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Genetic variation and differentiation among a native British and five
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CODIS forensic STR loci.

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Genetic variation and differentiation among a native British and five migrant South Asian populations of the East Midlands (UK) based on CODIS forensic STR loci.

Aim: Short Tandem Repeats (STRs) are widely used in population and forensic genetic studies. The objective of this study was to document the level and extent of genetic variation of the FBI Combined DNA Index System (CODIS) STR loci (D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, TH01, TPOX and CSF1PO) in 6 populations (British, Indian (Punjabis and Gujaratis), Pakistani, Bangladeshi and Sri Lankan) of the East Midlands (UK). There is a lack of genetic research on the migrant South Asian populations.

Methods: DNA samples (N=603) were analysed for 13 autosomal forensic STR loci along with the amelogenin locus following standard protocols. Data were analysed for genetic variation and a range of forensic indices.

Results: All loci were polymorphic in all populations with a variable degree of variation. Average observed heterozygosity was highest in Bangladeshi (0.803) and lowest in Punjabi (0.761). FGA locus had the highest power of discrimination (PD) in most populations.

Conclusion: FGA locus was most polymorphic and discriminatory among migrant populations demonstrating it as the marker with the highest potential in forensic analyses. These results could be useful for population and forensic genomic studies.

BACKGROUND

Short Tandem Repeats (STRs) are the genetic markers of choice in a wide range of genetic and forensic applications including analysis of mass disaster victims, kinship/paternity studies, migrations, population characterisation, genome mapping and crime detection through human identification (Butler, 2006). STRs account for $\approx 3\%$ of the human genome and are mostly located in non-coding DNA (Ellegren 2000, 2004; Payseur et al. 2011; Genovese et al. 2018), making them a marker of choice for forensic analyses. STRs are multiallelic, and alleles are designated based on the number of repeats present at a locus on a chromosome. Most alleles are complete repeats of either simple or complex motifs, but some also have partial repeats (e.g. TH01 allele 9.3; D21S11 allele 32.2, etc.). Most STRs in humans are dinucleotides and trinucleotides; these are not commonly used for forensic applications due to the high frequency of stutter peaks. Commonly used forensic STRs are tetranucleotide (4 base pair repeat motif) which exhibit lower stutter products (Butler, Coble and Vallone, 2007). Tetranucleotide repeats represent $\approx 9\%$ of total STRs in the human genome and are highly polymorphic (Li, 2015). Hypervariability in STRs arises from high mutation rates being between 10^{-3} and 10^{-6} per cell generation, which is higher than that of single nucleotide polymorphisms (SNPs) (average 2.5×10^{-8}) (Nachman and Crowell 2000; Gemayel et al., 2012). Multiple STRs are routinely amplified in a single or a few multiplex polymerase chain reactions (PCR). The typing of STR loci provides high sensitivity and high power of discrimination (PD) for characterisation of DNA samples. Approximately 40-60 SNPs are required to approximate the high PD or random match probabilities (pM) achieved by 13-15 STRs (Butler, Coble and Vallone, 2007).

The original FBI Combined DNA Index System (CODIS) nationwide DNA database focused on the analysis of 13 STR loci. These are commonly utilised for human identity testing both in forensic casework and paternity, mainly due to availability within many commercial human identification kits (Butler, 2006). The CODIS loci contained in AmpFISTR® Profiler Plus™ and AmpFISTR® COfiler™ kits (Applied Biosystems, Foster City, USA) included the autosomal tetranucleotide loci D3S1358, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D16S539, vWA, TPOX, FGA, CSF1PO and TH01. The Amelogenin locus is also included in these kits for

sex/gender identification. These loci (except D5S818 and CSF1PO) are located on different chromosomes, therefore are independently inherited. These loci are non-coding, disease-free markers used solely for forensic applications.

Many population and forensic genetic studies and databases have been established from these loci and other forensic STRs. A range of genetic variation has been documented at these loci among different local and global populations (Budowle et al., 2001; Budowle and Chakraborty, 2001; Ruitberg, 2001; Dobashi et al., 2003; Bindu et al., 2005; Eaaswarkhanth et al., 2009; Mastana et al., 2003, 2007; Illepuruma et al., 2009; Gosh et al., 2011; Silva et al., 2012; Shrivastava et al., 2015, 2017). There is a lack of forensic STR studies on migrant populations and their potential implications for forensic analyses. To address this gap in information, we have carried out a genetic analysis of a native British and five South Asian migrant populations in the East Midlands region of the UK.

