



Supplementary Material

Complete Mitochondrial Genome of Three Fish Species (Perciformes: Amblyopinae): Genome Description and Phylogenetic Relationships

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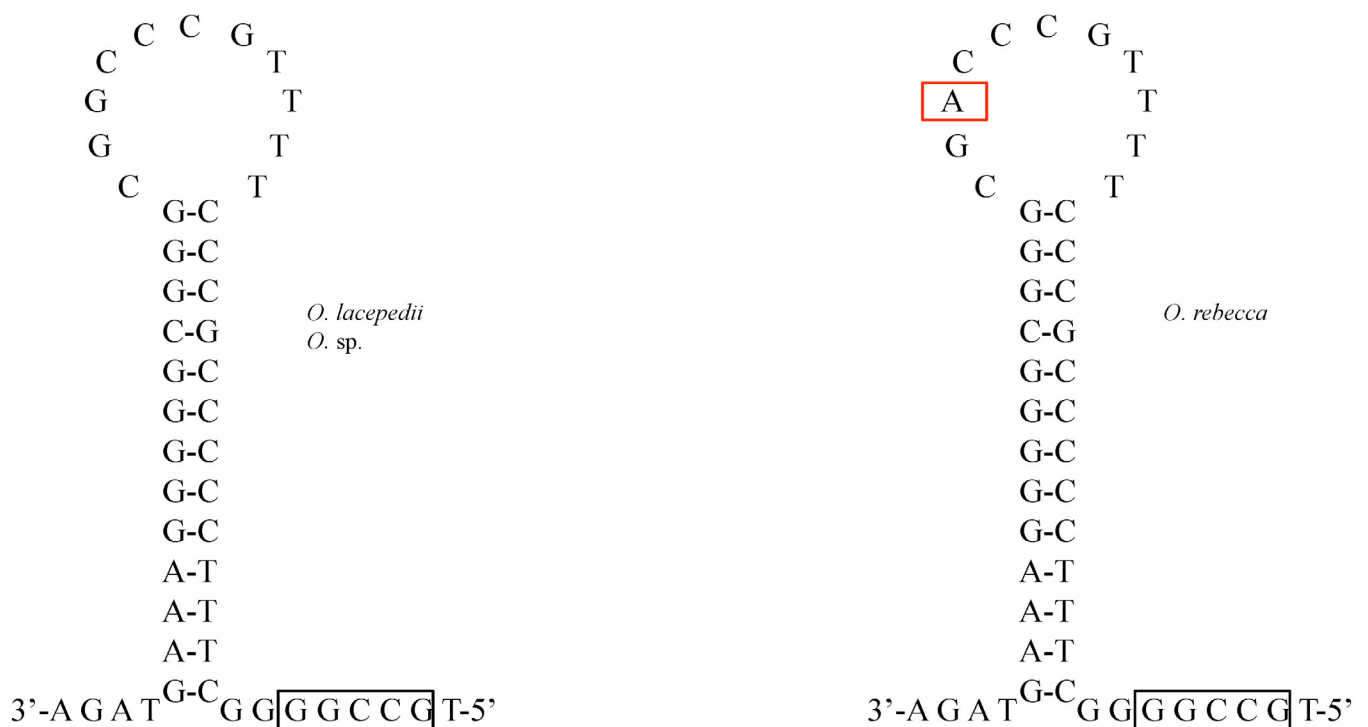


Fig. S1. Proposed the putative stem-loop secondary hairpin structures of O_L regions from *O. lacepedii*, *O. rebecca* and *O. sp.* These sequences are presented as H-strand sequences. The highly conserved sequence motif (GCCCG) found at the base of the stem within tRNA-Cys was associated to the transition from RNA to DNA synthesis which is illustrated by a box.

Supplementary Table S1.- Characteristics of the mitochondrial genome of three gobies.

