J Forensic Sci, May 2005, Vol. 50, No. 3
Paper ID JFS2004524
Published 6 April 2005
Available online at: www.astm.org

FOR THE RECORD

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STR Loci D19S400's Allele Frequency Distribution in Ten Populations*

POPULATIONS: Chengdu Han, Guanzhou Han, Jilin Han, Dali Bai, Nanning Zhuang, Hailaer Monggu, Yamamnash Japanese, Bremen Germany, Bratislava Slovakian, New York Black

KEYWORDS: forensic science, D19S400, short tandem repeat, DNA typing, population genetics

TABLE 1—*The allele frequencies of D19S400 locus in ten population groups.*

Populations	Samples Number	Allele										
		*7	*8	*9	*10	*11	*12	*13	*14	*15	*16	*17
Chengdu Han	154			.2208	.0227	.0519	.3441	.1494	.0942	.0682	.0455	.0032
Guanzhou Han	98	.0051	.0051	.1786	.0357	.1071	.3061	.1582	.0765	.0714	.0459	.0102
Jilin Han	99			.2070	.0354	.0707	.3030	.1869	.0859	.0707	.0404	
Dali Bai	88			.1477	.0511	.0739	.3693	.1477	.0398	.0739	.0795	.0170
Nanning Zhuang	88			.1932	.0739	.0682	.2273	.1307	.0625	.1307	.0852	.0284
Hailaer Monggu	91			.1044	.0714	.0659	.3242	.1923	.1209	.0879	.0275	.0055
Yamamnash Japanese	118	.0042	.0085	.2034	.0636	.0890	.3136	.1059	.0466	.1059	.0424	.0169
Bremen Germany	96		.0104	.1042	.0469	.0729	.1667	.1510	.1667	.1719	.0938	.0156
Bratislava Slovakian	95		.0053	.0737	.0263	.0842	.2211	.1684	.1947	.1263	.0842	.0156
New York Black	78			.0321	.0064		.1282	.0833	.1795	.2756	.2244	.0705

Blood Specimens were obtained from volunteer donors of ten different populations respectively, such as: Chengdu Han, Guanzhou Han, Jilin Han, Dali Bai, Nanning Zhuang, Hailaer Monggu, Yamamnash Japanese, Bremen Germany, Bratislava Slovakian, New York Black. DNAs were extracted from blood specimens using Chelex-100. (1) Genotyping were carried out by PCR in a PE9600 cycler. The components of a 20 μL reaction mixture were as follows: template DNA 20 ng, primer 0.2 μmol/L each, dNTPs 200 μmol/L each, KCl 50 μmol/L, Tris-HCl(pH8.3)10 mmol/L, $MgCl_2$ 1.5 mmol/L, Taq polymerase 1U. Primer sequences: D19S400:5′-cggtatgtctttatcagcag-3′,5′-atgacagctctaggaaggc-3′. PCR conditions: start at 94°C for 4 min, followed by 36 cycles consist of 35 s at 94°C, 40 s at 58°C, 50 s at 72°C followed by a 10 min extention at 72°C. The amplified products were electrophoresed in 6% polyacrylamide gel by using 100 bp ladder and allelic markers as size markers, followed by sliver staining. The amplified products were examined by an ABI PRISMTM 310 Genetic Analyzer. Data were analyzed by The Promega software, POWERSTATS.

The complete dataset is available to any interested researcher upon request.

Acknowledgment

The research was supported by grants from the Chinese Natural Sciences Foundation (No.-30171033) and State Ministry of Education (No. 20040610047).

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* The research was supported by grants from the Chinese Natural Sciences Foundation (No.-30171033) and State Ministry of Education (No. 01143) as well Sichuan Youth Foundation (2001–2).

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