

# Supporting Information

Nikaido et al. 10.1073/pnas.1115675108

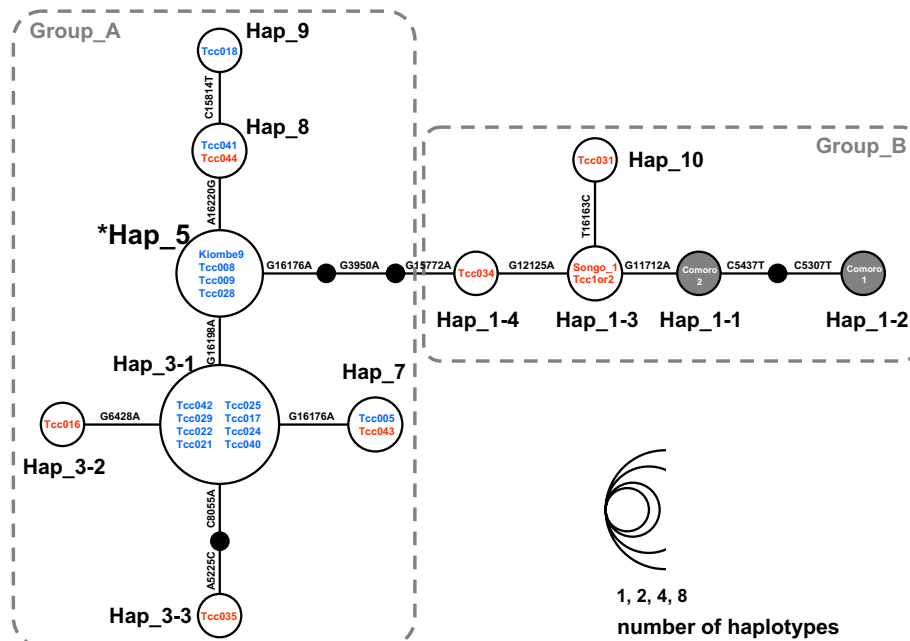


Fig. S1. Haplotype network tree of the entire mtDNA haplotypes of 23 Tanzanian and 2 Comoran coelacanths. The size of the circle corresponds to the number of occurrences. Nucleotide substitutions between haplotypes are shown above each branch. The haplotypes observed in northern Tanzania, southern Tanzania, and Comoros are indicated by blue, red, and white on gray characters, respectively. The hypothetical haplotypes that were not observed in the present study are shown in black circles. The haplotype names (1-Xs and 3-Xs) were used only for the analyses of full mtDNA.