SAMPLES AND METHODS

In this study we analyse genetic variation in 6 populations; one native (British) and five migrant South Asian populations (Indian Punjabi (Sikhs), Indian Gujarati, Pakistani, Bangladeshi and Sri Lankan) living in East Midlands area of the UK. In the 2011 census, the population of East Midlands was 4,533,222 and Indian population was the largest South Asian group (12%) followed by Pakistani (4.4%) and Bangladeshi (3%) (England and Wales 2011 Census). We hypothesised that there would be a significant genetic variation of STRs amongst the East Midlands populations based on different population and geographical origins, marriage and migration patterns.

Blood samples were collected from individuals in blood donation camps and community events as part of ongoing genetic studies in the region. All participants were unrelated to three generations and were volunteers aged 18-60 years. The assignment to the various populations was established by considering the population background of the four grandparents using a questionnaire. Each individual provided a blood sample after completion of written consent. The study had full ethical approval from Loughborough University and NHS blood donation service. The

sample consists of the European (N=115), Indian Punjabi (N=105), Indian Gujarati (74), Pakistani (N=102), Bangladeshi (N=103) and Sri Lankan (N=104) individuals. DNA extraction was carried out using the salting-out method. DNA amplification was carried out using AmpFISTR® Profiler Plus™ and AmpFISTR® COfiler™ (Applied Biosystems, Foster City, USA) kits as described by the manufacturer. All amplifications were completed on the GeneAmp 9700 PCR system (Applied Biosystems, Foster City, USA) and electrophoresis was carried out on ABI Prism 310 (Applied Biosystems, Foster City, USA). Samples were analysed using GeneScan Analysis 3.1, and genotypes were identified via Genotyper Software 2.5 (Applied Biosystems, Foster City, USA). Common loci (D3S1358, D7S820 and Amelogenin) in both kits produced consistent genotypes in both analyses for each participant. Amelogenin locus genotyping in both kits matched with the known gender of the participants.

Genotype data for each sample was collated in the Excel sheet and used for further analyses. Data analysis was carried out by a PowerStat Excel sheet (Tereba, 1999) to derive allele frequencies (AF) and forensic indices (pM, PD and typical paternity index (TPI)). GenAlEx 6.5 (Peakall and Smouse, 2012) was used to determine AF, private alleles within the studied East Midlands subpopulations, inbreeding coefficient (θ), Hardy-Weinberg Equilibrium chi-square (HWE, χ^2), observed and expected heterozygosities, analysis of molecular variance (AMOVA), Nei's unbiased genetic distance and pairwise population F_{ST} . All results from different software programmes were cross-referenced for consistency in addition to manual scrutiny.

RESULTS

Population and forensic genetic parameters are presented in Table 1 (1a-1f) for different groups. All loci were highly polymorphic in all populations with TH01 and TPOX loci showing the lowest number of alleles (5 –7) while FGA locus had the largest number of alleles (15 in European, Bangladeshi and Pakistani). Sri Lankan population documented the highest number of total alleles (119) across 13 loci, and the lowest was in Gujarati population (111) probably due to small sample size. Highest allele frequency was observed for TPOX locus (allele 8) in the British population (0.549). As expected, significant heterogeneity was observed at different

levels in individual locus by locus comparisons. Overall allelic diversity and variation are comparable to other European and South Asian populations (Budowle et al., 2001; Budowle and Chakraborty, 2001; Dobashi et al., 2003; Mastana et al., 2003, 2007; Eaaswarkhanth et al., 2009; Illepuruma et al., 2009; Gosh et al., 2011; Silva et al., 2012; Girotti and Talwar, 2013; Shrivastava et al., 2015, 2017; Anwar et al., 2018). Twenty private alleles (only observed in one study population) were found, with the highest number in the European followed by Gujarati population (6 and 5 respectively). Private alleles were observed in low frequencies (0.004-0.014) at all loci except vWA, TPOX, TH01 and D8S1179.

HWE was maintained for D13S317 locus among all populations, while other loci showed departure in one or more populations at initial analyses (24 out of 78 HWE χ^2 values were significant). After applying the Bonferroni correction (p-value $0.05/78 = <0.0006$), 11 population-loci combinations were still statistically significant; however, there was no consistent pattern to these departures. HWE departures witnessed in this study may be due to differences in origin, endogamy/inbreeding, differential migration, genetic drift and other evolutionary forces (Chen, Cole and Grond-Ginsbach, 2017) however alternatively, may be primarily due to small sample size. All homozygous genotypes were re-checked to ensure that this was not due to any issues in the automatic calling of genotypes.

