18S51, Penta E, D5S818, D13S317, D7S820, D16S539, CSF1PO, Penta D, vWA, D8S1179, TPOX, FGA, D19S433, D12S391, D6S1043, D2S1338, D1S1656	India	International Journal of Legal Medicine	Penta E	The locus "Penta-E" was most polymorphic the value 0.910 and 0.981, respectively. Whereas the locus TPOX was found least polymorphic the value 0.612 and 0.833.
Gasana Paul and colleagues et al (2021),	Genetic Polymorphism of 24 Autosomal STR in the Population of Rwanda	505 unrelated Individuals	24 Autosomal STR loci	D3S1358, D13S317, D7S820, D16S539, SE33, D10S1248, D5S818, D21S11, TPOX, D1S1656, D6S1043, D19S433, D22S1045, D8S1179, Penta E, D2S441, D12S391, D2S1338, vWA, Penta D, TH01, D18S51, CSF1PO and FGA.	Rwanda	Biochemical Genetics	SE33	SE33 presented the highest polymorphism (PIC=0.921) among these 24 loci, whereas D13S317 presented the lowest one (PIC=0.671).
Badiye et al. (2021)	A study of genomic diversity in populations of Maharashtra, India. Inferred from 20 autosomal STR markers.	158 unrelated Individuals	20 autosomal STR markers	D3S1358, D1S1656, D6S1043, D13S317, Penta E, D16S539, D18S51, D2S1338, CSF1PO, Penta D, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, FGA.	India	BMC Research Notes	Penta E	Observed heterozygosity viz. 0.690 to 0.918 for the admixed population and 0.696 to 0.942 for the Teli population.
Vivek Sahajpal et al. (2019).	Assessment of Genetic Polymorphism at 20 autosomal STR loci in scheduled caste population of Himachal Pradesh,	215 genetically unrelated individuals (114 males and 101 females)	20 autosomal STR markers	D3S1358, D1S1656, D6S1043, D13S317, Penta E, D16S539, D18S51, D2S1338, CSF1PO, Penta D, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433 and FGA)	India	International Journal of Legal Medicine	Penta E	Locus Penta E was found to be the most polymorphic and discriminative loci. The combined power of discrimination and the combined power of exclusion were 1 and 0.999.

	INDIA.							
R.K. Kumawat and Pankaj Shrivastava (2020)	Genomic blueprint of population of Rajasthan based on autosomal STR markers	317 healthy individuals	20 Autosomal STR loci	D3S1358, D1S1656, D6S1043, D13S317, PENTA-E, D16S539, D18S51, D2S1338, CSF1PO, PENTA-D, TH01, vWA, D21S11, D7S820, D5S818, TPOX, D8S1179, D12S391, D19S433, FGA	India	Annals of Human Biology	Penta E	The locus Penta-E was found to be the most polymorphic with a value of 0.90 in the studied population. The combined Power of discrimination (CPD) and Combined Power of Exclusion (CPE) were observed as >0.99999999 and 0.999999997.

CONCLUSION:

Based on the literature review encompassing genetic polymorphism studies of autosomal short tandem repeat (STR) loci in the population of Bangladesh, China, Rwanda, Algeria, Azerbaijan, Zimbabwe, Malaysia, Ghana, Pakistan, Italy, Kenya and India, several key conclusions can be drawn:

- Diversity across North Indian Populations:** The reviewed studies collectively reveal a significant level of genetic diversity within the North Indian population. This diversity can be attributed to various factors, including historical migrations, intermixing of different ethnic groups, and geographical variations need to more study in Bihar, Jharkhand, Rajasthan, Punjab and Odisha state.
- Utility of Autosomal STRs:** Autosomal STR markers have proven to be valuable tools for assessing genetic diversity and population structure in North India. These markers offer high discrimination power and are widely employed in forensic and anthropological studies.
- Regional Variations:** While North India is often treated as a homogeneous region, the literature suggests that there are notable genetic variations among different North Indian states and communities. These differences may be influenced by factors such as endogamy, caste, and social practices.
- Forensic Applications:** The studies emphasize the importance of autosomal STR markers in forensic investigations. Accurate population-specific allele frequency databases are crucial for forensic DNA analysis in the region, aiding in individual identification and criminal investigations.
- Historical Insights:** Genetic studies in North India have provided insights into historical events, migrations, and interactions among various populations. These insights contribute

to our understanding of the complex demographic history of the region.

- Future Research Directions:** The literature review suggests a need for continued research in this field, focusing on underrepresented populations, increased marker sets, and more extensive databases. This would enhance our ability to address forensic, anthropological, and medical genetic questions specific to North India.
- The genetic polymorphism studies of autosomal STR loci in North India have revealed a rich tapestry of genetic diversity and historical complexities within the region. These findings have practical applications in forensics and contribute to our broader understanding of human population genetics in this culturally and historically significant part of the world.

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