



Supplementary Materials:

Table S1. Summary of the base composition of the mitogenomes at each codon position of the concatenated 13 protein-coding genes (PCGs) across 32 species in the family Carangidae.

Species	Accession Number	Length (bp)	Entire Genome						Protein-Coding Genes		
			A(%)	G(%)	T(%)	C(%)	AT-Skew	GC-Skew	Length (bp)	AT-Skew	GC-Skew
<i>Alectis Indicus</i>	KP710215	16553	28.03	16.21	25.60	30.16	0.0453	-0.3008	3800	-0.0424	-0.3377
<i>Decapterus tabl</i>	MN102718	16545	27.28	17.05	25.02	30.65	0.0432	-0.2851	3799	-0.0480	-0.3250
<i>Alepes djedaba</i>	KP408222	16563	27.92	16.66	26.40	29.03	0.0279	-0.2707	3798	-0.0654	-0.3080
<i>Alectis ciliaris</i>	NC_025566	16570	28.32	16.16	26.77	28.75	0.0281	-0.2803	3640	-0.0597	-0.3183
<i>Alepes kleinii</i>	NC_023524	16571	28.06	16.45	27.02	28.47	0.0188	-0.2675	3651	-0.0685	-0.3049
<i>Atule mate</i>	NC_026222	16565	28.37	16.29	27.62	27.72	0.0133	-0.2597	3690	-0.0819	-0.2909
<i>Carangoides armatus</i>	NC_004405	16556	28.03	16.09	26.50	29.37	0.0280	-0.2921	3573	-0.0574	-0.3342
<i>Carangoides malabaricus</i>	NC_023968	16561	27.83	16.38	26.15	29.64	0.0311	-0.2881	3667	-0.0558	-0.3191
<i>Caranx ignobilis</i>	NC_022932	16588	28.83	16.05	25.81	29.30	0.0552	-0.2921	3637	-0.0334	-0.3232
<i>Caranx melampygus</i>	NC_004406	16593	28.95	15.84	26.28	28.93	0.0483	-0.2923	3568	-0.0324	-0.3299
<i>Caranx tille</i>	NC_029421	16593	28.95	15.84	26.26	28.95	0.0487	-0.2926	3633	-0.0316	-0.3303
<i>Decapterus macrosoma</i>	NC_023458	16545	27.05	17.17	25.39	30.39	0.0316	-0.2779	3674	-0.0569	-0.3173
<i>Decapterus macarellus</i>	NC_026718	16544	27.27	17.03	25.27	30.43	0.0380	-0.2822	3657	-0.0472	-0.3232
<i>Decapterus maruadsi</i>	NC_024556	16541	28.95	15.84	26.28	28.93	0.0483	-0.2923	3651	-0.0479	-0.3259
<i>Elagatis bipinnulata</i>	NC_029880	16542	27.93	16.76	25.81	29.49	0.0394	-0.2751	3639	-0.0475	-0.3093
<i>Kaiwarinus equula</i>	NC_025644	16588	26.31	18.13	25.33	30.24	0.0189	-0.2503	3652	-0.0797	-0.2745
<i>Megalaspis cordyla</i>	NC_025565	16566	28.83	15.93	25.81	29.43	0.0552	-0.2976	3637	-0.0275	-0.3299
<i>Parastrumateus niger</i>	KJ192332	16561	28.32	16.16	26.01	29.51	0.0425	-0.2923	3656	-0.0445	-0.3268
<i>Selar crumenophthalmus</i>	NC_023954	16610	27.18	16.77	26.57	29.48	0.0113	-0.2748	3648	-0.0706	-0.3117
<i>Selaroides leptolepis</i>	NC_029184	16560	27.77	16.76	26.53	28.94	0.0228	-0.2665	3624	-0.0613	-0.2964
<i>Seriola dumerili</i>	NC_016870	16530	26.84	17.60	25.50	30.05	0.0256	-0.2612	3661	-0.0586	-0.2961
<i>Seriola lalandi</i>	NC_016869	16535	26.67	17.80	25.34	30.20	0.0255	-0.2583	3643	-0.0614	-0.2912
<i>Seriola quinqueradiata</i>	NC_016868	16539	26.59	18.03	25.19	30.20	0.0270	-0.2523	3660	-0.0644	-0.2788
<i>Seriola rivoliana</i>	NC_027183	16599	27.30	17.15	25.74	29.80	0.0294	-0.2694	3656	-0.0502	-0.3064
<i>Seriolina nigrofasciata</i>	NC_028420	16531	26.67	17.50	25.84	29.99	0.0158	-0.2630	3656	-0.0627	-0.3000
<i>Trachinotus blochii</i>	NC_024026	16558	29.21	15.74	26.49	28.56	0.0488	-0.2893	3580	-0.0445	-0.3233
<i>Trachinotus carolinus</i>	NC_024184	16544	28.68	16.27	26.00	29.06	0.0490	-0.2822	3646	-0.0429	-0.3130
<i>Trachinotus ovatus</i>	NC_022707	16564	29.01	15.88	26.23	28.88	0.0490	-0.2903	3564	-0.0399	-0.3246

