



Title	Evolutionary and dispersal history of Eurasian house mice <i>Mus musculus</i> clarified by more extensive geographic sampling of mitochondrial DNA
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Table 1
Data summary for populations, haplotypes and nucleotide diversity of *Mus musculus*

Marker	Subspecies group	N	H	Hd	S	Pi (%)	k
Control Region (CR)							
	CAS	86	42	0.958	54	1.195	6.91
	MUS	132	66	0.981	58	0.842	5.16
	DOM	531	370	0.997	163	1.053	8.3
	GEN	6	6	1	16	1.029	6.26
	NEP*	2	2	1	12	1.376	12
	Nepal**	5	5	1	22	2.703	11
Cytochrome <i>b</i> (<i>Cytb</i>)							
	CAS	38	17	0.895	44	0.468	4.48
	MUS	88	49	0.956	67	0.407	4.62
	DOM	53	31	0.968	57	0.526	5.07
	NEP	2	1	1	12	1.053	12

Abbreviations: N, number of samples; H, number of haplotypes; Hd, haplotype diversity; S, number of polymorphic sites; Pi, nucleotide diversity; k, mean number of pairwise differences among sequences.

*NEP: HS1467, HS1523.

**Nepal: HS1467, HS1523, AF074524, AF074525, AF074526

Table 2

Divergence time estimation using mitochondrial cytochrome *b* sequences (1140 bp)

Node*	TMRCA estimated	Divergence time**	Confidence interval†
A	DOM/NEP and CAS/MUS	0.4591	0.3250 - 0.4808
B	CAS and MUS	0.4179	0.2863 - 0.5432
C	DOM and NEP	0.3719	0.2385 - 0.4805
D	CAS	0.2173	0.1340 - 0.2947
E	MUS	0.1509	0.0812 - 0.2136
F	DOM	0.1333	0.0690 - 0.1478
G	NEP	0.1408	0.0623 - 0.1852

*See Figure 7 for detail.

**Mean divergence times (million years ago; mya) were obtained from the BEAST analysis.

Divergence times were calculated on the assumption of 1.7 mya for the divergence of *Mus musculus* and *Mus spretus*.

†CI values are 95% highest posterior density interval.

Table 3

Estimation of population expansion times (year before present) based on mitochondrial cytochrome *b* sequences (1140 bp)

Group	Main range	N	<i>Pi</i> (%)	Tajima's <i>D</i>	<i>Tau</i> (Confidence interval)	SSD	Substitution rates (myr/site/lineage)		
							2.5%	10%	20%
CAS-1	S and E Asia	34	0.195	-1.93*	1.835 (1.279~2.556)	0.00353	32,200	8,000	4,000
CAS-1a	Yunnan, N Japan	17	0.08	-1.237	-				
CAS-1b	India, SE Asia	17	0.202	-2.583*	1.734 (0.436~3.676)	0.01005	30,000	7,600	3,800
MUS-1	N Eurasia	76	0.304	-2.257**	1.725 (1.724~2.352)	0.07956**	30,200	7,500	3,800
MUS-1a	E Europe	9	0.244	-0.255	-				
MUS-1b	N China	26	0.392	-1.952*	4.920 (2.941~6.468)	0.00451	86,000	21,000	10,800
MUS-1c	Korea, Japan	41	0.12	-2.190*	1.527 (0.746~2.535)	0.01595	26,000	6,600	3,300
MUS-2	China, Siberia	12	0.293	-0.353	-				
DOM	W Europe	53	0.526	-2.058*	5.464 (3.998~6.089)	0.00891*	95,900	23,900	12,000

Abbreviations: N, number of samples; SSD, sum of squares deviation. N, *Pi*, and Tajima's *D* values were calculated using DNASP v5 and *Tau* and SSD values were obtained using Arlequin.

* $P < 0.05$, ** $P < 0.01$.