Average observed heterozygosity was highest in the Bangladeshi population (0.803 ± 0.016) and lowest in Punjabi (0.761 ± 0.022). Overall average heterozygosities are similar to many STR studies on European and South Asian populations (Budowle et al., 2001; Budowle and Chakraborty, 2001; Dobashi et al., 2003; Mastana et al., 2003, 2007; Clark et al., 2009; Eaaswarkhanth et al., 2009; Illepuruma et al., 2009; Gosh et al., 2011; Silva et al., 2012; Girotti and Talwar, 2013; Shrivastava et al., 2015, 2017; Hossain et al., 2016; Anwar et al., 2018). Punjabi population has the highest average θ (0.043 ± 0.014) while Bangladeshi the lowest (-0.029 ± 0.024) (Tables 1 and 2). We expected that the British population would have higher heterozygosity reflective of non-endogamous marital patterns; however it was the Bangladeshi population that exhibited the highest heterozygosity in the majority of loci followed by British; Punjabi was noticeably the lowest. The reasoning for

Bangladeshi exhibiting greater heterozygosity than the British is likely to be the inclusion of samples from migrants from different parts of Bangladesh and small sample size. Higher heterozygosity among Bangladeshi population has been observed in other studies also; Dobashi et al. (2003) found Bangladeshi to have the higher average heterozygosity (0.792 vs Indonesian = 0.743) for nine CODIS loci studied.

AMOVA showed that 99% of the genetic variation was within individuals and populations, while 1% of the variation is between populations. Between-population variation is slightly high, but it reflects the nature of sampled migrant populations and their maintained levels of endogamy. The largest Nei's genetic distance is between British and Sri Lankan sample (0.064), while the lowest distance is between the Punjabi and Gujarati sample (0.003) (Table 3). As expected, British population showed the highest differences with other South Asian migrant populations. Within migrant populations, Bangladeshi population showed the highest distance with Sri Lankan followed by Pakistani and Punjabis. Pairwise F_{ST} shows a similar pattern (Table 3).

Pairwise population comparisons between Punjabi and Jat Sikhs from Punjab (Giroti and Talwar 2013) showed significant differences at two loci (D13S317 and FGA). British population did not differ significantly from a range of European populations at any loci (Budowle and Chakraborty, 2001; Budowle et al., 2001). Pakistani sample differed significantly at one locus (FGA) from Punjabi population from Pakistan (Anwar et al., 2018) but showed no differences compared to a Pakistani migrant sample in the UK (Clark et al., 2009). For Sri Lankan comparison, STR data was available for seven common loci on the Sinhalese population (Illepuruma et al., 2009), which did not lead to any statistically significant differences. Bangladeshi sample differed significantly from the native Bangladeshi population at three loci (THO1, vWA and TOPX) (Hossain et al., 2016). There was a lack of comparative data on native Gujarati population, but comparison with a migrant sample in the UK did not show significant differences at any loci (Clark et al., 2009). Caution should be exercised in the interpretations of these results as five populations in these analyses are migrant populations.

Power of discrimination (PD) and power of exclusion (PE) values were comparable in each studied population, suggesting no loss of information due to endogamy and the combination of all 13 loci have high forensic efficacy due to high combined PE and combined PD (Tables 1 and 2). The most discriminating locus across all populations except British was FGA, demonstrating it as the marker with the highest potential to identify individuals, followed by D21S11 and D18S51. Among the British population, D18S51 was the most discriminating with FGA and D21S11 the second and third (Table 1). TPOX was the least discriminating locus in five of six subpopulations. Overall pattern and range of PDs observed in this study is similar and comparable to those observed in British, European and South Asian populations ((Budowle et al., 2001; Budowle and Chakraborty, 2001; Dobashi et al., 2003; Mastana et al., 2003, 2007; Clark et al., 2009; Illepuruma et al., 2009; Shrivastava et al., 2015, 2017; Hossain et al., 2016; Anwar et al., 2018).

All combined typical paternity index and probability of paternity (POP) values were >399 and >99.99% respectively indicating that these markers have the potential to identify biological identities with high confidence (Table 2). Bangladeshi TPI values are ten times greater than the Punjabi population, which has the lowest average heterozygosity and highest θ . It is not unusual as the Punjabi sample mostly consists of Jat Sikh caste, which tends to marry within their caste, leading to a higher level of endogamy.

Comment

The present study is the first to have analysed the British and migrant South Asian sub-populations within the East Midlands, providing clear insight into inter-population differences. All STR loci analysed in this study were substantially polymorphic in all populations, and data generated here are suitable for population genetic and forensic analyses. These STRs provided strong PDs and high cumulative TPIs to identify the perpetrators and alleged fathers accurately. Larger sample size and additional STR loci (e.g. expanded CODIS loci set) will generate more robust

databases and reflective insight into the variability of populations, thus enhancing the forensic capacity of genomic DNA identification.

