Genetic polymorphism study at 15 autosomal locus in central Indian population

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Abstract
The analysis of 15 autosomal STR locus (TH01, D3S1358, vWA, D21S11, TPOX, D7S820, D19S433, D5S818, D2S1338, D16S539, CSF1PO, D13S317, FGA, D18S51, D8S1179) was done in 582 healthy unrelated individuals (Male-366, Female-216) originating from the various geographical regions of Madhya Pradesh, India. All locus fall under Hardy–Weinberg equilibrium except TPOX. These STR loci were highly informative and discriminating with combined power of discrimination (CPD) >0.99999. Locus wise allele frequencies of the studied population were compared with the other published populations. Also the Clustering pattern and genetic distance of studied populations is compared and presented with various populations. The studied population showed the genetic proximity with geographically close populations of India and significant genetic variation with distant populations which is also evident by clustering pattern of the NJ tree and the PCA plot.

Keywords: DNA typing, Autosomal STR, Central India, Population data, Forensic

Background
After almost 30 years since the first formal application of DNA technology (Jeffreys et al. 1985), short tandem repeats (STR’s) based DNA analysis (Edwards et al. 1992) was accepted as a core method in forensics, it is still being routinely used in cases of simple paternity testing (Zupanic Pajnic et al. 2001), identification of human remains testing (Zupanic Pajnic et al. 2010) and in complicated criminal casework analysis, including rape and mass rape. STR’s form approximately 3% of the total human genome and on an average are present once in every 10,000 nucleotides (Butler 2005). Due to ease of use due to multiplexing, these markers are routinely used in forensic, anthropological and medical studies. With the growing number of laboratories using STR analysis technology, more and more population STR data have been reported (Tandon et al. 2002; Sarkar and Kashyap 2002; Sahoo and Kashyap 2002; Gaikwad and Kashyap 2002; Rajkumar and Kashyap 2004; Narkuti et al. 2008; Dubey et al. 2009; Ghosh et al. 2011; Chaudhari and Dahiya 2014; Giroti and Talwar 2010; Shrivastava et al. 2015a; b).

India is the largest secular country with a polygenetic population. Various known religions are found in India and the Indian population belongs to various linguistic and ethnic groups of different castes and tribes and it is said to be the melting pot of various ethnic groups (Eaaswarkhanth et al. 2009). Human diversity in India is defined by 4693 differently documented population groups that include 2205 major communities, 589 segments and 1900 territorial units spread across the country (Singh 1998). Major population migrations, social structure and caste endogamy has influenced the genetic structure of Indian populations.

Madhya Pradesh, a state in Central India is the second largest state in the country by area. Population of Madhya Pradesh is 72,597,565 comprising 37,612,920 males and 34,984,645 females, contributing 6 percent to India’s total population (Census of India 2011). With these rationales 15 highly polymorphic autosomal microsatellite markers including 13 core forensic loci, have been analyzed and the distribution of alleles across various populations is compared with the previously published data on the same markers from different parts of India (caste specific available data) and other area specific reported data only one from India and rest from other parts of world, in order to decipher genetic delineation amongst the populations.
(Tables 1, 2). As the genetic data being reported here is area specific therefore, besides comparing the data with the population geographically close (caste specific) to the population of Madhya Pradesh and other parts of India, the data was also compared with the area specific available data.

**Methods**

The population and DNA extraction

The population sample consisted of 582 healthy, unrelated individuals (Male-366, Female-216) originating from different geographical regions of Madhya Pradesh. Samples were taken from routine casework performed by the first author at the DNA fingerprinting Unit, State Forensic Science Laboratory, Sagar, Madhya Pradesh, India from the period of 2007 to 2013 after written informed consent. Only fathers and mothers were selected from paternity trios and unrelated individuals were taken into consideration from complex kinship analyses. DNA was extracted from the peripheral blood samples by automated DNA extraction system 12 GC (Precision System Science Co., Ltd., Matsudo, Japan).

DNA quantitation

Real Time PCR ABI 7000 (Applied Biosystems, Foster City, CA, USA) was used for quantification of the isolated DNA using the Quantifiler DNA Quantification Kit (Applied Biosystems, Foster City, CA, USA) as per the recommended protocol by the manufacturer.

