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Genetic Polymorphism of 16 Autosomal STRs Loci of the PowerPlex ESX 17 System in a Population Sample from Bangladesh



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Abstract

Allele frequencies of 16 autosomal short tandem repeats loci, D18S51, D21S11, TH01, D3S1358, D16S539, D2S1338, D1S1656, D10S1248, FGA, D8S1179, VWA, D22S1045, SE33, D19S433, D12S391 and D2S441 were investigated in 95 unrelated Bangladeshi individuals using PowerPlex ESX 17 System Kit. Forensic efficiency parameters, the probability of match, power of discrimination, polymorphism information content, power of exclusion of paternity, observed heterozygosity and expected heterozygosity were calculated for the loci. The allele frequencies distribution and forensic statistical parameters indicated the usefulness of these loci in forensic investigation and personal identification in the Bangladeshi population. The combined probability of match (PM) and combined power of exclusion (PE) was 1.31×10^{-20} and 0.999736 for the loci. The PowerPlex ESX 17 System though was developed and recommended by ENFSI for DNA profile sharing across Europe, the system was also proved to be useful for forensic caseworks in Bangladeshi population.

Keywords: Allele Frequency; Power of Discrimination; Polymorphism; Heterozygosity; Forensic Investigation

Introduction

The PowerPlex® ESX 17 System loci primarily developed for use in European population. Forensic DNA assessment based on microsatellite sequences or short tandem repeats (STRs) has emerged as a powerful tool for human identification in criminal investigations, resolving parentage dispute and population genetic studies in recent days. Bangladesh is a South Asian country, bordered on the north, east and west side with India and, a short land and water frontier with Myanmar in the southeast. About 98% of the population in Bangladesh derives from Bengali ethno-liguistic group. The rest 2% are mainly etnic minorities living in the Chittagong Hill Tracts, Sylhet, Mymenshing and North Bengal regions of the country[1,2]. In this study we evaluated the effectiveness of thePowerPlex ESX 17 System loci primarily developed for use in European population.

Method

Whole blood or buccal cells were collected from randomly selected 95 individuals from Bangladeshi population Samples were taken with informed consent from all individuals following procedures that are in accordance with the Helsinki Declaration of 1964, revised in 1983 [3]. Ge

nomic DNA was extracted using the Chelex-100 method described by PS Walsh [4]. Extracted DNA was quantified by NanoDrop-1000 (Nano Drop Technologies, Inc, Washington DE 19810, USA). Approximately 1 to 2 ng of genomic DNA was used for PCR amplification procedure for each sample. The PCR amplification reaction was carried out by using VeritiThermal Cycler (Applied Biosystems, USA). The thermal cycling conditions were employed according to the manufacturer's instructions (Promega Corporation, USA). The PCR amplified products were separated and typed by capillary electrophoresis on ABI 3500 Genetic Analyzer (Applied Biosystems, USA) using POP-4 polymer and Data Collection Software v1.0. Peak sizing and genotype assignments were done by Gene Mapper ID-X v1.2. Allele frequencies and statistical parameters of forensic efficiency were calculated by using PowerStat Microsoft Excel Workbook version 1.2 [5]. The Hardy-Weinberg equilibrium and forensic efficiency parameters were calculated using Arlequin Software version 3.5 [6].

Results and Discussion

Allele frequency and forensic efficiency parameters for 16 STR loci are presented in Tables 1&2 respectively. A total of 75 alleles found at the 16 loci studied. For each locus, at least

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seven alleles were observed (Table 1). SE33 was the highest polymorphic locus bearing 33 different alleles and 71 genotypes compared to the other loci. The combined frequencies were used to calculate forensic efficiency parameters. Eight out of the 16 STR loci studied were in Hardy–Weinberg equilibrium (using a 5% significance level) the eight remaining loci, D18S51, D1S1656, D16S639, D22S1045, FGA, D12S391 and SE33, showed a slight deviation from expectations (0.002<P<0.05). The PIC value for all the STR loci were highly informative (PIC>0.7). The most informative locus among the 16 STR loci was SE33 (PIC = 0.94), while the least informative were D3S1358, D22S1045 and D2S441 (PIC=0.71). A large number of microvarient

and rare alleles (35 alleles) were observed and are shown in italics format (Table 1). The allele 29.3 at D21S11, allele 8 at D1S1656 and allele 19.3 at D12S391 were previously reported for Bangladeshi population [7,8]. and reported only once in STRBase [9]. Allele 11 was found to be the most frequent allele at D2S441 locus followed by allele 10 at D2S441 and allele 15 at D2S441 loci, respectively. Out of the sixteen loci studied, D2S1338 and SE33 were the most informative locus based on observed heterozygosity (0.895 and 0.884 respectively). The combined probability of match (PM), combined power of discrimination and combined power of exclusion for the studied loci were 1.31×10⁻²⁰, 1and 0.999736, respectively.

