

## Genetic variation and geographic distribution on the mitochondrial DNA in local populations of the musk shrew, *Suncus murinus*

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### ABSTRACT

The musk shrew (*Suncus murinus*) is widely distributed throughout Asia and East Africa. The mitochondrial DNA (mtDNA) of this species was analyzed in individuals from 31 local populations in nine Asian countries and Mauritius, using 17 restriction endonucleases. Although fourteen and nine mtDNA haplotypes were detected from Bangladesh and Nepal, respectively, one to four haplotypes were found in each Southeast Asian country, and one common haplotype existed in Japan, Philippines, Vietnam, Thailand and Indonesia. Clustering analysis of mtDNA haplotypes classified shrew populations to three groups—continental group (Bangladesh and Nepal), islands' group (insular countries and Vietnam) and Malay group. The average nucleotide diversity among these three groups was calculated to be about 3.5%. These results indicate that the origin of feral populations in this species might be old and their population sizes are extremely large in the continent, and suggest a rapid spread of this animal throughout the islands. Although we have not shown yet an evidence of close relationships between islands' and continental mtDNA haplotypes, it is likely that the musk shrew had migrated from the continent in South Asia to the islands in Southeast Asia recently.

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## 1. INTRODUCTION

The musk shrew is an insectivora animal inhabiting mainly the subtropics in South and Southeast Asia, and East Africa. This animal has a great degree of variation in body size, coat color and chromosome number according to locality. It was possible, however, to obtain fertile offspring between lines originating from different localities despite the large differences in body size (Ishikawa et al., 1987) or chromosomes (Ishikawa et al., 1989). This animal, therefore, could be classified as a single species, *Suncus murinus*.

We have examined mitochondrial DNA (mtDNA) haplotypes of musk shrews in laboratory lines and several wild populations (Yamagata et al., 1987, 1990) and reported that there were "mice-intersubspecific" differences between lines or populations from Bangladesh and Southeast Asia. In this study, we inspected shrew mtDNA haplotypes of wild populations from more localities in order to elucidate the genetic distribution and the relationship among shrew populations inhabiting the islands and the continent in Asia.

## 2. MATERIALS AND METHODS

Musk shrews were collected from 31 different localities in nine Asian countries and Mauritius (Table 1). The animals were dissected at these places and their organic samples were frozen by dry ice for transport to our laboratory. Samples were stored at  $-80^{\circ}\text{C}$  prior to the preparation of mtDNA.

The extraction of mtDNA from frozen kidney and liver of an individual was done by using the alkaline lysis procedure as described by Tamura and Aotsuka (1988). The mtDNA samples were digested completely by 17 restriction endonucleases—*AccI*, *BamHI*, *BanIII*, *BglI*, *BglII*, *BstEII*, *EcoRI*, *EcoRV*, *HindIII*, *PstI*, *PvuII*, *SacI*, *SalI*, *SmaI*, *StuI*, *XbaI* and *XhoI*. The fragments were then separated by agarose slab gel (0.6–1.2%) electrophoresis in TAE (0.089 M Tris-acetate, 0.002 M EDTA) or TBE (0.089 M Tris-borate, 0.002 M EDTA) buffer. The gel was stained with ethidium bromide and photographed under the illumination with ultraviolet light.

The proportion of nucleotide difference between mtDNA haplotypes was estimated by the cleavage site comparison method (equations (9) and (10) in Nei and Li, 1979). The nucleotide diversity within a population and the net of nucleotide diversity between populations were estimated by the formulae (10) and (24) in Nei and Tajima (1981), respectively. The phylogenetic trees among haplotypes and among local populations were constructed by using the neighbor-joining method of Saitou and Nei (1987).

Table 1. Mitochondrial DNA haplotypes of the wild musk shrews in each locality and their numbers

