



Supplementary Material

Complete Mitochondrial DNA Genome Sequences for Two Lineages in *Coilia mystus* (Clupeiformes: Engraulididae): Mitogenomic Perspective on the Phylogenetic Relationships of Genus *Coilia*

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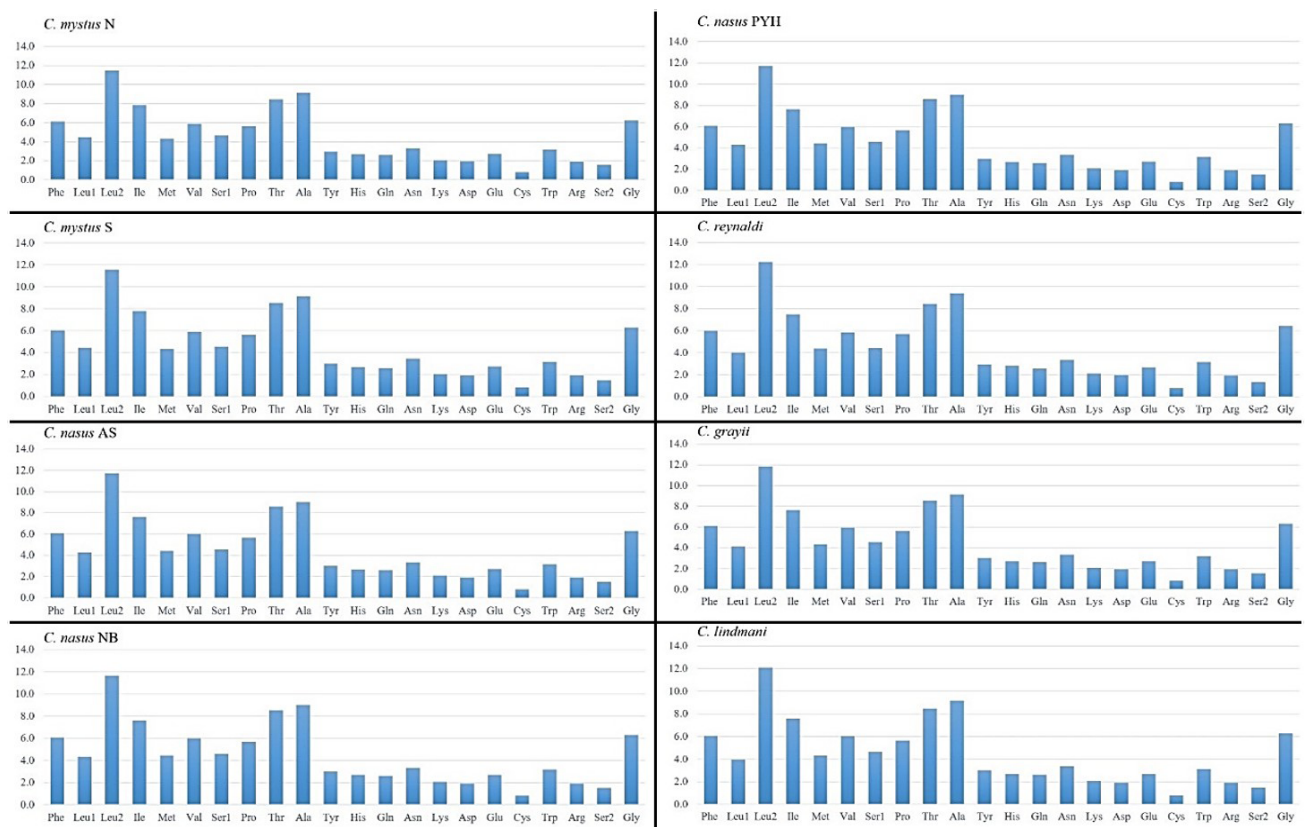
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Supplementary Fig. S1. Codon distributions in the mitochondrial genomes of *Coilia*.

Supplementary Table I.- Nucleotide composition and skews for mitochondrial 13 PCGs, tRNA, rRNA and control region (CR) in the genus *Coilia*.

Species	A(%)	T(%)	C(%)	G(%)	AT-skew	GC-skew	Species	A(%)	T(%)	C(%)	G(%)	AT-skew	GC-skew
<i>C. mystus S</i>	31.1	26.6	26.9	15.5	0.078	-0.269	<i>C. nasus PYH</i>	31.2	26.3	27.0	15.5	0.085	-0.271
PCGs	28.7	28.8	27.4	15.1	-0.002	-0.289	PCGs	29.0	28.5	27.5	14.9	0.009	-0.297
tRNA	31.5	24.22	25.3	19.0	0.130	-0.143	tRNA	31.4	24.0	25.5	19.0	0.134	-0.145
rRNA	33.9	20.1	25.6	20.5	0.255	-0.111	rRNA	34.0	20.1	25.4	20.5	0.256	-0.108
CR	34.5	33.1	19.3	13.2	0.021	-0.187	CR	33.6	33.5	19.1	13.8	0.002	-0.160
<i>C. mystus N</i>	30.9	26.9	26.5	15.7	0.069	-0.257	<i>C. reynaldi</i>	30.8	25.5	27.7	16.0	0.094	-0.267
PCGs	28.7	29.2	26.9	15.1	-0.009	-0.280	PCGs	28.0	27.6	28.3	16.1	0.008	-0.274
tRNA	31.3	23.7	25.7	19.3	0.137	-0.142	tRNA	30.8	23.7	26.0	19.5	0.131	-0.143
rRNA	33.7	20.0	25.6	20.7	0.256	-0.107	rRNA	34.9	18.8	26.4	19.9	0.299	-0.140
CR	34.2	33.2	19.3	13.3	0.016	-0.183	CR	35.8	33.4	18.9	11.9	0.035	-0.227
<i>C. nasus AS</i>	31.2	26.3	27.0	15.5	0.085	-0.270	<i>C. grayii</i>	31.1	26.1	27.2	15.6	0.088	-0.271
PCGs	29.0	28.5	27.5	15.0	0.007	-0.295	PCGs	29.0	28.4	27.6	15.0	0.009	-0.295
tRNA	31.3	24.0	25.6	19.2	0.133	-0.143	tRNA	31.4	24.0	25.5	19.1	0.133	-0.143
rRNA	34.0	20.0	25.5	20.5	0.258	-0.108	rRNA	33.9	19.8	25.8	20.5	0.264	-0.113
CR	33.4	33.3	19.2	14.1	0.001	-0.151	CR	32.9	32.4	19.9	14.9	0.008	-0.143
<i>C. nasus NB</i>	31.1	26.3	27.0	15.5	0.084	-0.269	<i>C. lindmani</i>	31.0	25.7	27.5	15.8	0.092	-0.270
PCGs	29.0	28.6	27.5	15.0	0.007	-0.295	PCGs	28.9	28.0	28.0	15.1	0.017	-0.298
tRNA	31.4	24.0	25.6	19.1	0.134	-0.145	tRNA	31.2	23.9	25.5	19.4	0.133	-0.138
rRNA	34.0	20.0	25.5	20.5	0.258	-0.108	rRNA	33.9	19.9	25.6	20.6	0.260	-0.107
CR	33.1	33.2	19.2	14.5	-0.002	-0.142	CR	32.4	31.3	21.1	15.2	0.017	-0.162