Amplification

1 ng of DNA template was used to simultaneously amplify 15 STR locus including 13 CODIS (D3S1358, TH01, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, CSF1PO, vWA, D8S1179, TPOX, FGA) and 2 additional loci (D2S1338 and D19S433), as well as the gender determining locus Amelogenin using AmpFlSTR Identifiler or AmpFlSTR Identifiler Plus kit (Applied Biosystems, Foster City, CA, USA). Similar amount of DNA was used in all PCR reactions. Amplification was carried out according to the manufacturer’s recommended protocol, with a modification of decreasing the total volume of each reaction to 12.5 μL. The PCR amplification was carried out in AB Gene Amp PCR System 9700 Thermal Cycler (Applied Biosystems, Foster City, CA, USA).
| Allele/n | D8S1179 | D21S11 | D7S820 | CSF1PO | D3S1358 | THO1 | D13S317 | D16S539 | D2S1338 | D19S433 | VWA | TPOX | D18S51 | D5S818 | FGA |
|---------|---------|--------|--------|--------|---------|------|---------|---------|---------|---------|-----|------|-------|-------|-----|
| 6       |         |        |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 7       | 0.021   | 0.003  |        | 0.090  | 0.001   | 0.077|         |         |         |         |     |      |       |       |     |
| 8       | 0.005   | 0.234  | 0.005  | 0.127  | 0.220   | 0.085|         |         |         |         |     |      |       |       |     |
| 9       | 0.007   | 0.067  | 0.003  | 0.293  | 0.107   | 0.149|         |         |         |         |     |      |       |       |     |
| 9.3     | 0.138   |        |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 10      | 0.168   | 0.232  | 0.193  | 0.006  | 0.090   | 0.093|         |         |         |         |     |      |       |       |     |
| 11      | 0.072   | 0.247  | 0.294  | 0.253  | 0.315   | 0.004|         |         |         |         |     |      |       |       |     |
| 11.2    |         | 0.002  |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 12      | 0.109   | 0.170  | 0.381  | 0.001  | 0.246   | 0.227|         |         |         |         |     |      |       |       |     |
| 12.2    |         | 0.004  |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 13      | 0.166   | 0.028  | 0.079  | 0.002  | 0.070   | 0.114|         |         |         |         |     |      |       |       |     |
| 13.2    |         | 0.171  |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 14      | 0.199   | 0.001  | 0.013  | 0.045  | 0.015   | 0.014|         |         |         |         |     |      |       |       |     |
| 14.2    |         | 0.060  |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 15      | 0.176   | 0.001  | 0.306  | 0.003  | 0.136   | 0.095|         |         |         |         |     |      |       |       |     |
| 15.2    |         | 0.087  |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 16      | 0.084   | 0.302  | 0.008  | 0.048  | 0.224   | 0.144|         |         |         |         |     |      |       |       |     |
| 16.2    |         | 0.021  |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 17      | 0.013   | 0.241  | 0.067  | 0.009  | 0.258   | 0.076|         |         |         |         |     |      |       |       |     |
| 17.2    |         | 0.007  |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 18      | 0.001   | 0.097  | 0.158  | 0.204  | 0.040   | 0.007|         |         |         |         |     |      |       |       |     |
| 18.2    |         | 0.001  |        |        |         |      |         |         |         |         |     |      |       |       |     |
| 19      | 0.008   |         | 0.144  | 0.092  | 0.033   | 0.049|         |         |         |         |     |      |       |       |     |
| 20      |         | 0.131  |        | 0.013  | 0.015   | 0.107|         |         |         |         |     |      |       |       |     |
| 20.2    |         | 0.053  |        | 0.001  | 0.008   | 0.143|         |         |         |         |     |      |       |       |     |
| 21      |         | 0.069  |        | 0.004  |         | 0.152|         |         |         |         |     |      |       |       |     |
| 21.2    |         | 0.168  |        | 0.001  |         | 0.183|         |         |         |         |     |      |       |       |     |
| 22      |         | 0.099  |        | 0.001  |         | 0.156|         |         |         |         |     |      |       |       |     |
| 22.2    |         | 0.006  |        | 0.006  |         | 0.009|         |         |         |         |     |      |       |       |     |
| 23      |         | 0.090  |        | 0.121  |         |       |         |         |         |         |     |      |       |       |     |
| Allele/n | D8S1179 | D21S11 | D7S820 | CSF1PO | D3S1358 | THO1 | D13S317 | D16S539 | D251338 | D19S433 | VWA | TPOX | D18S51 | D5S818 | FGA |
|---------|---------|--------|--------|--------|---------|------|--------|--------|---------|---------|-----|------|--------|--------|-----|
| 25      | 0.001   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 26      |         | 0.003  |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 27      | 0.008   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 28      | 0.143   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 29      | 0.209   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 29.2    | 0.004   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 30      | 0.187   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 30.2    | 0.027   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 31      | 0.045   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 31.2    | 0.125   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 32      | 0.008   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 32.2    | 0.182   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 33.2    | 0.048   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 34.2    | 0.012   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 35      | 0.001   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |
| 35.2    | 0.002   |        |        |        |         |      |        |        |         |         |     |      |        |        |     |

