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Data Article

Population dataset for 21 simple tandem repeat loci in the Akan population of Ghana

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ABSTRACT

Short tandem repeat (STR) loci are widely used as genetic marker for ancestral and forensic analyses. The latter application includes for paternity testing and DNA profiling of samples collected from scenes of crime and suspects. This survey provides the first dataset for 21 STR loci across the Akan population in Ghana by genotyping of 109 unrelated healthy individuals using Investigator 24plex kit. None of the STR loci screened deviated from Hardy-Weinberg equilibrium after applying Bonferroni correction. Overall, 224 unique alleles were observed with allele frequencies ranging from 0.005 to 0.518. The combined match probability, combined power of exclusion and combined power discrimination were 1 in 4.07×10^{-25} , 0.999999999 and 1, respectively. Principal co-

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ordinate analysis carried out using 21 STR allele frequency data mapped the Akans with Nigerian subpopulation groups (Hausa, Igbo and Yoruba), but separated from Thais of Thailand, Chechen of Jordan and Tijuana of Mexico.

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Specifications Table

Subject	Genetics
Specific subject area	DNA profiling
Type of data	Tables and figure
How data were acquired	Capillary electrophoresis of STR polymerase chain reaction amplified products on 3500XL Genetic Analyser (Applied Biosystems, USA)
Data format	Raw and analyzed
Parameters for data collection	Genomic DNA samples extracted from cheek cells were used as templates for amplification of 21 STR loci using Investigator 24plex QS kits (Qiagen, Germany)
Description of data collection	Comparison of separated STR fragments with standard allelic ladder included in the Investigator 24plex QS kit using the GeneMapper IDx v4.1 software (Applied Biosystems, USA).
Data source location	Forensic Science Program, School of Health Sciences, Health Campus, 16150 Kubang Kerian, Kelantan, Malaysia
Data accessibility	Data available in this article

Value of the data

- In the Sub-Saharan region of Africa, population data for these 21 STR loci are only available for Nigerian subpopulations. The 21 STR dataset for the Akans of Ghana reported in this article is thus the first from a different country.
- Our 21 locus STR dataset provides an important source of information to estimate their statistical value as DNA evidence (match probability, power of exclusion power etc.) for this population group
- Data from this survey also supports the general value of STR loci for population studies across the region; allele frequencies of the 21 STR loci can be used to examine the past history of population events in Akans including gene flow, natural selection and migration patterns.
- The population genetic data and forensic statistics reported for the Akans can be used as a reference standard in future studies of other sub-population groups in Ghana; Ewe, Mole-Dagbon, Ga-Dangbe and Guang.

1. Data description

The allelic scores for the 21 STR loci examined across 109 unrelated Akan individuals are shown in Supplementary Table 1. Their allele frequency data and forensic parameters are shown in Table 1. A total of 224 unique alleles were observed with corresponding allele frequency ranging from 0.005 to 0.518. The observed heterozygosity (H_o) ranged from 0.725 (TH01, DS5818 and D7S820 loci) to 0.917 (SE33 locus) while the expected heterozygosity (H_e) ranged from 0.669 (TH01 locus) to 0.927 (SEE33 locus). After applying Bonferroni correction ($p = 0.05/21$, at 95% significance level), no deviation from Hardy-Weinberg equilibrium (HWE) were observed. The highest power of discrimination (PD) and polymorphic information content (PIC) were 0.982 and 0.917 (respectively), recorded for the SE33 locus. Locus TH01 showed the lowest PIC (0.628) and PD (0.824) values. The combined matching probability (CMP), combined probability of exclusion (CPE) and combined discriminating power (CPD) were 1 in 4.07×10^{-25} , 0.999999999 and 1, respectively.

Table 1
Allele frequency data and forensic parameters for Akans of Ghana (n=109)

Allele	TH01	D3S1358	VWA	D21S11	TPOX	D1S1656	D12S391	SE33	D10S1248	D22S1045	D19S433	D8S1179	D2S1338	D2S441	D18S51	FGA	D16S539	CSF1PO	D13S317	D5S818	D7S820	
5	0.009																					
6	0.087				0.087																	
7	0.518				0.023																	
8	0.211				0.271				0.005	0.009							0.014	0.078	0.023	0.055	0.220	
9	0.101				0.257						0.005	0.009					0.220	0.028	0.009	0.005	0.119	
9.3	0.055																					
10	0.018				0.110	0.014			0.005	0.032	0.009	0.009		0.023			0.124	0.252	0.009	0.060	0.358	
11					0.220	0.037			0.050	0.096	0.110	0.028		0.362	0.009		0.358	0.239	0.252	0.234	0.239	
11.3														0.128								
12		0.005			0.023	0.069		0.005	0.138	0.064	0.101	0.133		0.124	0.083		0.138	0.239	0.472	0.353	0.055	
12.2											0.041											
13			0.028		0.005	0.133		0.014	0.174		0.303	0.147		0.106	0.009		0.147		0.174	0.257		
13.2											0.050											
14		0.064	0.050		0.005	0.239	0.005	0.046	0.312	0.174	0.179	0.339		0.225	0.041			0.069	0.050	0.032		
14.2											0.064											
15		0.298	0.280		0.188	0.087	0.050	0.220	0.197		0.037	0.257		0.032	0.211				0.009			
15.2											0.069											
15.3					0.023																	
16		0.427	0.220		0.115	0.069	0.050	0.078	0.179			0.046	0.064		0.156					0.005		
16.2											0.032											
16.3					0.087																	
17		0.161	0.220		0.028	0.133	0.092	0.018	0.206			0.028	0.073		0.170	0.005						
17.3					0.023																	
18		0.041	0.110		0.005	0.257	0.124		0.037			0.005	0.023		0.115	0.028						
18.2																0.009						
18.3					0.032	0.005																
19		0.005	0.055		0.009	0.183	0.138		0.005				0.151		0.106	0.055						
19.2																0.014						
20			0.032			0.138	0.096						0.050		0.060	0.018						
20.2																0.014						
21			0.005			0.050	0.060						0.174		0.023	0.083						
21.2																0.009						
22						0.050	0.028						0.133		0.005	0.206						
22.2							0.009									0.009						
23						0.005							0.101		0.009	0.142						
23.2							0.018									0.014						

