

Supplementary material:

$$N_c = n_1/F_1 + n_2/F_2 + n_3/F_3 + n_4/F_4 + n_5/F_5 + n_6/F_6$$

Where F_1, F_2, F_3 etc. are the average homozygosity estimates for Synonymous Family (SF) type 'i', and n_1, n_2, n_3 etc. are the contributions of each of the SF type. Average ENC was calculated for each species by taking average value for each protein coding gene.

Table 1: Variation in size, GC content and number of proteins, t-RNA and r-RNA coding genes in the mt-DNA of different species

Species	Size (bp)	GC content (%)	No. of Proteins	rRNA Species	tRNA Species
<i>Rhabdocalypus dawsoni</i>	18587	34	14	2	21
<i>Pista cristata</i>	15894	32	13	2	20
<i>Brugia malayi</i>	13657	24	12	2	22
<i>Caenorhabditis elegans</i>	13794	24	12	2	22
<i>Aedes aegypti</i>	16655	21	13	2	22
<i>Drosophila melanogaster</i>	19517	18	13	2	22
<i>Bombyx mori</i>	15643	19	13	2	22
<i>Manduca sexta</i>	15516	18	13	2	22
<i>Apis mellifera</i>	16343	15	13	2	22
<i>Oxya chinensis</i>	15443	24	13	2	22
<i>Periplaneta fuliginosa</i>	14996	25	13	2	22
<i>Tribolium castaneum</i>	15881	28	13	2	22
<i>Mytilus edulis</i>	16740	38	13	2	21
<i>Sepia officinalis</i>	16163	27	13	2	22
<i>Xenopus laevis</i>	17553	37	13	2	22
<i>Homo sapiens</i>	16567	44	13	2	22