Pm matching probability, PD power of discrimination, PIC polymorphism information content, PE power of exclusion, PI paternity index, Hobs observed heterozygosity, Hexp expected heterozygosity, P value HWE test
Typing

Multicapillary electrophoresis of the amplification products was performed on an ABI Prism 3100 Avant Genetic Analyzer (Applied Biosystems, Foster City, CA, USA) using LIZ 500 size standard (Applied Biosystems, Foster City, CA, USA) provided with the kit and the data was analysed using GeneMapper™ 3.5 Software (Applied Biosystems, Foster City, CA, USA). All steps were done according to the Laboratory’s internal control standards and respective kit controls, according to the IFSH recommendations (DNA recommendations 1994).

Quality control

Passed Proficiency testing of the GITAD, Spain http://gitad.ugr.es/principal.htm). Also, laboratory internal control standards and kit controls used.

Analysis of data

Allele frequency of the 15 STR loci was calculated by GenAlEx 6.5 software (Peakall and Smouse 2006). Several forensic parameters, i.e., polymorphism information content (PIC), power of discrimination (PD), power of exclusion (PE), matching probability (Pm) and paternity index (PI) was calculated using the PowerStatsV1.2 spreadsheet program (Tereba 1999). Observed heterozygosity (Hobs), Expected Heterozygosity (Hexp) and Hardy–Weinberg equilibrium (HWE) using exact test was calculated using Arlequin v3.5 (Excoffier et al. 2005). Allele frequencies of studied population were compared with other published populations using Fst pair wise distance by Arlequin v3.5 software (Excoffier et al. 2005). Nei’s genetic distances (Nei 1972) among compared populations were derived and subsequently used to generate a Neighbour joining (NJ) dendrogram using POPTREE2 program (Takezaki et al. 2009). The robustness of the phylogenetic relationship established by the NJ tree was assessed using bootstrap analysis with 1000 replications. Graphical representation of genetic distances was also performed based on Principle component analysis (PCA) plot using PAST 3.02a software (Hammer et al. 2001).

Table 4 The most common allele (MCA) and least common allele (LCA) in studied Central Indian population

| Allele    | MCA  | LCA  |
|-----------|------|------|
| D8S1179   | 14   | 18   |
| D21S11    | 29   | 35   |
| D7S820    | 11   | 14   |
| CSF1PO    | 12   | 15   |
| D3S1358   | 15   | 12   |
| THO1      | 9    | 10   |
| D13S317   | 11   | 14   |
| D16S539   | 11   | 15   |
| D2S1338   | 23   | 27   |
| D19S433   | 13   | 9    |
| vWA       | 17   | 16,2,17,18,2,21 |
| TPOX      | 11,8 | 7,13 |
| D18S51    | 14   | 9,23,24 |
| D5S818    | 11   | 8    |
| FGA       | 23   | 25,2 |