Table 1: Allele frequencies of 16 autosomal STR loci of PowerPlex® ESX 17 System in a population sample from Bangladesh (n = 95).

Allele	D3S1358	TH01	D21S11	D18S51	D10S1248	D1S1656	D2S1338	D16S639	D22S1045	vWA	D8S1179	FGA	D2S441	D12S391	D19S433	SE33
6	-	0.184	-	-	-	-	-	0.021	-	-	-	-	-	-	-	-
6.3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.005
7	-	0.137	-	-	-	-	-	-	-	-	-	-	-	-	-	-
8	-	0.158	-	-	-	0.026	-	0.032	0.011	-	0.016	-	-	-	-	-
8.3	-	0.026	-	-	-	-	-	-	-	-	-	-	-	-	-	-
9	-	0.279	-	0.011	0.016	-	-	0.163	0.011	-	0.005	-	0.011	-	-	-
9.3	-	0.174	-	-	-	-	-	0.021	-	-	-	-	-	-	-	-
10	0.011	0.026	-	0.005	-	0.016	-	0.084	-	0.05	0.226	-	0.332	-	-	-
11	-	0.005	-	0.032	-	0.168	-	0.284	0.3	-	0.074	0.005	0.342	-	0.016	0.005
11.3	-	-	-	-	-	-	-	0.021	-	-	-	-	0.047	-	-	-
12	-	0.011	-	0.089	0.032	0.074	-	0.221	0.005	-	0.084	-	0.063	-	0.132	-
12.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.021	-
12.3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
13	-	-	-	0.163	0.163	0.089	-	0.132	0.016	-	0.179	-	0.042	-	0.305	0.005
13.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.058	-
13.3	-	-	-	-	-	0.005	-	-	-	-	-	-	0.011	-	-	-
14	0.047	-	-	0.221	0.279	0.116	-	0.021	0.047	0.116	0.226	-	0.116	-	0.205	0.021
14.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.079	-
14.3	-	-	-	-	-	0.026	-	-	-	-	-	-	0.005	-	-	-
15	0.263	-	-	0.158	0.274	0.205	-	-	0.332	0.053	0.142	-	0.026	-	0.116	0.016
15.2	0.005	-	-	-	-	-	-	-	-	-	-	-	-	-	0.053	-
15.3	-	-	-	-	-	0.021	-	-	-	-	-	-	-	-	-	0.011
16	0.258	-	-	0.105	0.163	0.126	0.011	-	0.2	0.274	0.042	-	0.005	0.032	0.011	0.095
16.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.005	0.005
16.3	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.026
17	0.311	-	-	0.089	0.068	0.058	0.063	-	0.058	0.263	-	-	-	0.095	-	0.026
17.1	-	-	-	-	-	0.005	-	-	-	-	-	-	-	-	-	-
17.2	-	-	-	0.011	-	-	-	-	-	-	-	-	-	-	-	0.005
17.3	-	-	-	-	-	0.026	-	-	-	-	-	-	-	0.042	-	-
18	0.105	-	-	0.042	0.005	0.021	0.174	-	0.021	0.179	-	0.011	-	0.216	-	0.095
18.2	-	-	-	-	-	-	-	-	-	-	-	0.011	-	-	-	-
18.3	-	-	-	-	-	-	0.005	-	-	-	-	-	-	0.047	-	-
19	-	-	-	0.032	-	-	0.189	-	-	0.084	-	0.047	-	0.174	-	0.058
19.2	-	-	-	-	-	-	-	-	-	-	-	0.005	-	-	-	-
19.3	-	-	-	-	-	0.016	0.005	-	-	-	-	-	-	0.021	-	-
20	-	-	-	0.021	-	-	0.074	-	-	0.026	-	0.116	-	0.074	-	0.068