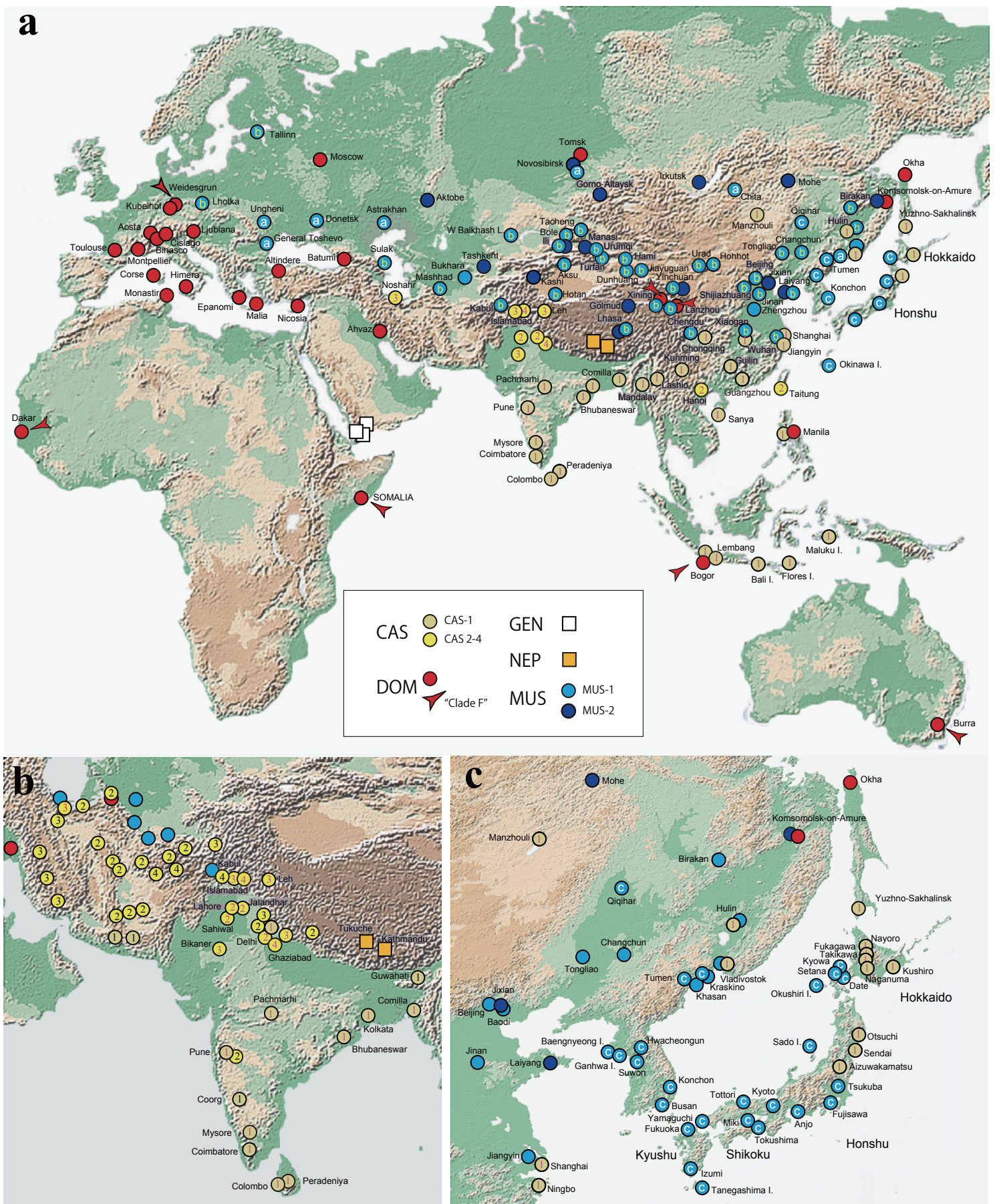


Figure 1