MCA most common allele, LCA least common allele

Table 5 Fst pairwise genetic distances and corresponding P value

| Locus     | Central India V/S | Bhil (Madhya Pradesh) | Balmiki (Punjab) | Mahadev Koli (Maharashtra) | Iyenger (Tamilnadu) | Kurumans (Tamilnadu) | Tripuri (Tripura) |
|-----------|-------------------|-----------------------|------------------|---------------------------|--------------------|---------------------|-------------------|
| D8S1179   | 0.009             | 0.001                 | 0.013            | 0.006                     | 0.025              | 0.000               | 0.395             |
| D21S11    | 0.001             | 0.230                 | -0.001           | 0.000                     | 0.479              | 0.042               | 0.000             |
| D7S820    | 0.000             | 0.458                 | -0.002           | 0.003                     | 0.150              | 0.000               | 0.412             |
| CSF1PO    | -0.002            | 0.826                 | 0.000            | -0.002                    | 0.624              | -0.003              | 0.742             |
| D19S433   | 0.002             | 0.078                 | 0.000            | 0.023                     | 0.000              | 0.007               | 0.031             |
| vWA       | 0.001             | 0.268                 | 0.006            | 0.018                     | 0.001              | 0.005               | 0.047             |
| TPOX      | 0.017             | 0.000                 | 0.000            | 0.019                     | 0.003              | 0.000               | 0.379             |
| D18S51    | 0.005             | 0.008                 | 0.000            | 0.014                     | 0.000              | -0.001              | 0.628             |
| D5S818    | 0.000             | 0.425                 | 0.011            | 0.007                     | 0.052              | 0.005               | 0.097             |
| THO1      | 0.006             | 0.011                 | 0.008            | 0.005                     | 0.050              | 0.004               | 0.101             |
| D13S317   | 0.000             | 0.414                 | 0.006            | 0.036                     | 0.000              | 0.008               | 0.023             |
| D16S539   | 0.001             | 0.286                 | 0.025            | 0.016                     | 0.000              | 0.000               | 0.437             |
| D2S1338   | 0.001             | 0.163                 | 0.000            | 0.015                     | 0.000              | -0.001              | 0.746             |
| D5S818    | 0.002             | 0.108                 | 0.006            | 0.006                     | 0.045              | -0.001              | 0.502             |
| FGA       | 0.002             | 0.126                 | 0.002            | 0.003                     | 0.118              | -0.001              | 0.566             |

P value <0.003 values
Results and discussion

The genetic variations in the allele-frequency distribution at 15 STR loci and statistical analysis of forensic parameters for the studied populations are shown in Table 3. In total, 158 alleles were observed in the central Indian population with corresponding allele frequencies ranging from 0.001 to 0.381 (Table 3). In which CSF1PO locus was found to have a maximum allele frequency with allele 12 (0.381) being the most frequent allele in this population. Locus wise distribution of the most common and least common allele in studied population is summarized and presented in Table 4. The peak high threshold was 50 RFU for heterozygous and 200 RFU for homozygous alleles. The combined power of exclusion (CPE) and
combined power of discrimination (CPD) for all 15 STR loci were 0.9999 and greater than 0.99999 respectively in studied population. The combined matching probability was found to be $1.51 \times 10^{18}$. Among all the studied locus, no significant deviations from Hardy–Weinberg expectations were observed even after Bonferroni correction (Bland and Altman 1995) except at locus TPOX ($p < 0.003$). At TPOX locus all the homozygotic peaks were found with a peak height of more than 200 RFU, thus removing the possibility of any heterozygous peak. Allele 11 (437 out of 1164) followed by allele 8 (410 out of 1164) were found to be the dominating alleles in this population.

