



Announcement of population data

Population data for the AmpF ℓ STR[®] Identifiler[™] PCR Amplification Kit in China Han in Jilin Province, China

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Abstract

Allele frequencies for the fifteen short tandem repeats (STR) loci D3S1358, vWA, FGA, D8S1179, D21S11, D18S51, D5S818, D13S317, D7S820, D19S433, THO1, D16S539, CSF1PO, TPOX, D2S1338 (AmpF ℓ STR[®] Identifiler[™] PCR Amplification Kit, Applied Biosystems) were determined in a population sample of unrelated China Han in Jilin Province, China. Statistical analyses were performed using Powerstats version 1.2 and GEP-ISFGWG. The results showed that all the loci met Hardy–Weinberg expectation.

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Keywords: STR; AmpF ℓ STR[®] Identifiler[™]; Jilin; China Han population

Population: A sample of 200 unrelated China Han from Jilin Province, China.

Extraction: The DNA was extracted from whole blood using John's method [1].

PCR: A 1.0 ng template following manufacturer's instructions (AmpF ℓ STR[®] Identifiler[™] PCR Amplification Kit, Applied Biosystems).

Typing: ABI Prism[®] 3100 using manufacturer's recommended protocol (AmpF ℓ STR[®] Identifiler[™] PCR Amplification Kit, Applied Biosystems), electrophoresis results were analyzed by GeneScan (version 3.7.1) and Genotyper (version 3.7).

Results: See Tables 1 and 2.

Analysis of data: Applied "PowerStats" program (Promega home page: <http://www.promega.com/geneticidtools/>) for power of discrimination (PD), polymorphism information content (PIC) and chance of exclusion (CE), and the

GEP-ISFGWG program (<http://www.gep-isfg.org>) for observed and expected heterozygosity (H_o , H_e).

Access of data: Available upon request: wsyang@mail.jlu.edu.cn.

Quality control: Laboratory internal control standards, kit controls and proficiency testing of the GEP-ISFGWG (<http://www.gep-isfg.org>). Twenty random samples (10% of all 200 samples) were genotyped twice to further ensure result reproducibility and accuracy.

Other remarks: An insignificant value of linkage disequilibrium was obtained for the locus D2S1338 ($P = 0.0003$). No significant deviations from Hardy–Weinberg expectation were observed for all other fourteen STR loci. The P value of D2S1338 was recalculated to be 0.113 according to the literature method [2], also indicating no significant deviation from Hardy–Weinberg expectation. Combined PD of all the 15 STR loci was determined to be more than 0.999999999999999993 and the value of CE was more than 0.999998 for the China Han population in Jilin Province. The verified statistic parameters of D19S433, THO1, D16S539, CSF1PO, TPOX, and D2S1338 loci of

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30.2	-	-	-	-	0.013	-	-	-	-	-	-	-	-	-	-
30.3	-	-	-	-	0.003	-	-	-	-	-	-	-	-	-	-
31	-	-	-	-	0.135	-	-	-	-	-	-	-	-	-	-
31.2	-	-	-	-	0.103	-	-	-	-	-	-	-	-	-	-
32	-	-	-	-	0.035	-	-	-	-	-	-	-	-	-	-
32.2	-	-	-	-	0.113	-	-	-	-	-	-	-	-	-	-
33	-	-	-	-	0.005	-	-	-	-	-	-	-	-	-	-
33.2	-	-	-	-	0.03	-	-	-	-	-	-	-	-	-	-
34	-	-	-	-	-	-	-	-	-	-	-	-	-	-	-
34.2	-	-	-	-	0.003	-	-	-	-	-	-	-	-	-	-

N: the number of samples.

Table 2
Statistical parameters for 15 STR loci in China Han in Jilin Province, China

Allele	D3S1358	vWA	FGA	D8S1179	D21S11	D18S51	D5S818	D13S317	D7S820	D19S433	TH01	D16S539	CSF1PO	TPOX	D2S1338
H_o	0.685	0.805	0.85	0.815	0.84	0.88	0.78	0.78	0.79	0.875	0.595	0.805	0.715	0.65	0.87
H_e	0.733	0.8	0.85	0.831	0.831	0.854	0.771	0.814	0.785	0.827	0.604	0.774	0.731	0.628	0.873
MP	0.117	0.077	0.045	0.053	0.056	0.047	0.093	0.064	0.079	0.062	0.21	0.09	0.114	0.204	0.038
PD	0.883	0.923	0.955	0.947	0.945	0.953	0.907	0.936	0.921	0.938	0.79	0.91	0.886	0.796	0.962
PIC	0.68	0.77	0.83	0.81	0.81	0.83	0.74	0.78	0.75	0.81	0.55	0.74	0.68	0.57	0.86
PE	0.398	0.608	0.695	0.637	0.695	0.755	0.562	0.562	0.572	0.735	0.297	0.61	0.452	0.355	0.735
TPI	1.56	2.56	3.33	2.78	3.33	4.17	2.27	2.27	2.33	3.85	1.27	2.58	1.75	1.43	3.85
P	0.7566	0.1094	0.0709	0.6356	0.2128	0.7438	0.3569	0.1847	0.4391	0.2041	0.5747	0.9957	0.8159	0.8156	0.1125

H_o , observed heterozygosity; H_e , expected heterozygosity; MP, matching probability; PD, power of discrimination; PIC, polymorphism information content; PE, power of exclusion; TPI, typical paternity index; P, Hardy-Weinberg equilibrium; exact test based on 3200 shuffling, for S.E. < 0.01.

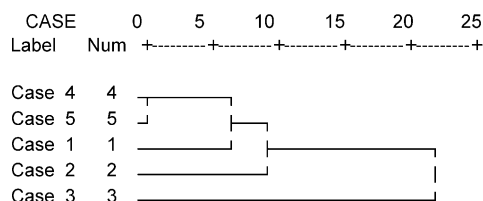


Fig. 1. Phylogenetic tree for China Han in different areas based on the available sets of loci: case (1) Jilin Province, China; case (2) Singapore; case (3) Henan Province, China; case (4) Beijing City, China; case (5) Shantou City, China.

or China Han populations in other regions of China [3–13]. We have compared our data with some published data on China Han [7,10,14,15] by using SPSS 13.0 for Windows program for affinity test. The resulting phylogenetic tree to compare China Han populations in Jilin Province, Henan Province, Beijing City and Shantou City, China, and in Singapore was given shown in Fig. 1. The results showed that Jilin-Han is in the nearest affinity with Beijing-Han and then Henan-Han.

This paper follows the guidelines for publication of population data requested by the journal [16].



China Han in Jilin Province reported here are useful for forensic and paternity purposes. So according to these statistical parameters, the combination of the AmpF ℓ STR[®] Identifier[™] PCR Amplification Kit is a powerful tool for forensic identification and paternity testing.

One rare and microvariant allele of 30.3 of D21S11 was observed in this study. This allele has been confirmed by retyping with Powerplex[™] 16 System Kit.

Jilin Province is one origin of Manchu population and China Han in Jilin Province is a peculiar member of Han. Many people of China Han in Jilin Province are crossbreed descendants of Han and Manchu populations and the population data are different from those reported for other ethnics

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