



A comparison of mtDNA and Y chromosome diversity in Malay populations

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Abstract. The mtDNA and Y chromosomes of the Malay population of peninsular Malaysia show high levels of diversity. Both the Malay and the indigenous Orang Asli populations showed a similar level of divergence between the different Y chromosome haplotypes. © 2005 Published by Elsevier B.V.

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1. Introduction

The Malaysian peninsula contains several distinct populations: the Malays, ethnic Chinese, Indian and the indigenous Orang Asli. Before using the Y chromosome as a forensic tool in Malaysia it is important to study the diversity within and between the populations. Previous studies have shown that the levels of mtDNA diversity within the Malay population are comparable to other Southeast Asian populations [1]; the mtDNA in the Orang Asli, the indigenous population within peninsular Malaysia, showed much lower levels of diversity.

In addition to the forensic application, the mtDNA and Y chromosome polymorphisms can provide information on the histories of different populations; analysis of some of the mtDNA lineages that are specific to the Orang Asli have dated them at approximately

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Table 1

The haplotypes of the Malay and Orang Asli samples (Obs=number of times observed)

	Obs	391	389I	439	389II	438	437	19	392	393	390	385a	385b
Malay	1	10	12	14	28	10	14	15	14	12	24	12	14
	1	11	13	13	29	10	14	16	13	14	25	15	20
	1	10	13	11	30	9	14	14	11	13	24	12	19
	1	10	12	12	28	11	14	15	13	14	24	12	12
	1	9	12	12	30	10	14	15	12	13	21	13	14
	1	10	14	10	30	10	14	16	12	13	22	13	14
	1	10	13	11	29	10	14	15	11	13	23	15	16
	1	11	14	12	30	11	16	15	13	13	21	14	14
	1	10	13	13	30	10	15	16	13	13	24	15	22
	1	10	13	13	29	9	14	14	11	12	23	14	17
	1	10	12	13	29	10	15	15	13	13	24	14	16
	1	10	13	11	29	10	14	15	10	14	24	14	16
	1	11	14	12	31	10	15	15	11	13	21	12	17
	1	10	13	12	29	11	16	14	11	14	23	13	17
	1	10	12	11	27	10	14	15	14	13	23	13	14
	1	10	12	12	28	11	15	14	14	13	24	13	18
	1	10	12	13	28	10	16	15	13	13	23	13	17
	1	10	12	11	28	10	14	15	11	12	21	11	16
	1	10	13	11	30	11	14	15	11	13	24	11	14
	1	10	12	12	27	10	14	15	14	13	23	13	14
	1	11	14	11	30	10	14	15	14	14	25	15	20
	1	10	13	12	30	10	14	15	13	14	23	15	20
	1	11	14	10	33	11	14	15	11	13	25	11	15
	1	10	13	11	30	9	14	17	13	14	25	13	17
	1	10	12	12	28	11	15	14	14	12	23	15	19
	1	10	14	11	30	9	15	14	11	13	23	13	18
	1	10	13	10	30	10	15	15	14	12	24	15	18
	1	10	12	13	28	10	15	15	13	13	24	12	16
	1	11	12	12	28	10	14	15	13	13	24	12	23
	1	10	13	12	29	10	14	16	13	14	24	15	20
	1	11	13	13	28	12	15	14	14	12	24	11	13
	1	10	13	11	31	10	14	13	11	13	24	16	17
	1	10	15	12	32	10	14	15	13	14	25	15	18
	1	10	14	11	30	10	16	14	10	14	23	13	19
	1	11	14	12	29	10	15	13	14	13	25	13	21
	1	10	12	12	28	9	15	15	11	12	23	12	18
Jahai	2	9	13	12	29	11	14	17	13	12	24	14	18
	1	10	12	13	28	10	15	15	13	13	24	13	15
	1	10	13	13	29	10	14	15	13	14	25	17	21
	1	10	13	13	28	11	14	15	13	14	25	15	20
	1	10	13	13	29	10	16	15	13	13	20	12	13
	1	10	14	11	29	9	14	15	11	12	22	14	15
	3	10	14	13	30	10	16	15	13	13	20	12	13
	1	11	13	10	30	11	15	16	11	13	25	11	14
	2	11	14	12	29	10	16	15	13	14	23	12	14
	2	11	14	13	29	10	16	15	13	14	23	11	12
Kensiu	1	10	12	12	28	10	14	14	13	13	24	12	16
	1	10	13	13	29	11	14	15	13	14	25	15	20
	1	10	14	12	30	10	14	15	13	15	25	15	20

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Table 1 (continued)

	Obs	391	389I	439	389II	438	437	19	392	393	390	385a	385b
Kensiu	3	11	13	10	30	11	15	16	11	13	25	11	15
	4	11	13	11	31	11	14	14	14	13	23	11	12
	2	11	13	12	31	11	14	14	14	13	23	11	12
	3	11	14	12	29	10	16	15	13	14	23	12	14
	3	11	14	13	30	9	14	16	13	14	25	14	15

50,000 to 60,000 years old—this has implications for the time and route taken during the dispersal of modern humans out of Africa [2].

2. Materials and methods

DNA samples from 69 males, 36 Malay and 33 Orang Asli were analysed using the PowerPlex® Y System (Promega).

3. Results and discussion

The Y chromosomes were analysed at 12 loci to produce haplotypes (Table 1).

A summary of the Y chromosome haplotype data along with the mtDNA haplotype data [1] is shown in Table 2.

The diversity of the Y chromosome does appear to be higher than the mtDNA, although this may be due in part to the small sample size. The level of Y chromosome diversity in the Malay population was high with no haplotype being observed twice; the gene diversity was 0.9999. The gene diversity was higher within the Jahai population (0.9428) than the Kensiu (0.8951). No haplotypes were common between the Orang Asli and the Malay.

Some mtDNA haplotypes are much more common within the Orang Asli than the Y chromosome haplotypes; in order to see whether this was because of a recent divergence of a small number of Y

Table 2

Population	Samples	Haplotypes	Most common haplotype	Power of exclusion
<i>(a) Summary of the mtDNA haplotype data [1]</i>				
Malay	106	75	6 (5.66%)	0.972
Orang Asli	59	14	18 (30.51%)	0.811
<i>(b) Summary of the Y chromosome haplotype data</i>				
Malay	36	36	1 (2.78%)	0.972
Orang Asli	33	17	5 (15.15%)	0.918

Table 3

The pairwise differences between Y chromosome haplotypes

Population	Average pairwise stepwise differences
Malay	13.90 ± 3.98
Jahai	15.02 ± 5.29
Kensiu	14.64 ± 4.86
Jahai vs. Kensiu	14.34 ± 5.08

chromosome haplotypes, due to the high mutation rate of Y STRs, the stepwise differences were calculated between the different Y chromosomes. All population comparisons produced an average of approximately 14 stepwise mutations between haplotypes ([Table 3](#))—illustrating the majority of haplotypes.

4. Conclusion

Y chromosome analysis has the potential to be a valuable tool for certain forensic applications within the Malay population.

In light of the deep roots that are found in the mitochondrial DNA [\[2\]](#) some of the Y chromosome lineages may also be representative of deep lineages; analysis of more slowly evolving loci [\[3\]](#) should help to address the dating of these Y chromosome lineages.

References

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