The expected heterozygosity and the power of discrimination calculated from allele frequencies obtained from central Indian population revealed that in combination, the 15 autosomal STRs have a high forensic efficacy. Locus wise allele frequencies of studied population were compared at all 15 loci with the other published Indian populations including geographically close populations viz. Chenchu (Andhra Pradesh), Lambadi (Andhra Pradesh), Yerucula (Andhra Pradesh) and Nai-kpood (Andhra Pradesh) (Bindu et al. 2005), Adimiong (Arunchal Pradesh) and Adipasi (Arunchal Pradesh) (Kritihika et al. 2007), Munda (Chotanagpur), Santal (Chotanagpur) and Oraon (Chotanagpur) (Banerjee et al. 2005), Kora (Bengal), Lodha (Bengal) and Maheli (Bengal) (Singh et al. 2006), Bhil (Gujrat) (Chaudhari and Dahiya 2014), Balmiki (Punjab), Sakaldwipi Brahmin (Jharkhand), Munda (Jharkhand), Konkanastha Brahmin (Maharashtra), Mahadev Koli (Maharashtra), Iyengar (Tamilnadu), Kurumans (Tamilnadu), Tripuri (Tripura) and Riang (Tripura) (Ghosh et al. 2011), Bhil (Madhya Pradesh) (Shrivastava et al. 2015b) populations using Pairwise Fst distance ranging from $-0.003$ to 0.247 (Tables 5, 6, 7, 8). Central Indian population showed a considerable genetic distance with other published indian population which were used for comparison (Table 1). Central Indian population showed significant variation at 14 loci with Lodha (Bengal), at 11 loci with Adi pasi population (Arunachal Pradesh) and Kora population (Bengal), at 10 loci with Yerukula population (Andhra Pradesh) and Maheli population (Bengal), at 9 loci with Adiminyong population (Arunachal Pradesh), at 8 loci with Naikpod Gond population (Andhra Pradesh) and Oraon population (Chotanagpur), at 7 loci with Riang population (Tripura) and Munda population (Chotanagpur), at 6 loci with Chencheu population (Andhra Pradesh), Santal population (Chotanagpur) and Mahadev koli population (Maharashtra), at 5 loci with Bhil (Gujrat), at 4 loci with Tripuri population (Tripura), at 3 locus with Munda population (Jharkhand) and Sakaldwipi brahmin population (Jharkhand), at 2 loci with Konkanastha Brahmin population (Maharashtra), Kurumans population (Tamilnadu), Balmiki population (Punjab) and Bhil population (Madhya Pradesh) and at 1 locus with Iyengar (Tamilnadu). Central Indian population showed no significant variation from Lambadi population (Andhra Pradesh). Neighbour Joining dendrogram (Figs. 1, 2) based on Nei’s genetic distance (Nei 1972)

### Table 8 Fst pairwise genetic distances and corresponding P value

| Locus          | Central India V/S Bhil (Gujrat) Fst | Central India V/S Sakaldwipi Brahmin (Jharkhand) Fst | Central India V/S Konkayastha Brahmin (Maharashtra) Fst |
|----------------|-------------------------------------|----------------------------------------------------|--------------------------------------------------------|
|                | P-value 0.000                        | P-value 0.007                                      | P-value 0.005                                          |
| D8S1179        | 0.005                               | 0.010                                              | 0.008                                                  |
| D21S11         | 0.002                               | 0.004                                              | 0.051                                                  |
| D7S820         | 0.001                               | 0.001                                              | 0.010                                                  |
| CSF1PO         | 0.002                               | −0.001                                             | 0.012                                                  |
| D19S433        | 0.001                               | 0.007                                              | 0.003                                                  |
| vWA            | 0.005                               | 0.002                                              | 0.006                                                  |
| TPOX           | 0.014                               | 0.003                                              | 0.007                                                  |
| D18S51         | 0.002                               | 0.012                                              | 0.002                                                  |
| D3S1358        | 0.000                               | 0.005                                              | 0.040                                                  |
| THR1           | 0.001                               | 0.032                                              | 0.000                                                  |
| D13S317        | 0.001                               | 0.027                                              | 0.008                                                  |
| D16S539        | 0.003                               | 0.005                                              | 0.010                                                  |
| D2S1338        | 0.005                               | 0.010                                              | 0.010                                                  |
| D5S818         | −0.001                              | 0.006                                              | −0.001                                                 |
| FGA            | 0.004                               | 0.001                                              | 0.018                                                  |

P value < 0.003 Values
showed genetic relationships of the studied population with other Indian published populations. The grouping of populations in PCA plot (Fig. 3) is also found consistent with the clustering pattern observed in the NJ tree.