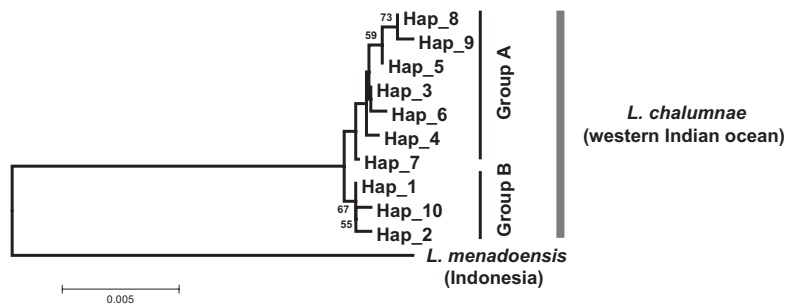
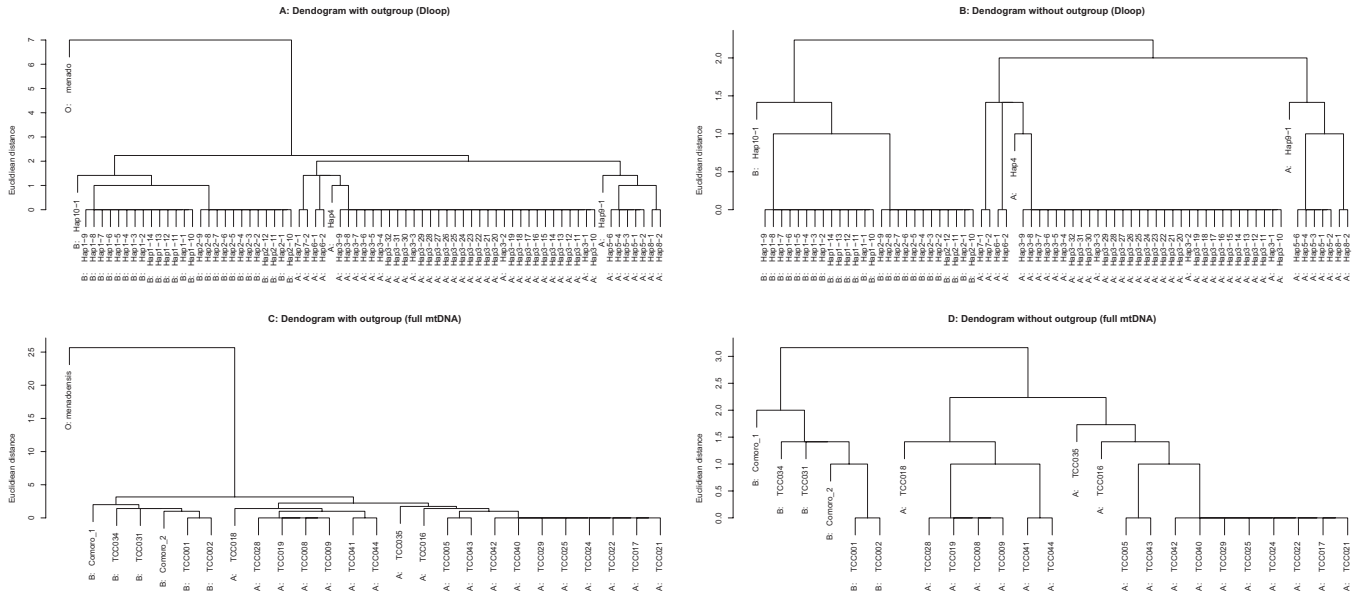


Fig. S2. Neighbor joining tree of 10 d-loop haplotypes of *Latimeria chalumnae*. The tree was constructed by using the sequence of *Latimeria menadoensis* as an outgroup. The haplotypes of *L. chalumnae* are divided into two subgroups, A and B. The bootstrap values higher than 50 are shown on each branch.



**Fig. S3.** The results of the clustering analyses. The clusters were identified and visualized using the `dist`, `hclust`, and `plot.hclust` functions in R (1). *A* and *B* use the haplotype labels, whereas *C* and *D* use sample labels from Table S1. *A* and *B* are for d-loop data and *C* and *D* show full mitochondrial data. *A* and *C* show clustering when the out group *L. menadoensis* is included, whereas *B* and *D* show the clustering when the outgroup is not included.

1. R Development Core Team (2011) *R: A Language and Environment for Statistical Computing* (R Foundation for Statistical Computing, Vienna, Austria).



**Table S2. Alignment of 12 entire mtDNA haplotypes of *L. chalumnae* in the western Indian Ocean**

	Gln	Ala	Asn	Tyr	CO I	ATP8	ND4	ND5	d-Loop					
	3	5	5	5	6	8	1	1	1	1	1	1	1	1
	9	2	3	4	4	0	1	2	5	5	6	6	6	6
	5	2	0	3	2	5	7	1	7	8	1	1	1	2
	0	5	7	7	8	5	1	2	7	1	6	7	9	2
Nucleotide position <sup>†</sup>							2	5	2	4	3	6	8	0
Hap_1-1	A	C	C	C	A	A	A	A	A	T	T	A	A	A
Hap_1-2	—	—	T	T	—	—	—	—	—	—	—	—	—	—
Hap_1-3	—	—	—	—	—	—	G	—	—	—	—	—	—	—
Hap_1-4	—	—	—	—	—	—	G	G	—	—	—	—	—	—
Hap_3-1	G	—	—	—	—	—	G	G	G	—	—	G	G	—
Hap_3-2	G	—	—	—	G	—	G	G	G	—	—	G	G	—
Hap_3-3	G	A	—	—	—	C	G	G	G	—	—	G	G	—
Hap_5	G	—	—	—	—	—	G	G	G	—	—	G	—	—
Hap_7	G	—	—	—	—	—	G	G	G	—	—	—	G	—
Hap_8	G	—	—	—	—	—	G	G	G	—	—	G	—	G
Hap_9	G	—	—	—	—	—	G	G	G	C	—	G	—	G
Hap_10	—	—	—	—	—	—	G	—	—	—	C	—	—	—

Residues identical to the top sequence are indicated by “—”.