Locality (Captured year)	mtDNA haplotype <sup>a</sup>	No. of animals <sup>b</sup>
Japan		
1. Okinawa Island (1987, 1990)	SEA-C	26 (25)
2. Tokunoshima Island (1988)	SEA-C	19 (19)
Philippines		
3. Los Baños, Laguna (1992)	SEA-C	21
	P-1	3
	P-2	2
Vietnam		
4. Hanoi (1993)	SEA-C	14
5. Phu Tho (1993)	SEA-C	5
6. Haiphong (1993)	V-1	2
7. Nha Trang (1992)	V-1	2
8. Ho Chi Minh (1992)	V-1	6
9. Chau Doc (1992)	V-1	2
10. Can Tho (1992)	V-1	3
Thailand		
11. Hat Yai (1992)	SEA-C	2
	MI-1	6
12. Song Khla (1992)	SEA-C	3
	MI-2	4
Malaysia		
13. Guar Chempedak (1993)	MI-1	4
14. Butterworth (1993)	MI-1	4
15. Petaling Jaya (1993)	MI-2	1
	MI-3	4
16. Serdang (1993)	MI-2	4
17. Keluang (1993)	MI-2	1
Indonesia		
18. Bogor, Java (1988, 1989, 1990)	SEA-C	33 (9)
	I-1	2
19. Lampung, Sumatra (1988, 1989, 1990)	I-2	7 (1)
20. Denpasar, Bali (1989, 1990)	SEA-C	2
	I-3	11
21. Bandjarmasin, Kalimantan (1990)	SEA-C	2
22. Ujung Pandang, Sulawesi (1990)	SEA-C	2
Sri Lanka		
23. Koralawella (1984)	S-1	6 (6)
	S-2	2 (2)
	S-3	1 (1)
Bangladesh		
24. Mymensingh (1983, 1985, 1992)	B-1	7 (4)
	B-2	19 (13)

Table 1. Continued

		B-3	2 (2)
		B-4	1 (1)
		B-9	1
		B-13	7
		B-14	2
25.	Dhaka (1993)	B-2	4
		B-5	2
		B-6	2
		B-10	1
		B-11	1
26.	Faridpur (1993)	B-5	3
		B-7	1
		B-8	4
		B-12	2
Nepal			
27.	Katmandu (1988, 1989)	NK-1	7
		NK-2	3
28.	Hetauda (1988)	NH-1	1
		NH-2	1
		NH-3	1
29.	Biratnagar (1988)	NB-1	1
		NB-2	1
30.	Pokhara (1989)	NP-1	2
		NP-2	1
Mauritius			
31.	Mauritius (1989)	Mr-1	4
		Mr-2	1

<sup>a</sup> See Table 3 for the mtDNA haplotype. SEA-C is the common type found in Southeast Asia. MI-1 and MI-2 are found in Malay Peninsula in Thailand and in Malaysia commonly. The rest of mtDNA haplotypes are unique at each country.

<sup>b</sup> Numbers in parentheses were data from our previous study (Yamagata et al., 1990). SEA-C was designated as J-2, and I-2 and B-4 were not discriminated from J-2 (SEA-C) and B-3, respectively, in the previous study.

### 3. RESULTS

We have already analyzed mtDNA haplotypes from wild musk shrew populations in Japan, Indonesia, Bangladesh and Sri Lanka (Yamagata et al., 1990). In the present study, we examined those from Philippines, Vietnam, Thailand, Malaysia, Nepal, Mauritius and other localities in Indonesia and Bangladesh. The following are the summarized results from these studies.

Polymorphisms in cleavage patterns of shrew mtDNA were revealed by 14 out of 17 restriction enzymes (Table 2). The cleavage patterns by *Xho*I were monomorphic and no cleavage sites were detected by *Sal*I and *Sma*I in any shrew mtDNA. Altogether, 39 mtDNA haplotypes were recognized as presented in

Table 2. Numbers of cleavage sites of musk shrew mtDNA for 17 restriction endonucleases and the lengths of their fragments in kilo base pairs (kb)