The central Indian population showed significant variations at maximum number of studied loci (14 out of 15) with Lodha (Bengal) and showed no significant disparity from Lambadi population (Andhra Pradesh). This finding is found consistent with the clustering pattern of observed in the NJ tree and PCA plot. We also compared central Indian population on the basis of locus wise allele frequencies at all the 15 loci with the other published populations from Palestinian_Iraq (AL-Zubaidi et al. 2014), Swedish (Montelius et al. 2008), Hungarian (Demeter et al. 2010), Shenyang_China (Hou et al. 2013), Guangdong (Zhu et al. 2005), Moroccan (Bentayebi et al. 2014), Tamil (Balamurugan et al. 2010), Croatian (Projić et al. 2007), Wallachia_Romania (Stanciu et al. 2009), Estonia (Sadam et al. 2014) and Latvia (Jemeljanova et al. 2015) populations using Pairwise Fst distance ranging from −0.001 to 0.266 (Table 9, 10). Central Indian population showed genetic detachment from all other area specific published population data (Table 2), used for comparison and also showed significant variation.

**Fig. 1** NJ tree based on Nei's genetic distance showing genetic distance of central Indian population with other reported Indian populations
**Fig. 2** NJ tree for the studied population with other reported populations from different countries based on Nei’s genetic distances

**Fig. 3** PCA plot of central Indian population showing distance pattern with other published Indian populations of India
at all 15 loci with Wallachia population. Central Indian population showed significant variations at 13 loci with Moroccan population and Estonian population, at 12 loci with Swedish population, at 11 loci with Shenyang population, at 10 loci with Hungarian population, at 9 loci with Latvia population and Croatian population, at 7 loci with Guangdong population and Palestinian Iraq population, at 5 loci with Tamil population (Table 9, 10). Neighbour Joining dendrogram (Fig. 2) based on Nei’s genetic distance (Nei 1972) showed genetic relatedness amongst same neighboring populations of India in the form of clustering pattern.

### Table 9 Fst pairwise genetic distances and corresponding P value

| Central Indian region V/S | Palestinian_Iraq | Swedish | Hungarian | Guangdong | Moroccan | Tamil |
|----------------------------|-------------------|---------|-----------|-----------|----------|-------|
|                            | Fst    | P-value | Fst    | P-value | Fst    | P-value | Fst    | P-value | Fst    | P-value | Fst    | P-value |
| D8S1179                    | 0.005  | 0.062   | 0.023  | 0.000   | 0.016  | 0.000   | 0.005  | 0.069   | 0.009  | 0.000   | 0.044  | 0.010   |
| D21S11                     | 0.062  | 0.000   | 0.043  | 0.000   | 0.043  | 0.000   | 0.057  | 0.000   | 0.047  | 0.000   | 0.061  | 0.000   |
| D7S820                     | 0.011  | 0.012   | 0.007  | 0.001   | 0.011  | 0.000   | 0.023  | 0.001   | 0.011  | 0.000   | 0.000  | 0.441   |
| CSF1PO                     | 0.006  | 0.088   | 0.003  | 0.059   | 0.019  | 0.000   | 0.000  | 0.376   | 0.020  | 0.000   | 0.001  | 0.265   |
| D19S433                    | 0.025  | 0.000   | 0.027  | 0.000   | 0.014  | 0.000   | 0.047  | 0.000   | 0.014  | 0.000   | 0.015  | 0.000   |
| vWA                        | 0.002  | 0.175   | NA     | NA      | 0.010  | 0.000   | 0.011  | 0.016   | 0.010  | 0.000   | 0.004  | 0.012   |
| TPOX                       | 0.010  | 0.028   | 0.070  | 0.000   | 0.019  | 0.000   | 0.055  | 0.000   | 0.115  | 0.000   | 0.013  | 0.001   |
| D18S51                     | 0.019  | 0.000   | 0.016  | 0.000   | 0.015  | 0.000   | 0.010  | 0.010   | 0.017  | 0.000   | 0.001  | 0.209   |
| D3S1358                    | 0.026  | 0.002   | 0.015  | 0.000   | 0.003  | 0.000   | 0.000  | 0.369   | 0.000  | 0.155   | −0.001 | 0.557   |
| THO1                       | 0.025  | 0.000   | 0.010  | 0.000   | 0.082  | 0.000   | 0.071  | 0.000   | 0.035  | 0.000   | 0.024  | 0.000   |
| D13S317                    | 0.016  | 0.002   | 0.008  | 0.000   | 0.006  | 0.009   | 0.004  | 0.129   | 0.028  | 0.000   | 0.000  | 0.430   |
| D16S539                    | 0.005  | 0.095   | 0.011  | 0.000   | 0.010  | 0.000   | 0.010  | 0.022   | 0.014  | 0.000   | 0.002  | 0.090   |
| D25S1338                   | 0.015  | 0.000   | 0.021  | 0.000   | 0.011  | 0.000   | 0.007  | 0.020   | 0.038  | 0.000   | 0.004  | 0.002   |
| D55S818                    | −0.002 | 0.623   | 0.007  | 0.004   | 0.006  | 0.009   | 0.091  | 0.000   | 0.009  | 0.000   | −0.001 | 0.817   |
| FGA                        | 0.003  | 0.135   | 0.006  | 0.000   | 0.002  | 0.083   | 0.026  | 0.000   | 0.002  | 0.047   | 0.003  | 0.018   |

