

**Text S2.** *Characteristics of mitochondrial (a) and nuclear (b) datasets used in this study*

(a)

<b>MITOCHONDRIAL</b>				
Studied gene	Number of taxa	Sequence length (in base pairs)	Number of informative sites within the intra group (%)	Evolution model
16S	36	522	128 (24.5 %)	-
12S	32	408	43 (10.5 %)	-
Cytb	36	346	92 (26.6 %)	-
CO1	36	1272	224 (17.6 %)	-
CO2	26	400	54 (13.5 %)	-
Total	37	2948	541 (18.4 %)	GTR+G

(b)

<b>NUCLEAR</b>				
Studied gene	Number of taxa	Sequence length (in base pairs)	Number of informative sites within the intra group (%)	Evolution model
EF1- $\alpha$	37	990	67 (6.8 %)	GTR+I+G
28S	28	1466	148 (10.1 %)	GTR+I+G
HexK	16	464	11 (2.4 %)	-
H3	33	329	10 (3 %)	-
18S	31	652	5 (0.8 %)	-
Total	37	3901	241 (6.2 %)	GTR+I+G