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			1	1		I	1		I	1						
20.1	-	-	-	-	-	-	-	-	-	-	-	0.005	-	-	-	-
20.2	-	-	-	-	-	-	-	-	-	-	-	0.005	-	-	-	0.005
20.3	-	-	-	-	-	-	-	-	-	-	-	-	-	0.021	-	-
21	-	-	-	0.005	-	-	0.047	-	-	-	-	0.105	-	0.053	-	0.058
21.2	-	-	-	-	-	-	-	-	-	-	-	0.011	-	-	-	0.011
22	-	-	-	-	-	-	0.074	-	-	-	-	0.142	-	0.1	-	-
22.1	-	-	-	-	-	-	-	-	-	-	-	0.005	-	-	-	-
22.2	-	-	-	-	-	-	-	-	-	-	-	0.016	-	-	-	0.011
23	-	-	-	0.011	-	-	0.179	-	-	-	-	0.184	-	0.089	-	0.005
23.1	-	-	-	-	-	-	-	-	-	-	-	0.016	-	-	-	-
23.2	-	-	-	-	-	-	-	-	-	-	0.005	0.026	-	-	-	0.037
24	-	-	-	0.005	-	-	0.063	-	-	-	-	0.137	-	0.026	-	0.005
24.1	-	-	-	-	-	-	-	-	-	-	-	0.005	-	-	-	-
24.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.053
25	-	-	-	-	-	-	0.063	-	-	-	-	0.074	-	0.011	-	-
25.1	-	-	-	-	-	-	-	-	-	-	-	0.005	-	-	-	-
25.2	-	-	-	-	-	-	-	-	-	-	-	0.005	-	-	-	0.021
26	-	-	0.005	-	-	-	0.042	-	-	-	-	0.047	-	-	-	0.005
26.2	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-	0.047
27	-	-	0.011	-	-	-	-	-	-	-	-	0.016	-	-	-	-
27.2	-	-	0.005	-	-	-	-	-	-	-	-	-	-	-	-	0.047
28	-	-	0.142	-	-	-	0.011	-	-	-	-	-	-	-	-	-
28.2	-	-	0.005	-	-	-	-	-	-	-	-	-	-	-	-	0.074
28.3	-	-	0.021	-	-	-	-	-	-	-	-	-	-	-	-	-
29	-	-	0.137	-	-	-	-	-	-	-	-	-	-	-	-	-
29.2	-	-	0.037	-	-	-	-	-	-	-	-	-	-	-	-	0.053
29.3	-	-	0.005	-	-	-	-	-	-	-	-	-	-	-	-	-
30	-	-	0.184	-	-	-	-	-	-	-	-	-	-	-	-	0.005
30.2	-	-	0.042	-	-	-	-	-	-	-	-	-	-	-	-	0.053
30.3	-	-	0.005	-	-	-	-	-	-	-	-	-	-	-	-	-
31	-	-	0.032	-	-	-	-	-	-	-	-	-	-	-	-	-
31.1	-	-	0.026	-	-	-	-	-	-	-	-	-	-	-	-	-
31.2	-	-	0.074	-	-	-	-	-	-	-	-	-	-	-	-	0.026
32	-	-	0.011	-	-	-	-	-	-	-	-	-	-	-	-	-
32.1	-	-	0.032	-	-	-	-	-	-	-	-	-	-	-	-	-
32.2	-	-	0.174	-	-	-	-	-	-	-	-	-	-	-	-	0.011
33.1	-	-	0.005	-	-	-	-	-	-	-	-	-	-	-	-	-
33.2	-	-	0.042	-	-	-	-	-	-	-	-	-	-	-	-	0.011
34.2	-	-	0.005	-	-	-	-	-	-	-	-	-	-	-	-	0.005

Table 2: Forensic and Paternity related parameters of PowerPlex® ESX 17 System kit loci in a population sample from Bangladesh (n=95)

Loci	Forensic efficiency parameters											
	PM	PD	PIC	PE	TPI	Но	Не	p				
D3S1358	0.114	0.886	0.71	0.561	2.26	0.779	0.758	0.044				
TH01	0.075	0.925	0.79	0.659	2.97	0.832	0.817	0.047				
D21S11	0.035	0.965	0.87	0.742	3.96	0.874	0.888	0.063				
D18S51	0.044	0.956	0.85	0.619	2.64	0.811	0.872	0.002				
D10S1248	0.084	0.916	0.76	0.58	2.38	0.789	0.792	0.105				
D1S1656	0.038	0.962	0.87	0.639	2.79	0.821	0.884	0.005				

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D2S1338	0.043	0.957	0.86	0.785	4.75	0.895	0.879	0.01
D16S639	0.064	0.936	0.79	0.453	1.76	0.716	0.821	0.002
D22S1045	0.109	0.891	0.71	0.404	1.58	0.684	0.758	0
vWA	0.082	0.918	0.77	0.505	1.98	0.747	0.804	0.003
D8S1179	0.064	0.936	0.81	0.679	3.17	0.842	0.835	0.076
FGA	0.032	0.968	0.88	0.561	2.26	0.779	0.895	0
D2S441	0.134	0.866	0.71	0.679	3.17	0.842	0.755	0.06
D12S391	0.038	0.962	0.87	0.58	2.38	0.789	0.886	0
D19S433	0.064	0.936	0.8	0.505	1.98	0.747	0.825	0.007
SE33	0.019	0.981	0.94	0.763	4.32	0.884	0.951	0
Overall	1.31 × 10 ⁻²⁰	1	-	0.999736	-	-	-	-

PM, probability of match; PD, power of discrimination; PIC, polymorphism information content; PE, power of exclusion of paternity; TPI, typical paternity index; Ho, observed heterozygosity; He, expected heterozygosity; p, Hardy-Weinberg equilibrium exact test.

Conclusion

Genotyping of the 16 autosomal STR loci including SE33 locus may provide a useful adjunct to the previously studied autosomal STR loci evaluated for this population in the past.

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