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Table 1a: Allele frequencies and population genetic and forensic parameters for British population (n=115)

Allele Number	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO
6											0.319		0.022
7									0.009		0.239	0.009	0.009
8				0.026				0.135	0.170	0.035	0.093	0.549	0.022
9				0.013		0.013	0.039	0.074	0.139	0.175	0.142	0.214	0.057
9.3											0.199		
10				0.087		0.018	0.035	0.074	0.243	0.127	0.009	0.022	0.259
10.2						0.004							
10.3													0.004
11				0.048		0.035	0.443	0.283	0.200	0.259		0.179	0.272
12				0.157		0.149	0.335	0.309	0.178	0.237		0.022	0.289
13	0.009			0.335		0.140	0.135	0.091	0.052	0.123		0.004	0.044
13.2													
14	0.135	0.143		0.213		0.149	0.013	0.035	0.009	0.039			0.018
14.2													
15	0.243	0.096		0.096		0.136				0.004			0.004
15.2	0.009												
16	0.235	0.239		0.026		0.136							
17	0.200	0.261	0.004			0.118							
17.2													
18	0.161	0.187	0.026			0.070							
19	0.009	0.070	0.070			0.013							
20		0.004	0.152			0.009							
20.2			0.004										
21			0.139			0.009							
21.2			0.004										
22			0.165										
22.2			0.004										
23			0.152										
23.2													
24			0.157										
24.2													
25			0.091										
25.2													
26			0.030										
27					0.048								
28					0.183								
28.2													
29					0.200								
29.2													
30					0.226								
30.2					0.026								
31					0.057								
31.2					0.083								
32					0.026								
32.2					0.122								
33					0.004								
33.2					0.022								
34.2													
35													
35.2					0.004								
36.2													
Total alleles	8	7	13	9	12	14	6	7	8	8	6	7	11
Observed Heterozygosity	0.852	0.791	0.843	0.800	0.843	0.886	0.730	0.748	0.765	0.781	0.841	0.723	0.807
Expected Heterozygosity	0.801	0.805	0.868	0.798	0.847	0.878	0.670	0.786	0.818	0.812	0.773	0.620	0.769
Inbreeding Coefficient (F/θ)	-0.063	0.017	0.028	-0.003	0.004	-0.009	-0.090	0.049	0.064	0.039	-0.088	-0.167	-0.050
Hardy-Weinberg Equilibrium													
Chi-square (χ^2)	131.23	25.08	84.08	79.42	68.89	97.47	12.14	16.95	36.60	84.32	52.78	12.33	40.26
Probability	<0.001	0.244	0.299	<0.001	0.380	0.302	0.669	0.714	0.128	<0.001	<0.001	0.930	0.932
Degrees of freedom	28	21	78	36	66	91	15	21	28	28	15	21	55
Significance	***	NS	NS	***	NS	NS	NS	NS	NS	***	***	NS	NS
Forensic Indices													
Discrimination Power	0.920	0.926	0.964	0.927	0.953	0.966	0.811	0.922	0.937	0.915	0.847	0.789	0.901
Power of Exclusion	0.699	0.583	0.682	0.599	0.682	0.767	0.477	0.506	0.536	0.564	0.677	0.465	0.612
Typical Paternity Index	3.382	2.396	3.194	2.500	3.194	4.385	1.855	1.983	2.130	2.28	3.139	1.806	2.591
Probability of Match	0.080	0.074	0.036	0.073	0.047	0.034	0.189	0.034	0.063	0.085	0.153	0.211	0.099

Table 1b: Allele frequencies and population genetic and forensic parameters for Indian-Punjabi population (n=105)