Restriction endonuclease	Type of cleavage pattern	Number of cleavage sites	Lengths of fragments (kb)						
<i>AccI</i>	A	6	7.0,	3.65,	2.58,	1.68,	1.26,	0.58	
	B	5	7.0,	3.65,	2.58,	1.83,	1.68		
	C	6	4.9,	3.65,	2.58,	2.10,	1.83,	1.68	
	D	5	7.0,	3.84,	3.65,	1.68,	0.58		
	E	7	7.0,	3.84,	2.00,	1.65,	1.30,	0.58,	0.4
	F	6	7.0,	5.5,	2.58,	2.50,	1.65,	0.58	
	G	7	4.25,	3.84,	3.65,	2.50,	1.65,	0.58,	0.25 <sup>a</sup>
	H	7	4.9,	3.65,	2.58,	2.10,	1.68,	1.26,	0.58
	I	5	7.0,	3.84,	1.94,	1.90,	1.63		
	J	6	3.84,	3.82,	3.65,	3.14,	1.68,	0.58	
	K	7	3.84,	3.82,	3.14,	2.00,	1.68,	1.65,	0.58
	L	6	5.35,	3.84,	3.65,	1.68,	1.65,	0.58	
	M	7	3.84,	3.82,	3.14,	2.58,	1.68,	1.26,	0.58
	N	8	4.5,	3.65,	2.58,	2.50,	1.68,	1.26,	0.58
	P	7	3.65,	3.55,	3.45,	2.58,	1.68,	1.26,	0.58
<i>BamHI</i>	A	2	10.1,	6.7					
	B	1	17.0						
<i>BanIII</i>	A	2	14.0,	2.73					
	B	3	7.3,	6.8,	2.73				
	C	5	4.35,	3.50,	3.28,	2.90,	2.73		
	D	4	7.3,	3.50,	3.28,	2.73			
<i>BglI</i>	O	0	—						
	A <sup>b</sup>	1	17.0						
	B <sup>b</sup>	1	17.0						
<i>BglII</i>	A	2	9.1,	7.7					
	B	3	7.7,	5.6,	3.50				
	C	4	7.7,	5.6,	3.00,	0.5			
	D	2	13.3,	3.50					
	E	2	11.2,	5.6					
<i>BstEII</i>	A	2	10.8,	6.0					
	B	3	10.8,	3.66,	2.32				
	C	3	10.8,	5.18,	0.80				
	D	3	7.7,	5.45,	3.66				
	E	2	9.7,	7.1					
	F	3	7.1,	6.0,	3.66				
	G	1	17.0						
	H	4	10.8,	2.85,	2.32,	0.80			
<i>EcoRI</i>	A	2	8.8,	8.0					
	B	3	8.0,	7.7,	1.10				
	C	2	12.0,	4.7					
	D	2	9.1,	7.7					
	E	1	17.0						
<i>EcoRV</i>	A	3	8.2,	7.5,	1.12				
	B	4	8.2,	4.85,	2.68,	1.12			
	C	5	8.2,	4.85,	1.48,	1.20,	1.12		
	D	4	7.1,	6.0,	2.68,	1.10			
	E	5	7.1,	4.85,	2.68,	1.12,	1.10		
	F	3	8.2,	6.0,	2.68				

Table 2. Continued

<i>Hind</i> III	A	5	6.6,	4.2,	2.62,	2.50,	0.89		
	B	6	6.6,	3.30,	2.62,	2.50,	0.94,	0.89	
	C	7	6.6,	3.30,	2.62,	1.32,	1.18,	0.94,	0.89
	D	6	6.6,	4.2,	2.62,	1.32,	1.18,	0.89	
	E	7	4.3,	4.2,	2.62,	2.30,	1.32,	1.18,	0.89
<i>Pst</i> I	A <sup>b</sup>	1	17.0						
	B	2	14.0,	3.00					
	C <sup>b</sup>	1	17.0						
<i>Pvu</i> II	A	3	14.0,	1.70,	0.72				
	B	4	12.5,	1.70,	1.60,	0.72			
	C	4	10.1,	3.7,	1.70,	0.72			
<i>Sac</i> I	O	0	—						
	A	1	17.0						
	B	2	9.6,	7.3					
<i>Sal</i> I	O	0	—						
<i>Sma</i> I	O	0	—						
<i>Stu</i> I	A	3	13.0,	2.97,	0.95				
	B	2	14.0,	2.97					
	C	5	10.0,	2.97,	1.55,	1.25,	0.95		
<i>Xba</i> I	A	4	9.4,	4.35,	1.95,	1.12			
	B	5	5.8,	4.35,	3.65,	1.95,	1.12		
<i>Xho</i> I	A	1	17.0						

<sup>a</sup> The presence of these fragments was confirmed by making the restriction map of mtDNA.

<sup>b</sup> The A and B types of cleavage patterns with *Bgl*I and the A and C with *Pst*I showed same one 17.0 kb fragment, but it was confirmed that each two types has a different cleavage site by double digestion method.

Table 3. Each haplotype was designated with the capital letter of the name of each country (or country and locality) where its type was found, and a number representing a haplotype, e.g., three different haplotypes found in Sri Lanka named S-1, S-2 and S-3. The J-1 type was detected in the two Japanese laboratory shrew lines (Yamagata et al., 1990), but their original wild populations were not examined. The SEA-C type (designated as J-2 previously) was found commonly in several countries of Southeast Asia (Philippines, Vietnam, Thailand and Indonesia) and Japan, while the MI-1 and MI-2 types were found in Malay Peninsula including Thailand and Malaysia (Table 1). The rest of haplotypes were unique to each country.

