

FOR THE RECORD

Li Rao,^{1,3} M.D.; Mei Yun Wu,^{2,3} M.D.; Wei Bo Liang,^{2,3} M.D.; and Lin Zhang,^{2,3} M.D., Ph.D.

Sequence Polymorphisms of the Mitochondrial DNA Control Region in 105 Chinese Han Population*

POPULATION: 105 unrelated persons, Southwest China

KEYWORDS: forensic science, DNA typing, mitochondrial DNA, hypervariable region I, hypervariable region II, population genetics, China

A total of 105 EDTA blood samples were collected from unrelated blood donors living in Chengdu, Southwest China. DNA was extracted according to the method of Miller et al. (1). The quantity of DNA was estimated by fluorometry.

The two hypervariable regions of the Mitochondrial DNA typing was carried out with 20 ng of genomic DNA in a total volume of 50 μ L reaction system, containing 0.2 μ M primer (2,3), 200 μ m each dNTP, 1 U Taq polymerase (Eurobio, Raunheim, Germany), 1X PCR buffer, 0.5 mM MgCl₂. The PCR was carried out in a thermal cycler (GeneAmp PCR System 2400; Perkin Elmer Corporation, Morwalk) for 30 cycles in such conditions as denaturation at 94°C for 45 s, annealing at 55°C for 30 s, and extension at 72°C for 3 min, followed by a final extension step at 72°C for 7 min.

PCR products were purified by using the QIAquick PCR purification kit (QIAGEN, Hilden, Germany) and then sequenced by cycle sequencing using fluorescent dideoxynucleotides (ABI PRISM™ Dye Terminator Cycle Sequencing Ready Reaction Kit) followed by capillary electrophoresis in an ABI Prism 310 Genetic Analyzer (Applied Biosystems, Foster City, CA).

The genetic diversity ($h = n(1 - \sum x^2)/(n - 1)$) is estimated to be 0.999, and the probability of two random individuals from the studied population with the identical mtDNA haplotype ($P = \sum x^2$) is 1.07%

Results obtained in this study are shown in Table 1 and 2 after aligned with a reference sequence (4).

L15997 5'—CAC CAT TAG CAC CCA AAG CT—3'
And H16401 5'—TGA TTT CAC GGA GGA TGG TG—3' for HVR-I

The HVR-I and HVR-II are amplified by two different sets of primers respectively which are shown as follows:

L00029 5'—GGT CTA TCA CCC TAT TAA CCA C—3'
And H00408 5'—CTG TTA AAA GTG CAT ACC GCC A—3' for HVR-II

The complete dataset is available to any interested parties and researchers upon request.

References

1. Miller SA, Dykes DD, Polesky HI. A simple salting out procedure for extracting DNA from human nucleotide cells. *Nucl Acid Res* 1088;16:1215.
2. Orrego C, King MC. Determination of familial relationships. In: Immis MA, Gelfand DH, Smisky JJ, White TJ, editors. PCR protocols. Academic Press, London and San Diego, 1990;416–426.
3. Sullivan KM, Hopgood R, Gill P. Identification of human remains by amplification and automated sequencing of mitochondrial DNA. *Int J Legal Med* 1992;105:83–6.
4. Anderson S, Bankier AT, Barrell BG, deBruijn MHL, Coulson AR, Drouin J, et al. Sequence and organization of the human mitochondrial genome. *Nature* 1981;290:457–65.

Additional information and reprint request:

Lin Zhang, M.D., Ph.D
College of Basic Medicine and Forensic Medicine
Sichuan University
Chengdu, 610041
P. R. China
Fax: +86-28-85405541
Tel: +86-28-85460532
E-mail: kjc@pridns.suc.edu.cn

¹ Department of Cardiology, The First Affiliated Hospital, 610041 Sichuan University.

² College of Basic Medicine and Forensic Medicine, 610041 Sichuan University.

³ Key Lab of Biotherapy of Human Diseases, Ministry of Education, P. R. China.

* This research was supported by grants from the National Natural Sciences Foundation of China (No.-30171033) and State Ministry of Education (No.01143) as well as the Chinese Medical Board of New York (No.00722).