<i>Trachurus japonicus</i>	NC_002813	16559	27.74	16.58	25.79	29.89	0.0364	-0.2864	3590	-0.0465	-0.3293
<i>Trachurus trachurus</i>	NC_006818	16559	27.71	16.62	25.76	29.91	0.0364	-0.2856	3594	-0.0487	-0.3271
<i>Uraspis helvola</i>	NC_033402	16555	28.15	16.25	25.84	29.77	0.0427	-0.2937	3647	-0.0518	-0.3281
<i>Uraspis secunda</i>	NC_029488	16554	28.17	16.23	25.81	29.78	0.0437	-0.2945	3667	-0.0514	-0.3280

Table S2. Nucleotide composition and skewness levels calculated for sequenced majority strand of the mitogenomes of *Alectis indicus*, *Decapterus tabl* and *Alepes djedaba*.

Region(s)/Genes	Size(bp)	Nucleotides Composition						AT-Skew	GC-Skew
		A	T	G	C	A+T	G+C		
<i>Alectis Indicus</i>									
Whole mitogenome	16553	28.03	25.60	16.21	30.16	53.63	46.37	0.045	-0.301
PCGs	11428	25.45	27.69	15.53	31.34	53.13	46.87	-0.042	-0.337
1st condon positions	3800	26.10	20.30	25.50	28.10	46.40	53.60	0.125	-0.048
2nd condon positions	3800	18.30	40.50	13.60	27.70	58.80	41.30	-0.378	-0.341
3rd condon positions	3800	31.90	22.10	7.60	38.40	54.00	46.00	0.181	-0.670
tRNAs	1556	27.96	26.48	23.84	21.72	54.43	45.57	0.027	0.046
rRNAs	2667	31.65	20.88	20.92	26.55	52.53	47.47	0.205	-0.119
Control region	861	32.06	30.66	14.63	22.65	62.72	37.28	0.022	-0.215
<i>Decapterus Tabl</i>									
Whole mitogenome	16545	27.28	25.02	17.05	30.65	52.30	47.70	0.043	-0.285
PCGs	11425	24.33	26.77	16.51	32.39	51.10	48.90	-0.047	-0.324
1st condon positions	3799	25.50	19.70	26.20	28.70	45.20	54.80	0.128	-0.045
2nd condon positions	3799	18.20	40.50	13.60	27.70	58.70	41.30	-0.380	-0.341
3rd condon positions	3799	29.10	20.00	9.90	41.00	49.10	50.90	0.185	-0.611
tRNAs	1555	27.78	26.75	23.99	21.48	54.53	45.47	0.018	0.055
rRNAs	2673	31.72	21.29	21.17	25.81	53.01	46.99	0.197	-0.099