In Southeast Asia, there were 1 to 3 haplotypes per locality and the SEA-C type, being common in Southeast Asia, was a major type in eight localities. On the other hand, 4 to 7 haplotypes were detected in 3 localities in Bangladesh, and all 4 localities in Nepal showed polymorphism, although only few animals were

Table 3. Restriction endonuclease cleavage patterns of mtDNA haplotypes in the musk shrew

mtDNA haplotype	Type of cleavage pattern															No. of animals
	Ac <sup>a</sup>	Bm	Bn	Bg1	Bg2	Bs	Ec1	Ec5	Hd	Ps	Pv	Sc	St	Xb	Xo	
SEA-C	A	A	A	A	A	A	A	A	A	A	A	A	A	A	A	129
J-1 <sup>b</sup>	A	A	A	O	A	A	A	A	A	A	A	A	A	A	A	—
P-1	N	A	A	A	A	A	A	A	A	A	A	A	A	A	A	3
P-2	P	A	A	A	A	A	A	A	A	A	A	A	A	A	A	2
V-1	A	A	A	A	A	A	A	A	A	A	C	A	A	A	A	15
MI-1	I	B	D	O	B	A	A	A	E	A	A	A	A	A	A	14
MI-2	A	A	A	O	A	G	A	A	A	A	A	A	A	A	A	10
MI-3	A	A	A	O	A	G	A	A	A	A	A	A	C	A	A	4
I-1	A	A	A	A	A	A	E	A	A	A	A	- <sup>c</sup>	-	-	A	2
I-2	A	A	A	O	A	B	A	A	A	A	A	-	A	-	A	7
I-3	H	A	A	A	A	A	A	A	A	A	A	-	-	-	A	11
S-1	C	A	A	O	A	A	A	B	A	A	A	A	A	A	A	6
S-2	F	A	B	O	C	A	C	D	A	A	A	A	A	B	A	2
S-3	B	A	-	-	A	-	A	C	A	-	-	-	-	A	-	1
B-1	D	A	C	O	B	B	B	B	B	B	A	A	A	A	A	7
B-2	E	A	C	O	C	B	A	C	B	A	C	B	A	B	A	23
B-3	J	B	C	O	D	B	B	B	C	B	A	A	A	A	A	2
B-4	J	B	D	O	D	B	B	B	C	B	A	A	A	A	A	1
B-5	J	B	C	O	D	B	B	A	C	B	A	A	A	A	A	5
B-6	J	B	C	O	D	B	B	A	D	B	A	A	A	A	A	2
B-7	D	B	C	O	B	C	B	A	C	B	A	A	A	A	A	1
B-8	D	B	C	O	B	H	B	A	C	B	A	A	A	A	A	4
B-9	D	B	C	O	B	H	B	A	C	B	A	O	A	A	A	1
B-10	G	B	C	O	A	H	B	A	C	B	A	A	A	A	A	1
B-11	G	B	C	O	B	H	B	A	C	B	A	A	A	A	A	1
B-12	K	B	C	O	D	B	B	A	C	B	A	A	A	A	A	2
B-13	L	B	C	O	B	H	B	A	C	B	A	A	A	A	A	7
B-14	M	B	C	O	D	B	B	A	C	B	A	A	A	A	A	2
NK-1	G	B	C	B	B	D	D	E	D	C	A	A	A	A	A	7
NK-2	G	B	C	B	B	D	D	F	D	C	A	A	A	A	A	3
NH-1	G	B	C	B	B	C	D	E	D	C	B	A	-	-	A	1
NH-2	D	B	C	B	E	E	B	E	D	C	A	A	A	-	A	1
NH-3	-	A	C	O	B	C	B	A	C	B	A	A	-	-	A	1
NB-1	-	B	C	O	B	B	D	A	D	B	A	B	-	-	A	1
NB-2	D	B	C	O	B	B	D	A	C	B	A	B	-	-	A	1
NP-1	-	B	C	O	B	F	B	E	D	C	A	A	-	-	A	2
NP-2	D	B	C	B	B	F	B	E	D	C	A	A	-	-	A	1
Mr-1	A	A	A	O	A	G	A	A	A	-	-	-	-	-	-	4
Mr-2	A	-	A	O	B	-	A	A	A	-	-	-	-	-	-	1

<sup>a</sup> Abbreviations of enzymes : Ac, *AccI*; Bm, *Bam*HI; Bn, *Ban*III; Bg1, *Bgl*I; Bg2, *Bgl*II; Bs, *Bst*EII; Ec1, *Eco*RI; Ec5, *Eco*RV; Hd, *Hind*III; Ps, *Pst*I; Pv, *Pvu*II; Sc, *Sac*I; St, *Stu*I; Xb, *Xba*I; Xo, *Xho*I.