(continued on next page)

Table 1 (continued)

Allele	TH01	D3S1358	VWA	D21S11	TPOX	D1S1656	D12S391	SE33	D10S1248	D22S1045	D19S433	D8S1179	D2S1338	D2S441	D18S51	FGA	D16S539	CSF1PO	D13S317	D5S818	D7S820	
24				0.005			0.018						0.119		0.005	0.165						
24.2								0.018								0.005						
25													0.087			0.087						
25.2																0.005						
26				0.005									0.014			0.073						
26.2								0.060														
27				0.018									0.009			0.037						
27.2								0.069														
28				0.303												0.018						
28.2								0.032														
29				0.202												0.005						
29.2								0.023														
30				0.165																		
30.2				0.014				0.014														
31				0.083																		
31.2				0.028																		
32				0.028																		
32.2				0.073																		
33				0.014																		
33.2				0.014																		
34				0.009																		
35				0.037																		
36				0.005																		
N	7	7	9	16	9	14	12	20	9	10	12	10	12	7	14	21	6	7	8	8	8	6
MP	0.176	0.149	0.066	0.052	0.089	0.039	0.050	0.018	0.091	0.052	0.055	0.087	0.029	0.099	0.050	0.033	0.093	0.082	0.149	0.109	0.112	
PD	0.824	0.851	0.934	0.948	0.911	0.961	0.950	0.982	0.909	0.948	0.945	0.913	0.971	0.901	0.950	0.967	0.907	0.918	0.851	0.891	0.888	
PIC	0.628	0.648	0.778	0.804	0.760	0.846	0.828	0.917	0.767	0.820	0.822	0.744	0.873	0.743	0.851	0.873	0.733	0.773	0.631	0.706	0.709	
PE	0.468	0.514	0.530	0.530	0.665	0.665	0.756	0.831	0.630	0.630	0.701	0.530	0.701	0.665	0.812	0.756	0.579	0.683	0.370	0.468	0.468	
TPI	1.817	2.019	2.096	2.096	3.028	3.028	4.192	6.056	2.725	2.725	3.406	2.096	3.406	3.028	5.450	4.192	2.370	3.206	1.473	1.817	1.817	
Ho	0.725	0.752	0.761	0.761	0.835	0.835	0.881	0.917	0.817	0.817	0.853	0.761	0.853	0.835	0.908	0.881	0.789	0.844	0.661	0.725	0.725	
He	0.669	0.701	0.809	0.828	0.795	0.864	0.850	0.927	0.800	0.844	0.842	0.779	0.888	0.777	0.869	0.887	0.771	0.805	0.683	0.750	0.753	
p-HWE	0.008	0.876	0.252	0.756	0.634	0.296	0.596	0.818	0.127	0.470	0.446	0.183	0.774	0.006	0.034	0.162	0.427	0.348	0.521	0.249	0.036	

N, number of loci; MP, matching probability; PD, power of discrimination; PIC, polymorphic information content; PE, power of exclusion; TPI, typical paternity index; Ho, observed heterozygosity; He, expected heterozygosity; p-HWE, p-value for Hardy-Weinberg equilibrium.

Principal coordinate (PCO) mapping performed using the allele frequency data across all 21 STR loci in the Akans and 7 other previously reported STR datasets (Supplementary Table 2) is shown in Fig. 1. The first and second axes accounted for 59.43% and 12.71% of genetic variability between datasets. The populations from Asia and North America are clustered in the upper left-hand quadrant. In contrast, the populations of Middle Eastern origin are plotted on the lower left quadrant. The Akans plotted closely with the Nigerian subpopulations in the lower right quadrant.

2. Experimental design, materials, and methods

2.1. Ethical clearance

This research was reviewed and approved by the Institutional Review Board of Nugochi Memorial Institute of Medical Research (NMIMR), University of Ghana (permit no: NMIMR-IRB CPN 118/15-16 revd. 2019) and the Human Ethics Committee of University Sains Malaysia (USMKK), Health Campus, Kelantan, Malaysia (permit no: USM/JEPeM/16050188).