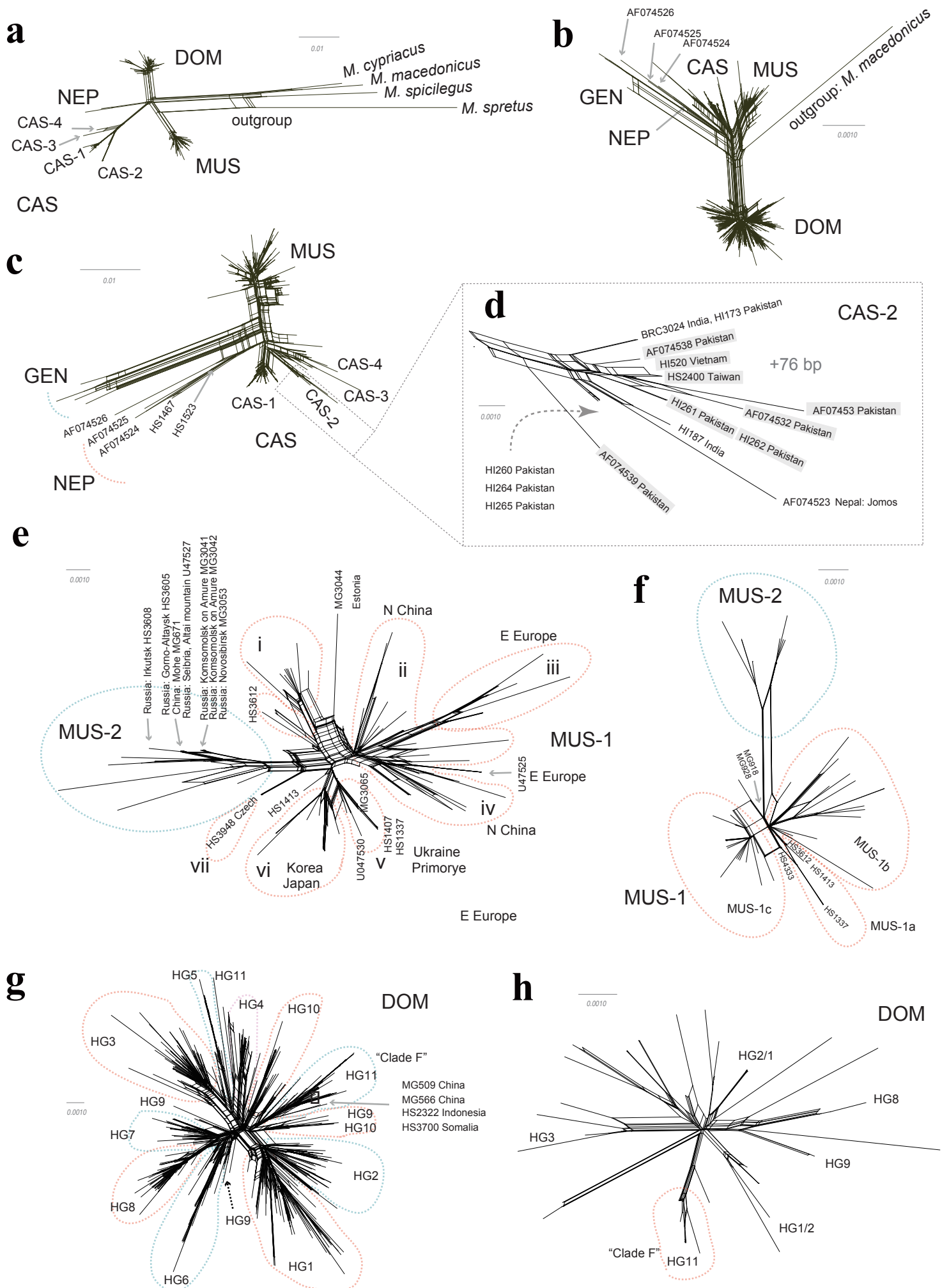


Figure 2

