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Announcement of Population Data

Forensic evaluation of STR data for the PowerPlex™ 16 System loci in a Bangladeshi population

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ABSTRACT

Allele frequencies of 15 autosomal STR loci included in PowerPlex™ 16 System were determined from a sample of 148 unrelated Bangladeshi individuals. Forensic efficiency parameters such as, the power of discrimination (PD), observed and expected heterozygosity (*H*), polymorphism information content (PIC), probability of match (PM), power of exclusion (PE), and typical paternity index were calculated for the loci. These parameters indicated the usefulness of the loci in paternity testing and personal identification in the Bangladeshi population.

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Population: A sample of 148 randomly selected unrelated Bangladeshi individuals was typed for 15 STR loci. Historically, there are four ethnic groups in Bangladesh: Dravidian, proto-Australian, Mongolian and Bangali. The Bangalis are by far the largest group of all, constituting about 98% of the total population. The Dravidian element of population is represented mainly the Oraons, a tribe of central Indian in origin. The proto-Australian group includes Khasia and Santals, mainly labourers in the tea garden at Sylhet district. The Mongolian group is confined to the hills along the southern spur of the Shilong plateau, in Chittagong hill tracts and Madhupur forest. Chakam, Tripura, Garo, Murang and Moghs are the major Mongolid tribes in Bangladesh. The individuals recruited in this study belongs to only the mainstream Bangali population.

DNA extraction: Genomic DNA from 148 unrelated individuals was isolated by Chelex method [1]. Whole blood and buccal cells were used as a DNA source.

PCR amplification: Approximately 1–2 ng of DNA was co-amplified using PowerPlex™ 16 PCR amplification kit. The PCR reaction was carried out in a GenAmp PCR system 2700 (Applied Biosystems) following the protocol provided by the manufacturer.

Typing: PCR amplified fragments were separated and analyzed on ABI Prism 3100-*avant* Genetic Analyzer (Applied Biosystems). Data were sized using GeneScan Software version 3.7 through the use of IL-600 internal size standard. Tabular data from

GeneScan was converted to genotype calls using Genotyper version 3.7 NT with the help of PowerTyper™ 16 Macros.

Results: Allele frequency for 15 STR loci and forensic efficiency parameters are presented in Tables 1 and 2.

Analysis of data: Allele frequencies and statistical parameters of forensic interest was calculated using PowerStat Microsoft Excel workbook template [2]. Deviations from Hardy-Weinberg expectations were evaluated by Fisher's exact test using Arlequin 2.0 software [3].

Quality control: Positive control DNA and allelic ladder provided in PowerPlex™ 16 kit. Fifteen random samples (~10%) of all 148 samples were genotypes twice to further ensure result reproducibility.

Other remarks: We have previously reported the allele frequency of 10 STR loci in a sample population of Bangladesh using AmpF_l SGM Plus PCR amplification kit (Applied Biosystems) [4]. The present study reports the allele frequency of 15 STR loci included in PowerPlex™ 16 PCR amplification kit (Promega Corporation, USA). Allele frequency of eight loci which were common in both the system is in good agreement. This study reports the allele frequency of seven more loci namely Penta E, D5S818, D13S317, D7S820, CSF1PO, Penta D and TPOX. All loci were in Hardy-Weinberg equilibrium except Penta E ($p = 0.015$). The most informative locus among the 15 STR loci was Penta E (PIC = 0.910), while the least informative was TPOX (PIC = 0.660). The observed heterozygosity showed >70% in all loci tested. The combined PM and PE for all 15 STR loci tested were 2.05×10^{-18} and 0.9999996, respectively. The 15 loci therefore, offer a highly discriminating system

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Table 1
Allele frequency of 15 autosomal STR loci in Bangladeshi population (n = 148).

