

FOR THE RECORD

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Allele Frequencies of Mitochondrial DNA STR Locus in Two Chinese Ethnic Groups

POPULATION: Chinese

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Blood specimens were collected from two Chinese ethnic groups, including 100 unrelated individuals from Han ethnic group in Beijing and 100 unrelated individuals from Uygur ethnic group in Kashi of Xinjiang province. Ethnic origin was determined by appearance and self declaration. DNA was extracted from blood specimens using Chelex 100 method (1). The mtDNA was amplified using PCR with primers L16419 5'-caatattcccgcacaaagagtg-3' and H00672 5'-tagaaagcgtaggaccaaacc t-3'. The primers were numbered according to the location of their 3' ends in Anderson reference sequence (2) and "L" and "H" designated the light and the heavy strands of the mtDNA molecule, respectively. Each PCR contained 1 ng human genomic DNA, 1 × Taq buffer, 1.5 mM MgCl₂, 200 mM per nucleotide, 1.5 U Taq polymerase, 0.25 mM per primer in a total volume of 50 μL. In PCR protocol, DNA was initially denatured at 95°C for 200 s, which was followed by 94°C for 30 s, 55°C for 30 s and 72°C for 90 s. A total of 35 cycles were carried out in GeneAmp PCR System 9600. The PCR products were separated from residual primers by Wizard Purification system (Promega Corporation, Madison, WI). The purified DNA was directly sequenced by BigDye Terminator Cycle Sequencing ready reaction 2.0 (PE Applied Biosystems, Foster City, CA). Both strands were sequenced using primers H00672 5'-tagaaagcgtaggaccaaacc t-3' and L00374 5'-cacagcctaacagatttc-3', re-

spectively. The ABI 377 DNA Sequencer (PE Applied Biosystems, Foster City, CA) was used for separation and detection of the fluorescence-labeled chain termination products. The sequences were automatically analyzed by ABI Prism Sequencing Analysis Software (Version 2.1.2). The CA-repeat at position 514-523 described by Bodenteich et al. (3) were manually checked and then compared with Anderson sequence (2) by Seq/Ede Software 2.5. Following the recommendations of the International Society of Forensic Genetics (4), the allele classification of STR with CA-repeat was based on the number of repeat motifs. The parameters dealing with forensic genetics were calculated according to Hou's method (5).

The dataset can be accessed at <http://www.legalmed.org/dna/mtDNA01.htm>

TABLE 1—Allele frequencies of STR for mtDNA in two Chinese ethnic groups.

Referenced Sequence*	Allele	Uygur Ethnic Group	Han Ethnic group
(CA) ₅ - 2	3	0.010	
(CA) ₅ - 1	4	0.200	0.330
(CA) ₅	5	0.690	0.670
(CA) ₅ + 1	6	0.010	
(CA) ₅ + 3	8	0.090	
Total		1.000	1.000

* The (CA)₅ repeat was at position 514–523 and nucleotide substitutions were neglected.

Gene Diversity for Han ethnic group = 0.4467, Standard Error = 0.0103.

Gene Diversity for Uygur ethnic group = 0.4804, Standard Error = 0.0115.

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