Gene / Region	<i>O. lacepedii</i>				<i>O. rebecca</i>				<i>O. sp.</i>				Strand
	Position	Codon		Inter-vening spacer	Position	Codon		Inter-vening spacer	Position	Codon		Inter-vening spacer	
		Start	Stop			Start	Stop			Start	Stop		
tRNA ^{Phe}	1-68			0	1-68			0	1-68			0	H
12S rRNA	69-1017			+2	69-1018			+2	69-1017			+2	H
tRNA ^{Val}	1020-1091			0	1021-1092			0	1020-1091			0	H
16S rRNA	1092-2784			0	1093-2787			0	1092-2783			0	H
tRNA ^{Leu(UUR)}	2785-2859			0	2788-2862			0	2784-2858			0	H
ND1	2860-3834	ATG	TAA	+4	2863-3837	ATG	TAA	+4	2859-3833	ATG	TAA	+4	H
tRNA ^{Ile}	3839-3908			-1	3842-3911			-1	3838-3907			-1	H
tRNA ^{Gln}	3908-3978			-1	3911-3981			-1	3907-3977			-1	L
tRNA ^{Met}	3978-4047			0	3981-4050			0	3977-4046			0	H
ND2	4048-5094	ATG	TAA	+1	4051-5097	ATG	TAA	0	4047-5093	ATG	TAA	+1	H
tRNA ^{Trp}	5096-5166			+2	5098-5168			+2	5095-5165			+2	H
tRNA ^{Ala}	5169-5237			+1	5171-5239			+1	5168-5236			+1	L
tRNA ^{Asn}	5239-5311			0	5241-5313			0	5238-5310			0	L
O _L	5312-5346			0	5314-5348			0	5311-5345			0	-
tRNA ^{Cys}	5347-5410			0	5349-5412			0	5346-5409			0	L
tRNA ^{Tyr}	5411-5481			+1	5413-5483			+1	5410-5480			0	L
COI	5483-7045	GTG	AGG	-9	5485-7044	GTG	AGG	-9	5481-7043	GTG	AGG	-9	H
tRNA ^{Ser(UCN)}	7037-7107			0	7036-7106			0	7035-7105			0	L
tRNA ^{Asp}	7108-7179			+2	7107-7178			+2	7106-7177			+2	H
COII	7182-7872	ATG	T--	0	7181-7871	ATG	T--	0	7180-7870	ATG	T--	0	H
tRNA ^{Lys}	7873-7948			+4	7872-7947			+4	7871-7946			+4	H
ATPase8	7953-8120	ATG	TAG	-4	7952-8119	ATG	TAG	-4	7951-8118	ATG	TAG	-4	H
ATPase6	8117-8802	ATA	TA-	-1	8116-8801	ATA	TA-	-1	8115-8800	ATA	TA-	-1	H
COIII	8802-9585	ATG	T--	0	8801-9584	ATG	T--	0	8800-9583	ATG	T--	0	H
tRNA ^{Gly}	9586-656			0	9585-9655			0	9584-9654			0	H
ND3	9657-10005	ATG	T--	0	9656-10004	ATG	T--	0	9655-10003	ATG	T--	0	H
tRNA ^{Arg}	10006-10074			0	10005-10073			0	10004-10072			0	H
ND4L	10075-10371	ATG	TAA	-7	10074-10370	ATG	TAA	-7	10073-10369	ATG	TAA	-7	H
ND4	10365-11745	ATG	T--	0	10364-11744	ATG	T--	0	10363-11743	ATG	T--	0	H
tRNA ^{His}	11746-11814			+1	11745-11813			+1	11744-11812			+1	H
tRNA ^{Ser(AGY)}	11816-11883			+2	11815-11882			+2	11814-11881			+2	H
tRNA ^{Leu(CUN)}	11886-11958			+1	11885-11957			+1	11884-11956			+1	H
ND5	11960-13798	ATG	TAA	-4	11959-13797	ATG	TAA	-4	11958-13796	ATG	TAA	-4	H
ND6	13795-14316	ATG	TAG	0	13794-14315	ATG	TAG	0	13793-14314	ATG	TAA	0	L
tRNA ^{Glu}	14317-14385			+4	14316-14384			+4	14315-14383			+4	L
Cyt <i>b</i>	14390-15530	ATG	T--	0	14389-15529	ATG	T--	0	14388-15528	ATG	T--	0	H
tRNA ^{Thr}	15531-15603			+1	15530-15602			+1	15529-15601			+1	H
tRNA ^{Pro}	15605-15674			0	15604-15673			0	15603-15672			0	L
Control region	15675-17245				15674-17009				15673-17004				H

a: TA and T represent incomplete stop codons; b: Numbers correspond to the nucleotides separating adjacent genes. Negative numbers indicate overlapping nucleotides.