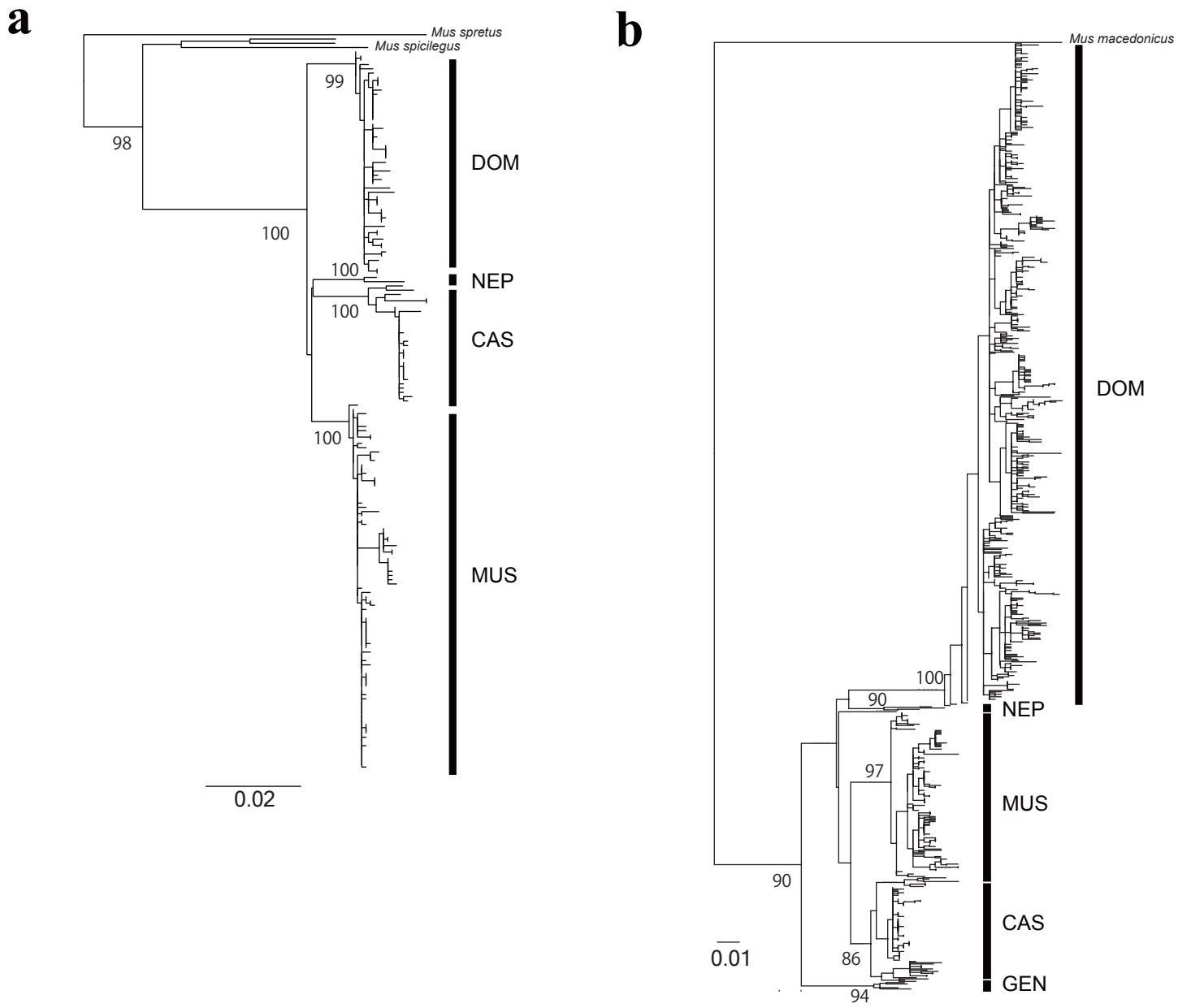


Figure 3