2.2. Sample collection

A total of 109 healthy unrelated individuals of Akan ethnicity aged between 18 to 45 years were recruited for this research. Each individual provided written informed consent and have at least three generations of un-admixed history. The sampling locations included Accra, Koforidua and Kumasi of Ghana.

2.3. DNA isolation and STR amplification

Cheek cells were collected using buccal swab sticks and genomic DNA was extracted from them using Invisorb® Spin Forensic kit (STRATEC Molecular GmbH, Germany). Total genomic DNA was quantified using Investigator Quantiplex Hyres kit according to manufacturer's recommendation (Qiagen, Hilden, Germany). The Investigator 24plex QS amplification kits (Qiagen, Germany) was utilized to amplify the sex-determining marker Amelogenin, 1 Y-STR locus, 2 quality sensors and 21 autosomal STR loci namely CSF1PO, D10S1248, D12S391, D13S317, D16S539, D18S51, TPOX, D19S433, D1S1656, D21S11, D22S1045, D2S1338, D2S441, D3S1358, D5S818, D7S820, FGA, D8S1179, SE33, TH01 and vWA on the GeneAmp PCR System 9700 thermal cyclers (Applied Biosystems, USA) in total of 12.5 ul reaction volume. PCR products were separated by multi-capillary electrophoresis in 3500XL Genetic Analyzer (Applied Biosystems, Foster City, CA, USA). The STR alleles were systematically called using the GeneMapper IDX v4.1 software (Applied Biosystems, USA). Allele designations were determined by comparison of the sample fragments with those of allelic ladders provided in the kit.

2.4. Statistical analysis

The HWE and the expected heterozygosity (He) values were calculated using Arlequin v3.5.2.2 [1,2]. The significance level for deviation from HWE (<0.05) was adjusted to $p > 0.00238$ after Bonferroni correction ($p = 0.05/21 = 0.00238$, where 21 is the number of loci and 0.05 is the standard HWE significance value). Allele frequencies for the 21 STR loci, PD, power of exclusion (PE), MP, typical paternity index (TPI), PIC and Ho values were computed using the Powerstats software version 1.2 [3]. PCO data mapping was used to compare and visualize genetic relatedness between Akans (Ghana), Thais [4], Tijuans [5], Chechens living in Jordan [6], Saudis [7], and

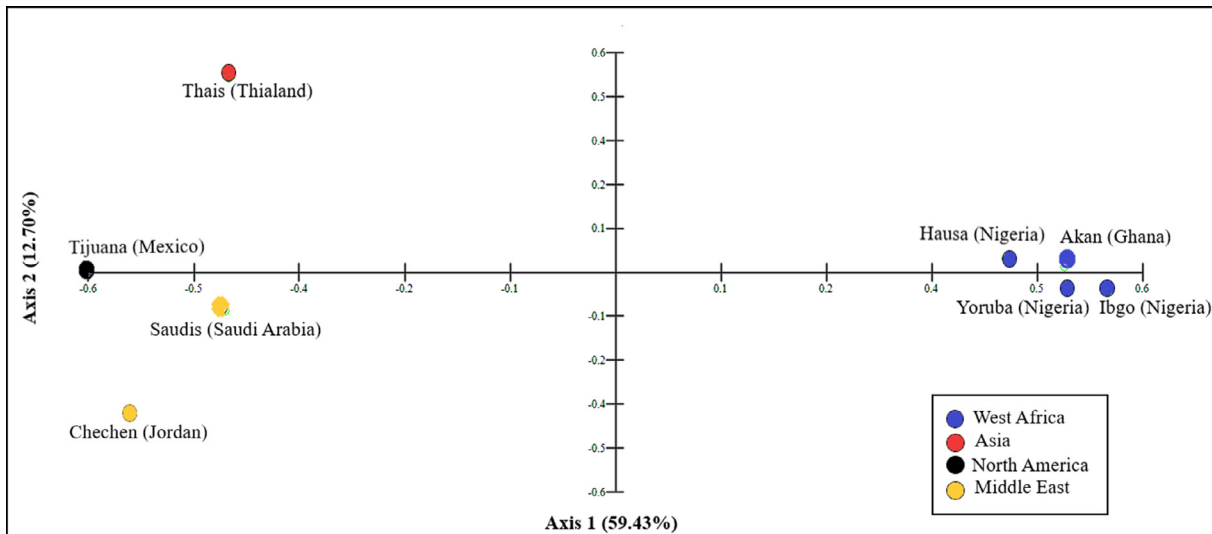


Fig. 1. PCO plot of 21 STR loci allele frequency data obtained from present survey of Akans and other reference populations.

Nigerians [8]). The PCO analysis was performed using the MVSP software version 3.22 [9] and STR datasets for PCO analysis are provided as Supplementary table 2.

Declaration of Competing Interest

The authors declare that they have no known competing interests or personal relationships that could have appeared to influence the work reported in this paper.

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Supplementary materials

Supplementary material associated with this article can be found, in the online version, at doi:10.1016/j.dib.2020.105746.

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