NA not available
P value <0.003

### Table 10 Fst pairwise genetic distances and corresponding P value

| Central Indian region V/S | Croatian | Wallachia | Estonian | Shenyang | Latvian |
|----------------------------|----------|-----------|----------|----------|---------|
|                            | Fst      | p-value   | Fst      | p-value  | Fst     |
| D8S1179                    | 0.028    | 0.000     | 0.022    | 0.000    | 0.027   |
| D21S11                     | 0.067    | 0.000     | 0.050    | 0.000    | 0.041   |
| D7S820                     | 0.009    | 0.002     | 0.010    | 0.000    | 0.007   |
| CSF1PO                     | 0.000    | 0.304     | 0.007    | 0.000    | 0.017   |
| D19S433                    | 0.016    | 0.000     | 0.011    | 0.000    | 0.018   |
| vWA                        | −0.001   | 0.671     | 0.002    | 0.001    | 0.002   |
| TPOX                       | 0.037    | 0.000     | 0.018    | 0.000    | 0.068   |
| D18S51                     | 0.004    | 0.031     | 0.011    | 0.000    | 0.015   |
| D3S1358                    | 0.005    | 0.026     | 0.008    | 0.000    | 0.012   |
| THO1                       | 0.066    | 0.000     | 0.056    | 0.000    | 0.078   |
| D13S317                    | 0.004    | 0.051     | 0.004    | 0.000    | 0.019   |
| D16S539                    | 0.011    | 0.001     | 0.006    | 0.000    | 0.011   |
| D25S1338                   | 0.021    | 0.000     | 0.017    | 0.000    | 0.028   |
| D55S818                    | 0.004    | 0.063     | 0.009    | 0.000    | 0.004   |
| FGA                        | 0.077    | 0.000     | 0.003    | 0.000    | 0.005   |

P value <0.003
NA not available
Conclusion
The data generated here will add to the databank of various studies conducted on Indian populations. With respect to the distribution of alleles at each STR locus, all the 15 STR loci were found to be substantially polymorphic in this population. The virtue of being polymorphic makes these 15 STR loci specific and valuable in individual identification. Central Indian population showed genetic distance from all the compared (published) populations.

Authors' contributions
PS designed the study, did genotyping of samples and contributed significantly in data analysis and manuscript preparation. TJ carried out data management, statistical analysis and drafted the manuscript. VBT helped in data analysis contributed in drafting the manuscript. All authors read and approved the final manuscript.

Compliance with ethical guidelines

Competing interests
The authors declare that they have no competing interest.

We declare that our research was carried out according to our institution's ethical guidelines and that all subjects gave their consent to participate in this study.

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