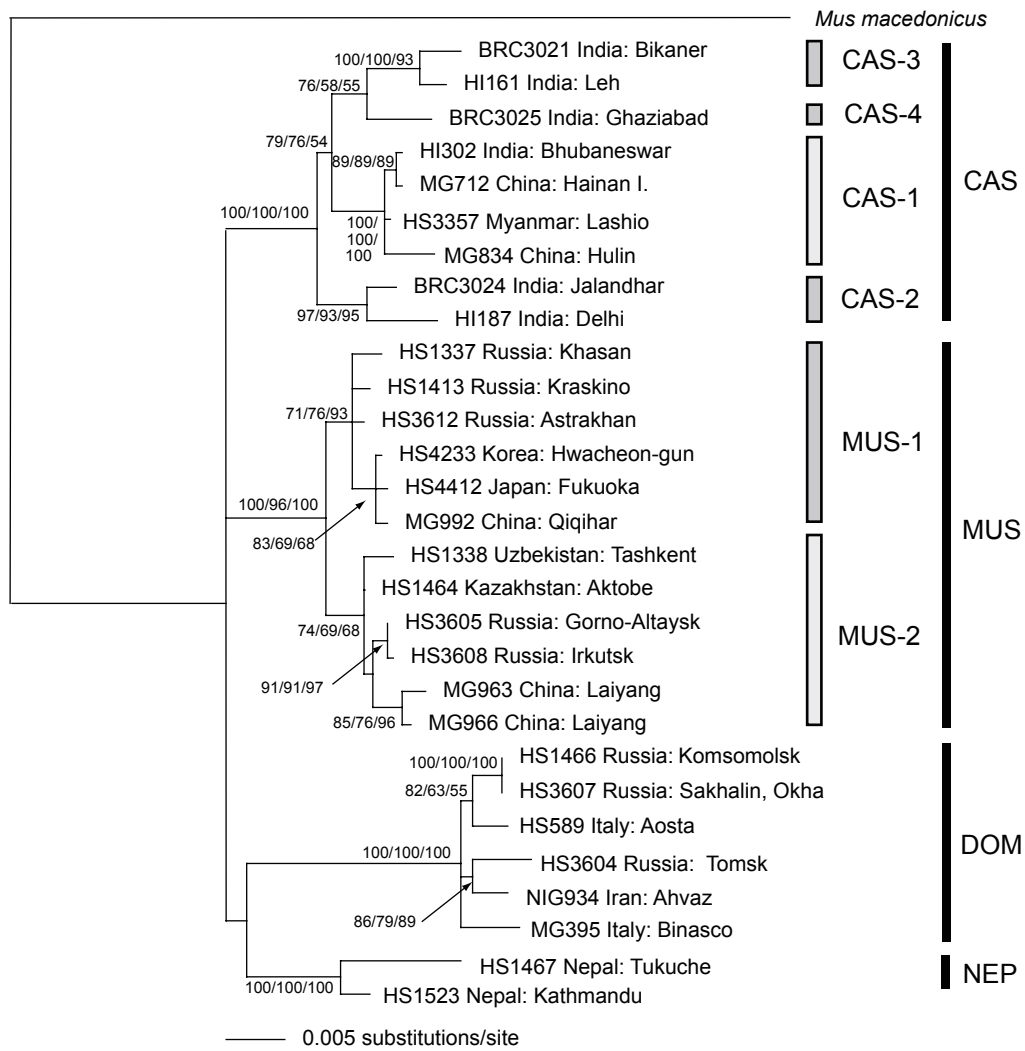


Figure 4

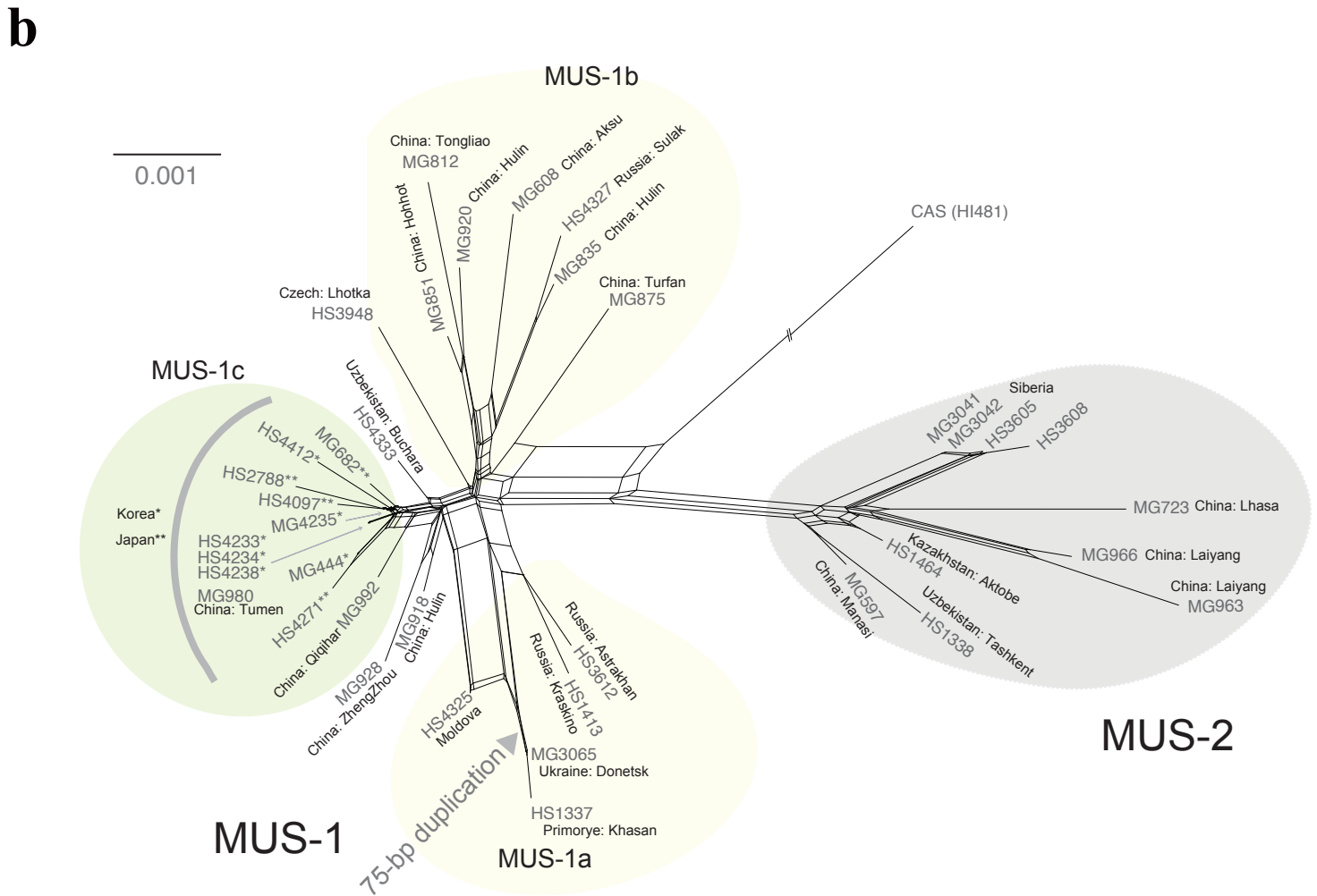
