

Mitochondrial DNA profiling of modern Malay and Orang Asli populations in peninsular Malaysia

Z. Zainuddin^a, W. Goodwin^{b,*}

^a*Department of Forensic Medicine and Science, University of Glasgow, Glasgow, UK*

^b*Department of Forensic and Investigative Science, University of Central Lancashire, Preston, PR1 2HE, UK*

Abstract. A study was undertaken to assess the utility of mtDNA as a forensic tool in the Malay Peninsular. Two populations, modern Malay and Orang Asli, were sampled and their mitochondrial DNA (mtDNA) analysed. Comparing the different haplogroups that were found, there are clear differences between the two populations. As a forensic tool, the use of mtDNA in the Orang Asli is limited as many individuals share the same haplotype, reducing the power of discrimination. In the Malay population, the power of discrimination is sufficiently high to make it a valuable tool. © 2003 Elsevier B.V. All rights reserved.

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1. Introduction

Mitochondrial DNA has proven to be a useful tool for human identification as well as understanding modern human evolution and migrations. Malaysian populations are underrepresented in the published data, and therefore, before using mtDNA as a forensic tool in Malaysia, it is important to study the population. This is particularly so when there are distinct populations within the main population, such as the Orang Asli. In addition to providing useful information for forensic studies, this information will also provide information on the relationships of the Malay population with neighboring populations.

2. Materials and methods

In total, 102 samples were collected from 11 states of Peninsular Malaysia and 58 samples from two populations of Orang Asli (Kensiu and Jahai) were collected. DNA was extracted using Puregene[®] DNA Extraction kit. The HVI region was amplified using L15926 and H16431 primers and sequenced. Polymorphisms were reported by

* Corresponding author. Tel.: +44-1772-894254; fax: +44-1772-894981.

E-mail address: whgoodwin@uclan.ac.uk (W. Goodwin).

Table 1

Population	Samples	Haplotypes ^a	Power of exclusion ^b
Malay	102	73 (6)	0.0203
Orang Asli	58	12 (18)	0.1961

^a Total number of haplotypes observed (most frequently occurring haplotype in brackets).

^b The probability that two samples chosen at random would have the same haplotype.

aligning the sequence obtained to the Anderson Reference Sequence [1]. RFLP analysis of the coding region was performed to examine the following mutations: +10394/+10397 *DdeI/AluI* [2,3], +13262 *AluI* [4], –5176 *AluI* [4,5], –12406 *HincII* [6], +12308 *HinfI* [7], –1715 *DdeI* [7,8] and –7025 *AluI* [5,8]. The haplogroups were determined using a combination of the HVI sequence and RFLP analysis (haplogroup nomenclature was in accordance with the above references and M. Richards, personal communication).

3. Results

Analysis of the hypervariable region I was used to place the samples into haplogroups. A summary of the mtDNA diversity is shown in Table 1.

Additional information from RFLP sites located outside of the hypervariable regions was used, in some cases, to place the samples into more highly resolved haplogroups. The different haplogroups along with their defining polymorphisms and the frequencies of these haplogroups in the tested populations are shown in Table 2.

From the data, it is clear that there are large differences between the modern Malay and the Orang Asli populations, both in the power of discrimination and in the haplogroups composition.

Table 2

The distribution of haplogroups within the modern Malay and Orang Asli populations

Haplogroup	Defining polymorphisms	Population frequencies	
		Malay	Orang Asli
M ^a	+10394/+10397 <i>DdeI/AluI</i>	39.12	5.17
M21a	+10394/+10397 <i>DdeI/AluI</i>	5.88	34.48
M21b	+10394/+10397 <i>DdeI/AluI</i>	–	1.72
M-D	+10394/+10397 <i>DdeI/AluI</i> , –5176 <i>AluI</i>	1.96	–
M-C	+10394/+10397 <i>DdeI/AluI</i> , +13262 <i>AluI</i>	0.98	–
B4	9-bp deletion	7.84	–
B5	9-bp deletion	10.78	6.90
E	+10394/+10397 <i>DdeI/AluI</i> , –7598 <i>HhaI</i>	1.96	–
F1a	–10394/–10397 <i>DdeI/AluI</i> , –12406 <i>HincII</i>	16.67	–
N9a	–10394/–10397 <i>DdeI/AluI</i>	2.94	3.45
R	–10394/–10397 <i>DdeI/AluI</i>	7.84	–
R21	+10394/–10397 <i>DdeI/AluI</i> , –1715 <i>DdeI</i>	1.96	48.28
Y	+10394/–10397 <i>DdeI/AluI</i>	1.96	–

^a Includes all variations of the M super haplogroup that are not specified.

4. Discussion

As in other populations, mtDNA can be a powerful tool for human identification when used in the Malay population. However, the differences between the Malay and Orang Asli populations highlight the need for care in interpreting any results in a forensic context. Further studies examining the nuclear autosomal and Y-chromosome loci will provide an improved understanding of the genetic composition in different populations in Peninsular Malaysia.

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