Allele Number	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO
6											0.245		
7								0.020	0.019		0.136		0.016
8				0.020		0.005		0.196	0.189	0.070	0.098	0.408	
9			0.005	0.005			0.029	0.103	0.107	0.124	0.337	0.120	0.005
9.3											0.174		
10				0.193			0.155	0.098	0.199	0.048	0.005	0.054	0.179
10.2													
10.3													
11				0.074			0.354	0.299	0.291	0.323	0.005	0.391	0.299
12				0.158		0.055	0.257	0.191	0.175	0.258		0.016	0.348
13				0.129		0.090	0.189	0.069	0.019	0.134		0.011	0.114
13.2													
14	0.062	0.175		0.158		0.265	0.015	0.020		0.043			0.033
14.2													
15	0.310	0.063		0.178		0.145							0.005
15.2													
16	0.305	0.223		0.069		0.200							
17	0.205	0.223		0.010		0.135		0.005					
17.2				0.005									
18	0.105	0.209	0.029			0.030							
19	0.005	0.087	0.039			0.045							
20	0.010	0.019	0.150			0.020							
20.2													
21			0.146			0.005							
21.2			0.019										
22			0.121			0.005							
22.2			0.019										
23			0.146										
23.2			0.005										
24			0.160										
24.2													
25			0.107										
25.2			0.010										
26			0.034										
27			0.010		0.029								
28					0.157								
28.2													
29					0.181								
29.2													
30					0.167								
30.2					0.029								
31					0.034								
31.2					0.098								
32					0.015								
32.2					0.172								
33					0.010								
33.2					0.098								
34.2					0.005								
35													
35.2					0.005								
36.2													
Total alleles	7	7	15	11	13	12	6	9	7	7	7	6	8
Observed Heterozygosity	0.762	0.796	0.845	0.832	0.853	0.780	0.738	0.814	0.718	0.796	0.696	0.554	0.707
Expected Heterozygosity	0.754	0.814	0.879	0.853	0.863	0.836	0.747	0.810	0.797	0.787	0.768	0.663	0.743
Inbreeding Coefficient (F/θ)	-0.010	0.022	0.039	0.025	0.011	0.067	0.012	-0.005	0.099	-0.011	0.095	0.164	0.049
Hardy-Weinberg Equilibrium													
Chi-square (χ^2)	25.07	12.21	188.55	53.53	121.00	93.75	27.77	44.83	47.20	23.41	19.12	111.94	45.81
Probability	0.244	0.934	0.000	0.531	0.001	0.014	0.023	0.149	0.001	0.322	0.577	<0.001	0.018
Degrees of freedom	21	21	105	55	78	66	15	36	21	21	21	15	28
Significance	NS	NS	***	NS	**	*	*	NS	***	NS	NS	***	*
Forensic Indices													
Discrimination Power	0.892	0.937	0.964	0.959	0.959	0.948	0.887	0.916	0.924	0.903	0.909	0.825	0.891
Power of Exclusion	0.530	0.592	0.684	0.689	0.701	0.562	0.489	0.625	0.512	0.591	0.422	0.240	0.438
Typical Paternity Index	2.100	2.452	3.219	3.269	3.400	2.273	1.907	2.684	2.012	2.447	1.643	1.122	1.704
Probability of Match	0.108	0.063	0.036	0.041	0.041	0.052	0.113	0.052	0.076	0.097	0.091	0.175	0.109

Table 1c: Allele frequencies and population genetic and forensic parameters for Indian-Gujarati population (n=73)

Allele Number	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO
6											0.254		
7									0.029	0.008	0.167		
8							0.007	0.193	0.171	0.063	0.127	0.435	0.008
9				0.007			0.035	0.114	0.036	0.135	0.246	0.129	0.04
9.3											0.167		
10				0.087		0.029	0.099	0.093	0.343	0.095	0.032	0.097	0.198
10.2													
10.3													
11				0.080		0.029	0.415	0.257	0.236	0.317	0.008	0.323	0.302
12	0.007	0.007		0.138		0.051	0.232	0.243	0.179	0.270		0.016	0.365
13	0.007			0.174		0.065	0.183	0.086		0.103			0.071
13.2													
14	0.021	0.211		0.196		0.283	0.028	0.014	0.007	0.008			0.016
14.2													
15	0.308	0.063		0.196		0.196							
15.2													
16	0.219	0.183		0.101		0.109							
17	0.274	0.296		0.014		0.145							
17.2				0.007									
18	0.158	0.148				0.029							
19	0.007	0.063	0.058			0.036							
20		0.028	0.123			0.022							
20.2			0.007										
21			0.152			0.007							
21.2			0.029										
22			0.138										
22.2			0.022										
23			0.167										
23.2			0.014										
24			0.138										
24.2													
25			0.072		0.007								
25.2													
26			0.080										
27					0.029								
28					0.193								
28.2													
29					0.221								
29.2					0.014								
30					0.150								
30.2													
31					0.029								
31.2					0.114								
32					0.014								
32.2					0.121								
33													
33.2					0.071								
34.2					0.029								
35													
35.2													
36.2					0.007								
Total alleles	8	8	12	10	13	12	7	7	7	8	7	5	7
Observed Heterozygosity	0.836	0.775	0.836	0.870	0.814	0.797	0.746	0.800	0.800	0.794	0.746	0.645	0.746
Expected Heterozygosity	0.757	0.804	0.879	0.850	0.855	0.838	0.728	0.808	0.763	0.784	0.802	0.680	0.729
Inbreeding Coefficient (F/Θ)	-0.105	0.036	-0.005	-0.023	0.048	0.049	-0.025	0.010	-0.048	-0.012	0.070	0.051	-0.023
Hardy-Weinberg Equilibrium													
Chi-square (X ²)	154.31	41.27	72.44	27.01	118.03	123.68	39.12	25.25	17.85	18.87	14.98	10.36	15.83
Probability	<0.001	0.051	0.274	0.985	0.002	<0.001	0.009	0.236	0.659	0.902	0.824	0.410	0.779
Degrees of freedom	28	28	66	45	78	66	21	21	21	28	21	10	21
Significance	***	NS	NS	NS	**	***	**	NS	NS	NS	NS	NS	NS
Forensic Indices													
Discrimination Power	0.883	0.922	0.960	0.952	0.948	0.941	0.872	0.922	0.898	0.916	0.930	0.843	0.872
Power of Exclusion	0.667	0.553	0.763	0.734	0.626	0.594	0.504	0.599	0.599	0.581	0.503	0.356	0.503
Typical Paternity Index	3.042	2.219	4.313	3.833	2.692	2.464	1.972	2.500	2.500	2.385	1.969	1.432	1.969
Probability of Match	0.117	0.078	0.040	0.048	0.052	0.059	0.128	0.059	0.102	0.084	0.070	0.162	0.128