<sup>b</sup> J-1 type was found in the two Japanese laboratory lines, but their original wild populations were not examined.

<sup>c</sup> Not tested.

tested at each locality except in Katmandu. In eight localities of these two countries and Sri Lanka, 26 haplotypes—two-thirds of the entire types were detected (Table 1).

The number of recognition cleavage sites shared by each pair of mtDNA haplotypes and the nucleotide difference between haplotypes were shown in Table 4. The nucleotide diversity within local populations and the net of nucleotide diversity between populations were presented in Table 5. Based on the matrices of these values for nucleotide differences and nucleotide diversities, phylogenetic

Table 4. The number of cleavage sites shared by each pair of shrew mtDNA haplotypes and nucleotide difference between shrew mtDNA haplotypes

		Number of cleavage sites shared																		
mtDNA																				
haplotype <sup>a</sup>	SEAC	J-1	P-1	P-2	V-1	MI-1	MI-2	MI-3	I-1	I-2	I-3	S-1	S-2	S-3	B-1	B-2	B-3	B-4	B-5	
SEA-C	(38) <sup>b</sup>	37	38	38	38	33	36	36	29	32	30	36	34	23	36	35	34	34	34	
J-1	0.23	(37)	37	37	37	33	36	36	28	32	29	36	34	23	36	35	34	34	34	
P-1	0.45	0.69	(40)	38	38	33	36	36	29	32	30	36	34	23	36	35	34	34	34	
P-2	0.22	0.46	0.66	(39)	38	33	36	36	29	32	30	36	34	23	36	35	34	34	34	
V-1	0.22	0.46	0.67	0.45	(39)	33	36	36	29	32	30	36	34	23	36	35	34	34	34	
MI-1	2.88	2.66	3.33	3.11	3.09	(40)	32	32	24	28	25	32	33	19	36	34	36	36	36	
MI-2	0.47	0.24	0.93	0.70	0.70	2.96	(36)	36	27	31	28	35	33	23	35	34	33	33	33	
MI-3	0.92	0.70	1.38	1.15	1.15	3.41	0.47	(38)	27	31	28	35	33	23	35	34	33	33	33	
I-1	0.29	0.61	0.88	0.59	0.58	4.16	0.93	0.93	(29)	28	29	27	26	18	27	27	25	25	25	
I-2	0.53	0.27	1.05	0.79	0.79	3.36	0.55	1.07	0.90	(33)	29	31	29	19	32	30	30	30	30	
I-3	0.29	0.59	0.85	0.57	0.57	4.02	0.90	0.90	0.59	0.87	(31)	29	26	19	28	28	26	26	26	
S-1	0.93	0.70	1.39	1.16	1.15	3.42	0.96	1.41	1.53	1.08	0.87	(38)	34	23	36	34	34	34	33	
S-2	2.79	2.57	3.23	3.01	3.00	3.73	2.87	3.30	3.04	2.99	3.60	2.80	(42)	21	36	36	35	35	34	
S-3	1.10	1.10	1.81	1.45	1.10	4.08	1.10	1.10	1.84	1.33	1.76	1.45	4.04	(25)	23	22	21	21	20	
B-1	2.43	2.22	2.85	2.64	2.63	2.84	2.49	2.91	3.44	2.25	3.34	2.43	3.24	2.12	(45)	42	43	42	42	
B-2	3.33	3.13	3.76	3.55	3.53	4.24	3.42	3.83	4.23	3.84	4.11	3.84	3.64	3.91	1.55	(47)	41	40	41	
B-3	3.41	3.21	3.84	3.63	3.62	2.85	3.51	3.92	4.78	3.37	4.64	3.42	3.72	3.71	0.77	1.97	(45)	44	44	