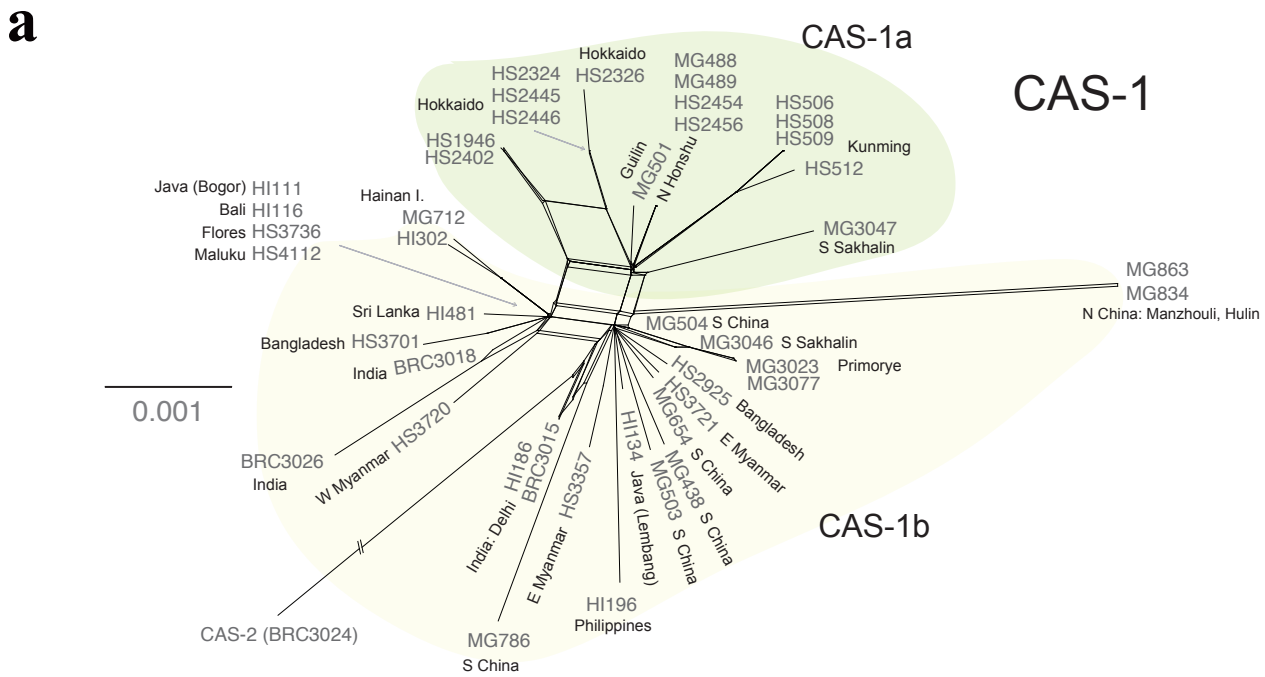