Table 1d: Allele frequencies and population genetic and forensic parameters for Pakistani population (n=102)

Allele Number	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO
6											0.227		
7							0.005	0.005	0.030		0.122	0.006	
8				0.005			0.010	0.116	0.203	0.029	0.174	0.401	0.006
9				0.005			0.025	0.172	0.079	0.169	0.308	0.151	0.061
9.3											0.157		
10				0.126			0.157	0.116	0.238	0.122	0.012	0.081	0.195
10.2													
10.3													
11				0.045		0.021	0.404	0.207	0.248	0.256		0.355	0.305
12		0.015		0.101		0.089	0.258	0.217	0.158	0.297		0.006	0.305
13				0.197		0.141	0.126	0.121	0.040	0.105			0.116
13.2						0.005							
14	0.069	0.136		0.242		0.286	0.010	0.040		0.023			0.012
14.2													
15	0.240	0.081		0.207		0.188		0.005	0.005				
15.2													
16	0.358	0.278		0.045		0.099							
17	0.216	0.268		0.020		0.068							
17.2													
18	0.113	0.172	0.031	0.005		0.031							
19	0.005	0.040	0.052			0.021	0.005						
20		0.010	0.077			0.042							
20.2													
21			0.077			0.005							
21.2			0.005										
22			0.139			0.005							
22.2			0.005										
23			0.232										
23.2			0.005										
24			0.206										
24.2			0.005										
25			0.103										
25.2													
26			0.041										
27			0.005		0.040								
28			0.015		0.131								
28.2					0.005								
29					0.182								
29.2													
30					0.177								
30.2					0.025								
31					0.051								
31.2					0.141								
32					0.005								
32.2					0.146								
33													
33.2					0.091								
34.2					0.005								
35													
35.2													
36.2													
Total alleles	6	8	15	11	12	13	9	9	8	7	6	6	7
Observed Heterozygosity	0.745	0.828	0.876	0.818	0.879	0.823	0.747	0.848	0.792	0.791	0.779	0.651	0.634
Expected Heterozygosity	0.750	0.795	0.856	0.829	0.864	0.837	0.729	0.837	0.807	0.791	0.784	0.684	0.759
Inbreeding Coefficient (F/Θ)	0.007	-0.042	-0.024	0.013	-0.017	0.017	-0.025	-0.014	0.019	0.000	0.006	0.048	0.164
Hardy-Weinberg Equilibrium													
Chi-square (χ^2)	9.99	59.36	94.67	71.08	58.06	53.59	18.66	26.47	27.30	13.68	8.10	7.88	44.85
Probability	0.821	<0.001	0.755	0.071	0.746	0.984	0.992	0.877	0.502	0.883	0.920	0.928	0.002
Degrees of freedom	15	28	105	55	66	78	36	36	28	21	15	15	21
Significance	NS	***	NS	NS	NS	NS	NS	NS	NS	NS	NS	NS	**
Forensic Indices													
Discrimination Power	0.895	0.921	0.957	0.946	0.957	0.949	0.883	0.943	0.930	0.925	0.919	0.848	0.900
Power of Exclusion	0.501	0.653	0.747	0.633	0.752	0.642	0.505	0.692	0.584	0.582	0.561	0.357	0.334
Typical Paternity Index	1.962	2.912	4.042	2.750	4.125	2.824	1.980	3.300	2.405	2.389	2.263	1.433	1.367
Probability of Match	0.105	0.079	0.043	0.054	0.043	0.051	0.117	0.051	0.070	0.075	0.081	0.152	0.100