<sup>†</sup>Number of nucleotide positions are according to Sasaki et al. (1)

- Sasaki T, et al. (2007) Mitogenomic analysis for coelacanths (*Latimeria chalumnae*) caught in Tanzania. *Gene* 389:73–79.

**Table S3. The data fail to reject the molecular clock hypothesis**

	d-Loop	Full mtDNA
Rate differences ( $\Delta K$ )		
Jukes Cantor 1 parameter	-0.0010302	-4.17634e-05
Kimura 2 parameter	-0.00106145	-4.2553e-05
<i>P</i> values		
Jukes Cantor 1 parameter	0.64177	0.744653
Kimura 2 parameter	0.647428	0.748696

Rate differences for various combinations of data and nucleotide substitution models, and *P* values for the magnitudes of the corresponding cells listed under “rate differences.” For both rate differences and *P* values, columns represent data sources analyzed and rows represent the nucleotide substitution models used.

**Table S4. Estimated age of the sharing of the last common ancestor between *L. chalumnae* populations of northern Tanzania and Comoros**

		<i>L. chalumnae</i> – <i>L. menadoensis</i> divergence time (years ago) from the literature				
		4,700,000	6,300,000	28,000,000	30,000,000	40,000,000
		Holder et al., 1999 (1)	Sudarto et al., 2010 (2)		Inoue et al., 2005 (3)	
Divergence time between Groups A and B (years ago)	Min	202,000	271,000	1,200,000	1,290,000	1,720,000
	Median	315,000	422,000	1,880,000	2,010,000	2,680,000
	Mean	348,000	466,000	2,070,000	2,220,000	2,960,000
	Max	517,000	693,000	3,080,000	3,300,000	4,400,000

Divergence times were estimated according to the rate of pair-wise nucleotide substitutions between individuals of mtDNA haplotype Groups A and B to those between *L. chalumnae* and *L. menadoensis*: 0.043, 0.067, 0.074, and 0.11 for minimum (Min), median, mean, and maximum (Max) values, respectively.

1. Holder MT, Erdmann MV, Wilcox TP, Caldwell RL, Hillis DM (1999) Two living species of coelacanths? *Proc Natl Acad Sci USA* 96:12616–12620.
2. Sudarto, et al. (2010) Mitochondrial genomic divergence in coelacanths (Latimeria): Slow rate of evolution or recent speciation? *Mar Biol* 157:2253–2262.
3. Inoue JG, Miya M, Venkatesh B, Nishida M (2005) The mitochondrial genome of Indonesian coelacanth *Latimeria menadoensis* (Sarcopterygii: Coelacanthiformes) and divergence time estimation between the two coelacanths. *Gene* 349:227–235.

**Table S5. Nucleotide differences in mtDNA control region sequences of *L. chalumnae* of Tanzania and Comoros**

mtDNA differences	Tanzania (whole)	Tanzania (northern)	Tanzania (southern)	Comoros
<i>n</i>	23	15	8	38
<i>S</i>	6	4	5	4
hd (SD)	0.779 (0.071)	0.676 (0.105)	0.857 (0.108)	0.679 (0.023)
$\pi$ (SD)	0.00204 (0.00033)	0.00128 (0.00033)	0.00267 (0.00043)	0.00239 (0.00013)
<i>k</i>	1.598	1.029	2.143	1.916
Tajima's D	-0.01676	-0.54965	0.50437	2.44763*

hd, haplotype diversity; *k*, average nucleotide difference per sequence; *n*, number of samples; *S*, number of segregating sites; SD indicates standard deviation;  $\pi$ , average nucleotide difference per site; \**P* < 0.05.



**Movie S1.** Coelacanth individuals that inhabited off Tanga, a northern coastal region of Tanzania. The movie was recorded by an international coelacanth research team (Aquamarine Fukushima, African Coelacanth Ecosystem Program, Sustainable Seas Trust, Tanzania Fisheries Research Institute) during the underwater surveys off Tanga using remotely operated vehicles in 2007. This was a unique observation of the Tanzania coelacanths in their natural habitat. The movie shows the coelacanths swimming head down, known to be a typical behavior of this animal.

[Movie S1](#)