Supplementary Table S2.- Base composition for protein-coding, rRNA, and rRNA genes of three gobies mitogenome (ND6 and eight tRNA genes which were encoded on the L-strand were converted to completely strand sequences.

	<i>O. lacepedtii</i>					<i>O. rebecca</i>					<i>O. sp.</i>							
	T	C	A	G	A+T	Total number	T	C	A	G	A+T	Total number	T	C	A	G	A+T	Total number
Complete genome	27.2	27.4	30.2	15.3	57.4	17245	27.2	27.3	30.2	15.3	57.4	17009	27.2	27.5	29.9	15.4	57.1	17004
ND1	30.0	29.4	26.4	14.1	56.5	972	29.7	29.5	26.9	13.9	56.6	972	29.8	30.0	25.8	14.3	55.7	972
ND2	24.8	33.5	30.8	10.8	55.7	1044	24.1	33.8	31.5	10.5	55.6	1044	24.0	33.9	30.8	11.2	54.9	1044
COI	31.2	24.9	26.0	17.9	57.2	1560	31.0	25.1	26.3	17.6	57.3	1557	31.0	25.1	25.6	18.3	56.6	1560
COII	29.3	26.7	28.4	15.7	57.7	690	29.1	27.0	28.4	15.5	57.5	690	29.6	26.4	28.3	15.8	57.8	690
ATPase8	28.5	25.5	30.3	15.8	58.8	165	29.1	24.2	30.9	15.8	60.0	165	29.7	24.2	29.7	16.4	59.4	165
ATPase6	30.0	30.8	26.8	12.4	56.7	684	31.1	30.0	26.6	12.3	57.7	684	30.3	30.4	26.8	12.6	57.0	684
COIII	28.7	28.2	26.7	16.3	55.4	783	29.1	28.0	26.3	16.6	55.4	783	29.8	27.5	26.6	16.2	56.3	783
ND3	31.9	30.7	22.1	15.2	54.0	348	33.9	28.2	22.7	15.2	56.6	348	32.8	29.9	22.1	15.2	54.9	348
ND4	27.5	29.9	28.5	14.1	56.0	1380	28.1	29.1	29.0	13.8	57.1	1380	27.9	29.8	28.0	14.3	55.9	1380
ND4L	27.6	34.7	24.5	13.3	52.0	294	29.3	33.0	23.5	14.3	52.8	294	27.2	35.4	24.1	13.3	51.4	294
ND5	29.0	29.9	27.9	13.2	56.9	1836	28.4	30.0	28.6	13.0	57.0	1836	29.1	29.7	28.3	12.9	57.4	1836
Cytb	31.4	28.6	25.6	14.4	57.0	1140	32.6	27.4	26.1	13.9	58.7	1140	31.4	28.4	26.1	14.1	57.5	1140
ND6	41.0	12.5	13.3	33.1	54.3	519	41.4	11.6	13.1	33.9	54.5	519	40.5	12.7	13.5	33.3	53.9	519
Protein- coding genes																		
1st	22.0	27.6	26.0	24.6	48.0	3804	22.0	27.5	25.9	24.6	47.9	3802	21.0	27.7	26.9	24.6	47.9	3806
2nd	40.0	27.5	19.2	13.3	59.2	3802	40.0	28.0	19.0	13.1	59.0	3805	40.0	27.5	18.5	14.2	58.5	3803
3rd	28.0	30.1	34.6	7.8	62.6	3809	28.0	28.6	35.6	7.8	63.6	3805	29.0	29.8	34.2	7.2	63.2	3806
Total	29.7	28.4	26.6	15.2	56.3	11415	29.9	28.0	26.9	15.1	56.8	11412	29.8	28.3	26.5	15.3	56.3	11415
rRNA	20.5	25.0	34.6	19.8	54.6	2642	20.3	25.3	34.4	20.0	54.7	2645	20.4	25.0	35.0	19.6	55.4	2641
tRNA	28.8	28.2	26.7	16.3	55.5	1555	25.7	24.2	30.9	19.1	56.6	1555	25.4	24.3	30.9	19.4	56.3	1554
D-loop	31.5	28.6	25.6	14.4	57.1	1571	30.5	20.0	38.0	11.5	68.5	1336	31.2	20.3	37.8	10.7	68.9	1332