Control region	848	32.55	30.31	15.33	21.82	62.85	37.15	0.036	-0.175
<i>Alepes Djedaba</i>									
Whole mitogenome	16563	27.92	26.40	16.66	29.03	54.31	45.69	0.028	-0.271
PCGs	11427	25.12	28.59	16.03	30.25	53.71	46.29	-0.064	-0.307
1st condon positions	3798	25.80	21.00	25.90	27.30	46.80	53.20	0.103	-0.026
2nd condon positions	3798	18.20	40.50	13.70	27.60	58.70	41.30	-0.380	-0.337
3rd condon positions	3798	31.10	24.20	8.60	36.10	55.30	44.70	0.124	-0.615
tRNAs	1552	27.90	26.68	23.52	21.91	54.57	45.43	0.022	0.035
rRNAs	2680	31.68	22.09	21.23	25.00	53.77	46.23	0.178	-0.082
Control region	857	33.72	30.11	15.17	21.00	63.83	36.17	0.057	-0.161

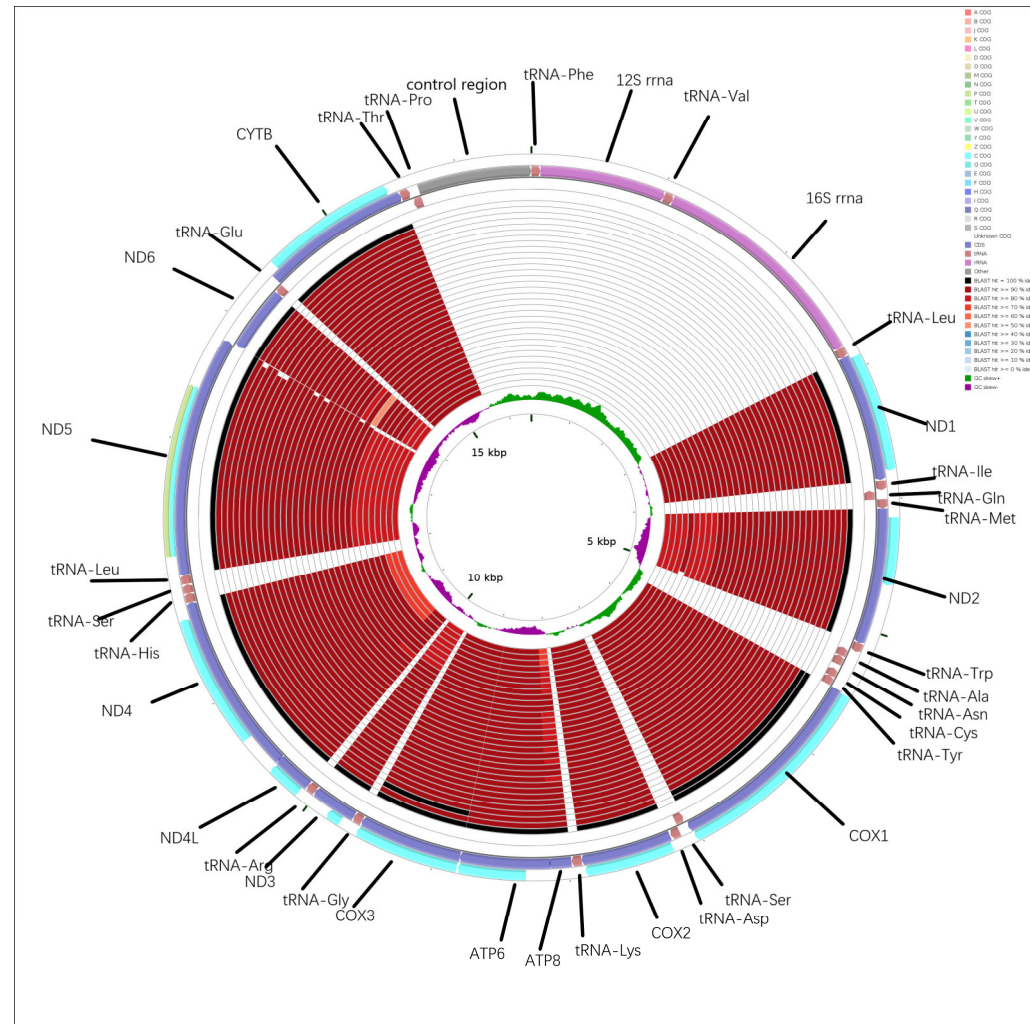