Table 1e: Allele frequencies and population genetic and forensic parameters for Bangladeshi population (n=103)

Allele Number	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO
6											0.263		
7							0.005	0.020	0.010		0.279		
8				0.010			0.005	0.212	0.217	0.016	0.068	0.547	
9				0.010			0.060	0.141	0.071	0.247	0.316	0.174	0.032
9.3											0.068		
10				0.118			0.180	0.116	0.212	0.168	0.005	0.042	0.207
10.2													
10.3													
11				0.074		0.010	0.330	0.263	0.313	0.379		0.205	0.271
12		0.010		0.059		0.051	0.260	0.162	0.146	0.116		0.032	0.378
13	0.015			0.172		0.179	0.150	0.056	0.025	0.063			0.096
13.2													
14	0.063	0.211		0.211		0.230	0.010	0.030	0.005	0.011			0.016
14.2						0.005							
15	0.286	0.054		0.240		0.173							
15.2													
16	0.325	0.211		0.098		0.138							
17	0.223	0.299		0.005		0.092							
17.2			0.005										
18	0.073	0.127	0.025	0.005		0.031							
19	0.010	0.078	0.084			0.031							
20	0.005	0.001	0.109			0.020							
20.2													
21			0.153			0.026							
21.2			0.010										
22			0.168			0.010							
22.2			0.005										
23			0.168										
23.2			0.015										
24			0.119			0.005							
24.2													
25			0.104										
25.2													
26			0.020										
27			0.005		0.015								
28			0.010		0.129								
28.2					0.010								
29					0.203								
29.2													
30					0.173								
30.2					0.040								
31					0.040								
31.2					0.084								
32					0.020								
32.2					0.213								
33					0.005								
33.2					0.069								
34.2													
35													
35.2													
36.2													
Total alleles	8	8	15	11	12	14	8	8	8	7	6	5	6
Observed Heterozygosity	0.757	0.765	0.812	0.843	0.881	0.796	0.760	0.818	0.869	0.853	0.863	0.726	0.691
Expected Heterozygosity	0.753	0.796	0.874	0.836	0.851	0.852	0.765	0.822	0.783	0.749	0.744	0.625	0.730
Inbreeding Coefficient (F/θ)	-0.006	0.040	0.072	-0.009	-0.035	0.066	0.006	0.005	-0.110	-0.138	-0.160	-0.162	0.053
Hardy-Weinberg Equilibrium													
Chi-square (χ^2)	22.01	25.80	70.13	49.85	100.30	189.65	22.24	15.80	20.19	19.16	45.30	26.86	26.55
Probability	0.781	0.584	0.996	0.671	0.004	0.000	0.770	0.969	0.857	0.575	<0.001	0.003	0.033
Degrees of freedom	28	28	105	55	66	91	28	28	28	21	15	10	15
Significance	NS	NS	NS	NS	**	***	NS	NS	NS	NS	***	**	*
Forensic Indices													
Discrimination Power	0.890	0.928	0.966	0.944	0.944	0.956	0.901	0.941	0.905	0.879	0.826	0.774	0.876
Power of Exclusion	0.522	0.535	0.621	0.681	0.757	0.591	0.527	0.633	0.732	0.700	0.721	0.470	0.415
Typical Paternity Index	2.060	2.125	2.658	3.188	4.208	2.450	2.083	2.750	3.808	3.393	3.654	1.827	1.621
Probability of Match	0.110	0.072	0.034	0.056	0.056	0.044	0.099	0.044	0.095	0.121	0.174	0.226	0.124

Table 1f: Allele frequencies and population genetic and forensic parameters for Sri Lankan population (n=104)

