

Table S3 Pairwise differences between the 14 kb mitochondrial genomes of the six members of Clade 1

	MA	MM	CR	HR	LH	MQ
MA	--	5/1	191/2	5/1	30/2	35/1
MM	<i>0.04</i>	--	192/3	3/0	29/1	34/2
CR	<i>1.4</i>	<i>1.4</i>	--	191/3	207/4	190/5
HR	<i>0.04</i>	<i>0.02</i>	<i>1.4</i>	--	31/1	32/2
LH	<i>0.22</i>	<i>0.21</i>	<i>1.5</i>	<i>0.22</i>	--	47/3
MQ	<i>0.26</i>	<i>0.26</i>	<i>1.4</i>	<i>0.26</i>	<i>0.33</i>	--

Above the diagonal: the number of substitutions above the slash marks and the number of indels below. Below the diagonal, in italics: the percent difference, counting substitutions and indels together. Based on full mitochondrial sequences from Lasek-Nesselquist 2012.