Figure S1. Graphical map of the blast results showing the mitochondrial coding DNA sequence (CDS) identity between *A. indicus* and 31 other Carangidae. Clusters of Orthologous Groups of proteins (COG), gene region, blast identity, and AT-skew are shown from outside to inside. The species from outside to inside are as in Figure 7.

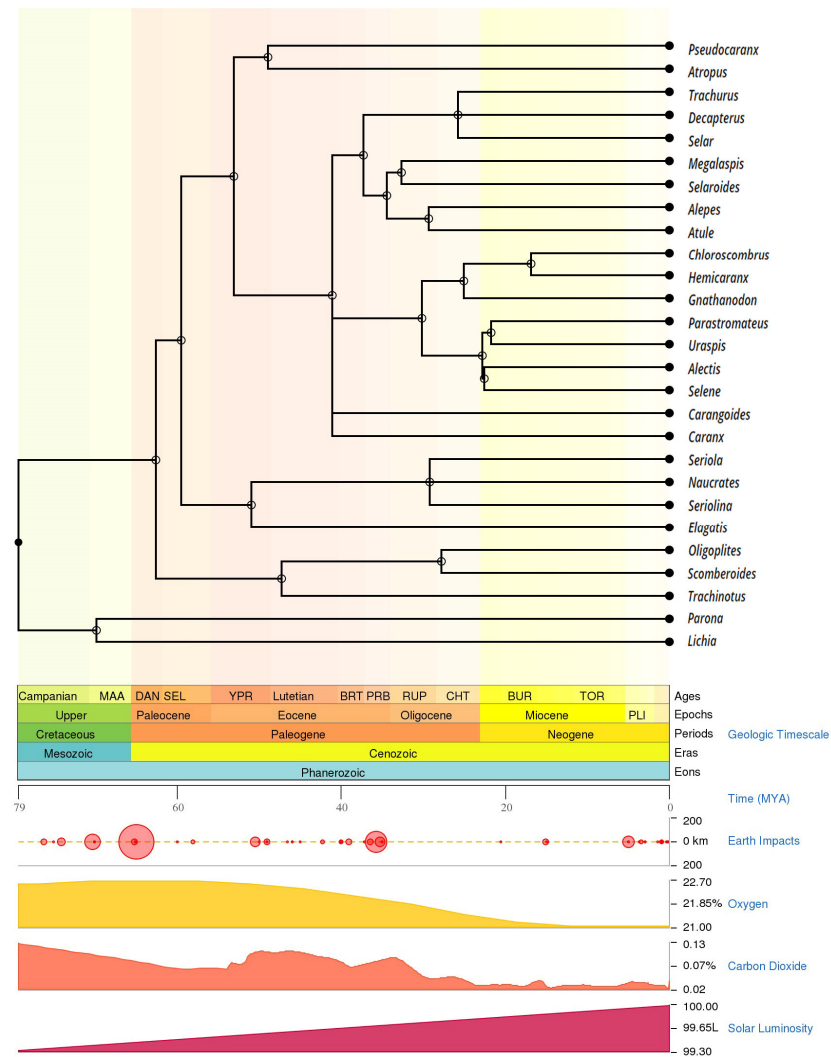


Figure S2. The divergence times of 27 genera of Carangidae generated by the TimeTree database. Changes in environmental parameters during the differentiation of the Carangidae, including earth impacts, changes in the oxygen and carbon dioxide contents, and solar luminosity, are also shown.