Allele Number	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D16S539	TH01	TPOX	CSF1PO
6											0.240		
7								0.014	0.019		0.123	0.005	
8				0.010				0.245	0.188	0.083	0.152	0.294	0.005
9				0.005			0.029	0.087	0.063	0.142	0.319	0.157	0.015
9.3											0.162		
10				0.231		0.010	0.072	0.077	0.279	0.113		0.108	0.245
10.2													
10.3													
11				0.087		0.029	0.380	0.250	0.264	0.319	0.005	0.368	0.279
12		0.014		0.106		0.063	0.337	0.260	0.154	0.221		0.059	0.382
13	0.005			0.077		0.096	0.168	0.048	0.029	0.093		0.010	0.064
13.2						0.005							
14	0.043	0.139		0.178		0.274	0.010	0.019	0.005	0.020			0.005
14.2													
15	0.341	0.096		0.216		0.207	0.005			0.010			0.005
15.2													
16	0.322	0.221		0.063		0.159							
17	0.159	0.279		0.024		0.077							
17.2				0.005									
18	0.115	0.163	0.005			0.019							
19	0.014	0.053	0.038			0.014							
20		0.034	0.130			0.034							
20.2													
21			0.173			0.005							
21.2			0.005										
22			0.178			0.005							
22.2			0.005										
23			0.192										
23.2													
24			0.144			0.005							
24.2			0.005										
25			0.091										
25.2			0.005										
26			0.029										
27					0.005								
28					0.106								
28.2													
29					0.221								
29.2													
30					0.168								
30.2					0.038								
31					0.048								
31.2					0.106								
32					0.014								
32.2					0.207								
33					0.005								
33.2					0.072								
34.2					0.005								
35					0.005								
35.2													
36.2													
Total alleles	7	8	13	11	13	15	7	8	8	8	6	7	8
Observed Heterozygosity	0.721	0.769	0.894	0.827	0.817	0.808	0.712	0.712	0.760	0.745	0.814	0.696	0.696
Expected Heterozygosity	0.739	0.814	0.853	0.839	0.848	0.835	0.708	0.794	0.788	0.801	0.776	0.739	0.711
Inbreeding Coefficient (F/θ)	0.024	0.055	-0.048	0.014	0.037	0.033	-0.005	0.104	0.036	0.070	-0.048	0.057	0.021
Hardy-Weinberg Equilibrium													
Chi-square (χ^2)	23.30	26.21	279.60	56.97	77.33	114.56	22.48	23.17	79.41	31.56	10.36	19.81	16.52
Probability	0.328	0.561	<0.001	0.402	0.500	0.246	0.373	0.725	<0.001	0.293	0.797	0.533	0.957
Degrees of freedom	21	28	78	55	78	105	21	28	28	28	15	21	28
Significance	NS	NS	***	NS	NS	NS	NS	NS	***	NS	NS	NS	NS
Forensic Indices													
Discrimination Power	0.881	0.935	0.954	0.945	0.953	0.950	0.846	0.926	0.912	0.926	0.909	0.888	0.856
Power of Exclusion	0.462	0.543	0.784	0.650	0.632	0.613	0.446	0.446	0.526	0.501	0.625	0.422	0.422
Typical Paternity Index	1.793	2.167	4.727	2.889	2.737	2.600	1.733	1.733	2.080	1.962	2.684	1.645	1.645
Probability of Match	0.119	0.065	0.046	0.055	0.047	0.050	0.154	0.050	0.088	0.074	0.091	0.112	0.144

Table 2: Average population and forensic indices for six East Midlands populations

Population	Average Observed Heterozygosity and SE	Combined θ	CPE	CpM	CPD	TPI
British	0.801 $\pm$ 0.014	-0.021 $\pm$ 0.019	9.9E-01	2.828E-15	9.9E-01	237797.395
Indian Punjabi	0.761 $\pm$ 0.022	0.043 $\pm$ 0.014	9.9E-01	1.635E-15	9.9E-01	33146.770
Indian Gujarati	0.789 $\pm$ 0.017	0.002 $\pm$ 0.014	9.9E-01	5.214E-15	9.9E-01	120743.750
Pakistani	0.786 $\pm$ 0.021	0.012 $\pm$ 0.014	9.9E-01	1.619E-15	9.9E-01	123036.620
Bangladeshi	0.803 $\pm$ 0.016	-0.029 $\pm$ 0.024	9.9E-01	8.850E-15	9.9E-01	306181.960
Sri Lankan	0.767 $\pm$ 0.017	0.027 $\pm$ 0.012	9.9E-01	3.437E-15	9.9E-01	33621.720

Legend: θ = Inbreeding coefficient; CPE= Combined power of exclusion; CpM = Combined probability of Match; CPD = Combined power of discrimination; TPI = Combined typical paternity index.

	British	Indian Punjabi	Indian Gujarati	Pakistani	Bangladeshi	Sri Lankan
British		0.009	0.007	0.008	0.009	0.011
Indian Punjabi	0.052		0.004	0.004	0.006	0.003
Indian Gujarati	0.031	0.003		0.004	0.006	0.004
Pakistani	0.043	0.009	0.007		0.007	0.004
Bangladeshi	0.048	0.025	0.023	0.029		0.007
Sri Lankan	0.064	0.004	0.009	0.015	0.034	

Table 3: Nei's unbiased genetic distance (DA) (below diagonal) and average pairwise FST (above diagonal)