Figure 5

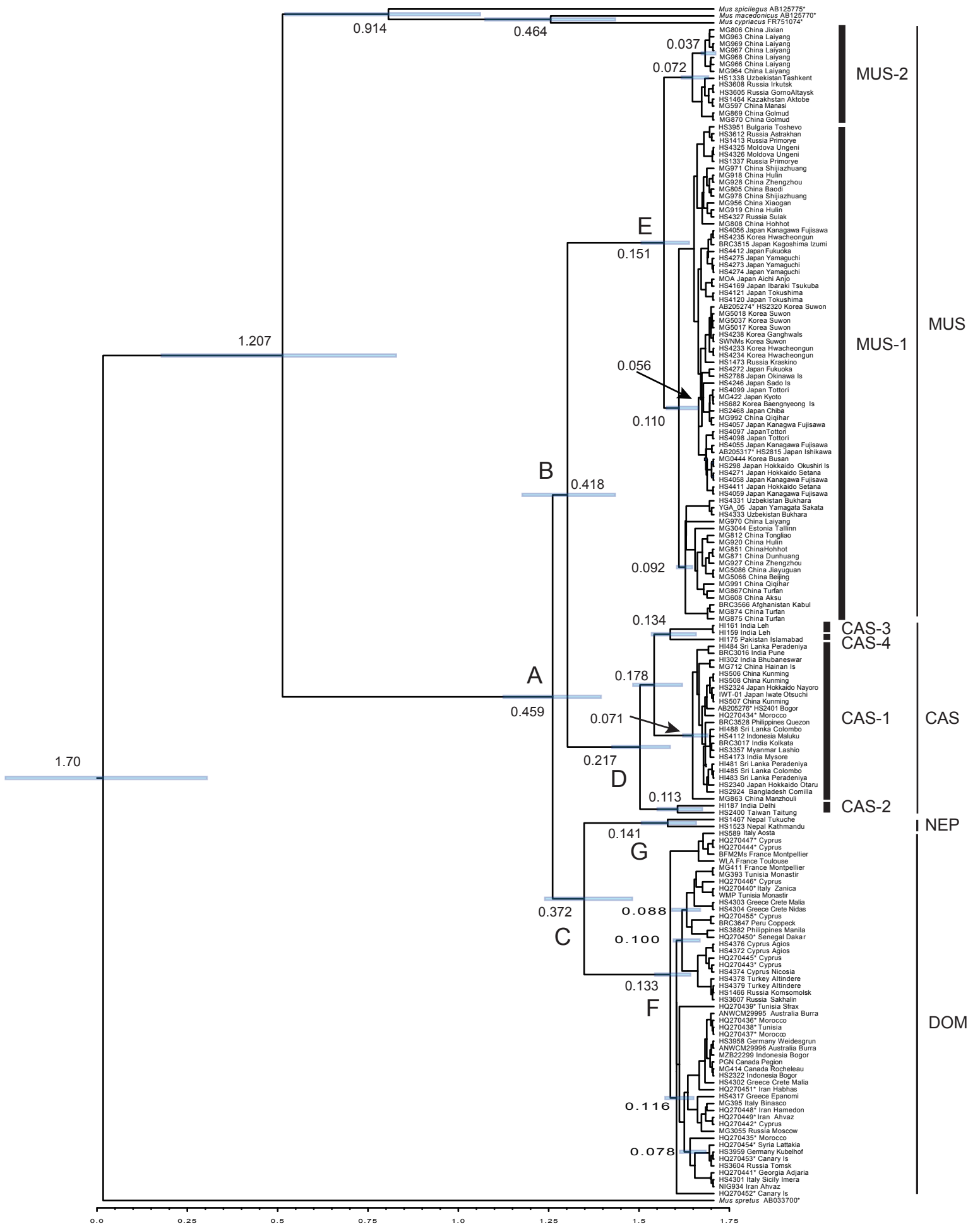


Fig. 6