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
5	–	–	–	–	0.0439	–	–	–	–	–	–	–	–	–	–
6	–	0.1756	–	–	0.0033	–	–	–	–	–	0.0067	–	–	–	–
7	–	0.1655	–	–	0.0743	0.0033	0.0101	0.0236	–	0.0033	0.0033	–	0.0033	–	–
8	–	0.1554	–	–	0.0033	–	0.2500	0.1993	0.0743	0.0067	0.0168	–	0.0169	0.3581	–
9	–	0.3141	–	–	0.0135	0.0168	0.1081	0.0574	0.1587	0.0236	0.2263	–	0.0033	0.1351	–
9.3	–	0.1824	–	–	–	–	–	–	–	–	–	–	–	–	–
10	–	0.0067	–	0.0067	0.0472	0.1486	0.0979	0.2229	0.1114	0.2027	0.1790	0.0033	0.2060	0.0945	–
11	–	–	–	0.0168	0.1520	0.3378	0.2060	0.2398	0.3209	0.2871	0.3006	–	0.0777	0.3682	–
12	–	–	–	0.0912	0.0979	0.3310	0.2229	0.2297	0.2128	0.3783	0.1216	0.0033	0.1216	0.0439	–
13	–	–	–	0.1351	0.0608	0.1486	0.0844	0.0168	0.1114	0.0878	0.0844	0.0033	0.1689	–	–
14	0.0574	–	–	0.2364	0.0641	0.0101	0.0202	0.0101	0.0101	0.0101	0.0506	0.1351	0.1824	–	–
15	0.3513	–	–	0.2060	0.0912	–	–	–	–	–	0.0067	0.0844	0.1452	–	–
16	0.2972	–	–	0.1182	0.1148	0.0033	–	–	–	–	0.0033	0.2331	0.0540	–	–
17	0.2128	–	–	0.0641	0.0945	–	–	–	–	–	–	0.2364	0.0168	–	0.0033
18	0.0709	–	–	0.0506	0.0675	–	–	–	–	–	–	0.1959	0.0033	–	0.0033
19	0.0101	–	–	0.0371	0.0202	–	–	–	–	–	–	0.0945	–	–	0.0540
20	–	–	–	0.0236	0.0270	–	–	–	–	–	–	0.0101	–	–	0.0844
21	–	–	–	0.0101	0.0101	–	–	–	–	–	–	–	–	–	0.1554
21.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.0033
22	–	–	–	0.0033	0.0101	–	–	–	–	–	–	–	–	–	0.1317
22.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.0135
23	–	–	–	–	0.0033	–	–	–	–	–	–	–	–	–	0.1756
24	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.1689
24.2	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.0101
25	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.1385
26	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.0439
27	–	–	0.0135	–	–	–	–	–	–	–	–	–	–	–	0.0135
28	–	–	0.1148	–	–	–	–	–	–	–	–	–	–	–	–
29	–	–	0.2094	–	–	–	–	–	–	–	–	–	–	–	–
29.2	–	–	0.0033	–	–	–	–	–	–	–	–	–	–	–	–
30	–	–	0.2195	–	–	–	–	–	–	–	–	–	–	–	–
30.2	–	–	0.0304	–	–	–	–	–	–	–	–	–	–	–	–
31	–	–	0.0405	–	–	–	–	–	–	–	–	–	–	–	–
31.2	–	–	0.1216	–	–	–	–	–	–	–	–	–	–	–	–
32	–	–	0.0067	–	–	–	–	–	–	–	–	–	–	–	–
32.2	–	–	0.1587	–	–	–	–	–	–	–	–	–	–	–	–
33.2	–	–	0.0608	–	–	–	–	–	–	–	–	–	–	–	–
34.2	–	–	0.0202	–	–	–	–	–	–	–	–	–	–	–	–

Table 2
Statistical parameters of forensic interest for 15 autosomal STR loci in Bangladeshi population.

Allele	D3S1358	TH01	D21S11	D18S51	Penta E	D5S818	D13S317	D7S820	D16S539	CSF1PO	Penta D	vWA	D8S1179	TPOX	FGA
Ho	0.7432	0.7838	0.8514	0.8581	0.9324	0.7973	0.7703	0.7838	0.7703	0.7365	0.8378	0.8581	0.8514	0.6622	0.8176
He	0.7346	0.7857	0.8479	0.8521	0.9133	0.7318	0.8165	0.7961	0.7961	0.7250	0.8015	0.8170	0.8503	0.7071	0.8676
PM	0.121	0.084	0.043	0.040	0.020	0.129	0.059	0.075	0.074	0.129	0.077	0.067	0.044	0.132	0.036
PD	0.879	0.916	0.957	0.960	0.980	0.871	0.941	0.925	0.962	0.871	0.923	0.933	0.956	0.868	0.964
PIC	0.690	0.750	0.830	0.840	0.910	0.690	0.790	0.760	0.770	0.680	0.770	0.790	0.830	0.660	0.850
PE	0.498	0.569	0.698	0.711	0.862	0.594	0.545	0.569	0.545	0.487	0.671	0.711	0.698	0.372	0.632
TPI	1.95	2.31	3.36	3.52	7.40	2.47	2.18	2.31	2.18	1.90	3.08	3.52	3.36	1.48	2.74
P	0.918	0.944	0.447	0.091	0.015	0.144	0.917	0.593	0.699	0.084	0.257	0.239	0.100	0.955	0.156

Ho, observed heterozygosity; He, expected heterozygosity; PM, probability of match; PD, power of discrimination; PIC, polymorphism information content; PE, power of exclusion of paternity; TPI, typical paternity index; P, Hardy–Weinberg equilibrium, exact test based on Monte Carlo Simulation using a 5% significance level.

for use in parentage testing and forensic identification of individuals in this population.

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