B-4	3.21	3.00	3.64	3.42	3.41	2.66	3.30	3.72	4.52	3.13	4.38	3.22	3.52	3.71	0.99	2.21	0.19	(44)	43	
B-5	3.21	3.00	3.64	3.42	3.41	2.65	3.30	3.72	4.52	3.13	4.38	3.73	4.02	4.22	0.99	1.79	0.19	0.39	(44)	
B-6	3.00	2.79	3.44	3.22	3.21	2.44	3.08	3.51	4.26	2.89	4.12	3.52	3.82	3.88	1.20	2.02	0.39	0.60	0.20	
B-7	2.70	2.49	3.13	2.92	2.91	2.17	2.78	3.20	3.83	3.12	3.71	3.21	4.02	3.36	0.98	0.97	0.99	1.20	0.79	
B-8	2.91	2.70	3.33	3.12	3.11	2.37	2.99	3.40	4.09	2.80	3.97	3.41	4.21	3.36	0.77	1.15	0.77	0.99	0.58	
B-9	3.20	2.99	3.63	3.41	3.40	2.64	3.28	3.70	4.09	2.80	3.97	3.72	4.53	3.36	0.98	1.37	0.99	1.20	0.79	
B-10	3.13	2.93	2.58	3.35	3.33	2.59	3.22	3.63	4.38	3.05	4.25	3.64	4.95	3.73	1.37	1.75	1.37	1.60	1.18	
B-11	3.33	3.13	2.78	3.55	3.53	2.79	3.42	3.83	4.64	3.28	4.50	3.84	4.63	4.06	1.15	1.53	1.16	1.37	0.97	
B-12	3.42	3.22	3.86	3.64	3.63	2.86	3.52	3.94	4.80	3.38	4.65	3.95	4.23	4.58	1.18	1.56	0.38	0.59	0.19	
B-13	3.12	2.92	3.55	3.33	3.32	2.58	3.21	3.62	4.36	3.04	4.90	3.63	4.41	3.71	0.96	1.34	0.97	1.18	0.78	
B-14	3.42	3.22	3.86	3.64	3.63	2.38	3.52	3.94	4.80	3.38	4.65	3.95	4.75	4.58	1.18	1.98	0.38	0.59	0.19	
NK-1	4.67	4.47	4.03	4.89	4.87	4.04	4.26	4.67	5.76	4.80	6.29	4.69	4.44	4.06	2.20	3.47	2.21	2.45	2.45	
NK-2	4.80	4.59	4.14	5.03	5.01	4.16	4.38	4.80	5.98	4.96	6.52	4.82	4.56	4.25	2.26	3.56	2.26	2.52	2.52	
NH-1	5.37	5.13	4.57	5.63	5.61	4.59	5.58	5.58	5.33	5.58	5.83	5.39	4.82	4.93	2.87	3.02	2.88	3.18	3.18	
NH-2	4.54	4.30	5.03	4.79	4.77	3.83	4.70	5.18	5.69	4.70	5.48	4.55	4.64	3.67	2.27	3.72	2.28	2.56	2.56	
NH-3	3.16	2.87	3.16	3.16	3.45	2.03	3.29	3.29	3.73	3.29	3.29	3.16	4.01	3.24	1.04	0.25	1.34	1.64	1.08	
NB-1	4.03	3.73	4.03	4.03	4.33	2.11	4.20	4.20	3.57	3.11	3.89	4.03	4.16	4.28	1.64	1.90	1.38	1.70	1.11	
NB-2	3.95	3.70	4.48	4.22	4.20	3.23	4.09	4.09	3.56	3.18	4.11	4.62	4.70	4.73	1.18	1.86	1.18	1.45	0.95	
NP-1	5.11	4.81	5.11	5.11	5.40	3.05	4.51	4.51	5.89	4.51	5.33	4.33	4.44	3.24	1.90	2.74	1.64	1.97	1.97	
NP-2	4.85	4.60	5.37	5.11	5.09	4.08	4.35	4.35	5.46	4.35	5.29	4.87	5.18	3.49	1.89	3.08	1.90	2.19	2.19	
Mr-1	0.74	0.37	1.46	1.10	0.74	4.80	0	0	1.15	0.74	1.10	1.52	4.22	1.33	3.53	4.50	5.20	4.88	4.88	
Mr-2	0.85	0.43	1.68	1.27	0.85	3.93	0.43	0.43	1.33	0.43	1.27	1.76	3.90	1.95	2.80	3.90	4.07	3.71	3.71	
Nucleotide difference (%)																				

Nucleotide difference (%)

<sup>a</sup> See Table 3 for the mtDNA haplotypes.<sup>b</sup> Numerals in parentheses are numbers of cleavage sites found for each mtDNA haplotype.