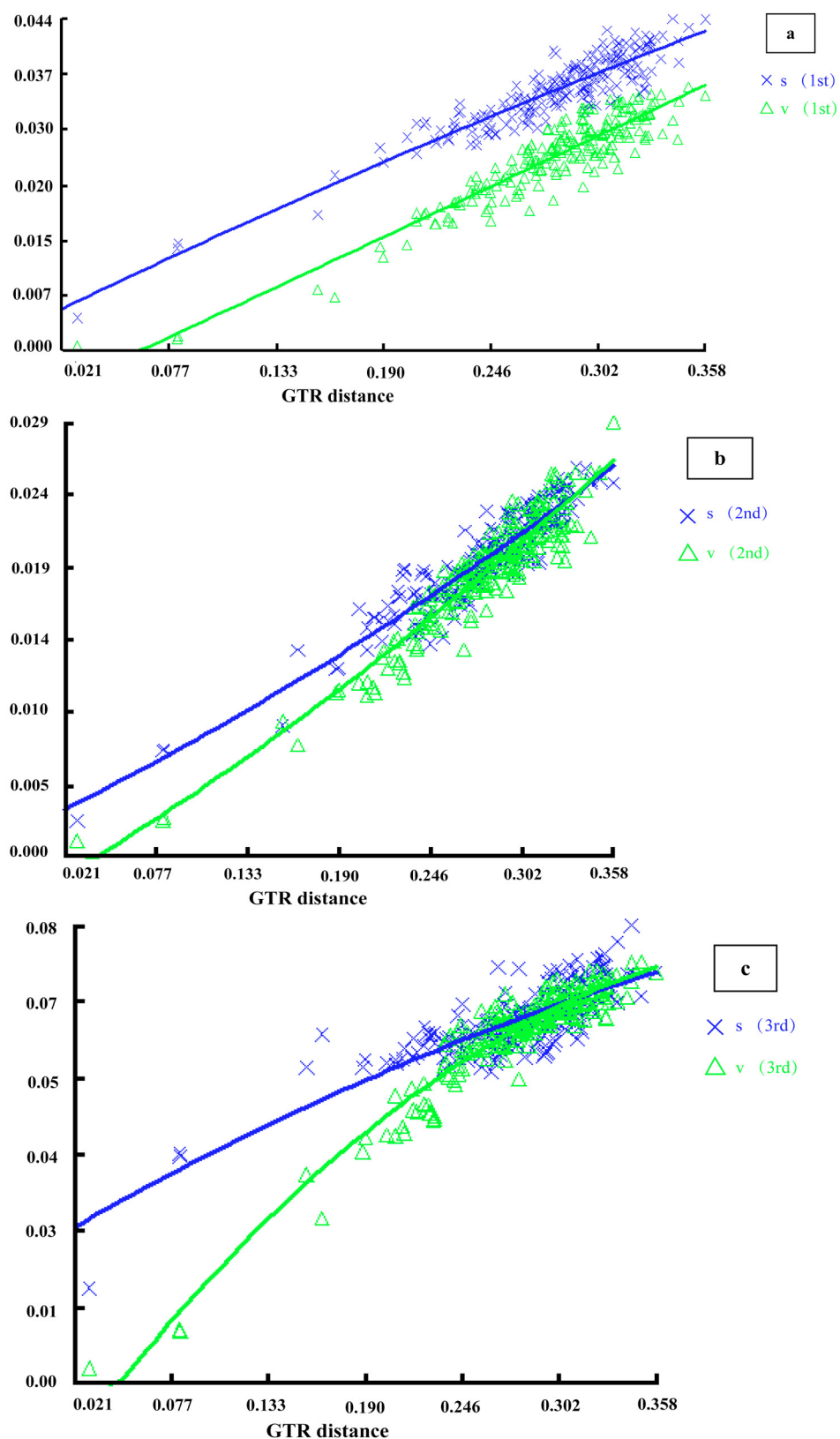


Fig. S2. Saturation plot for the substitutions at the first codon position of protein gene sequences (a). Saturation plot for the substitutions at the second codon position of protein gene sequences (b). Saturation plot for the substitutions at the third codon position of protein gene sequences (c). Values on the x-axis indicate the GTR distance. Number of transition substitution(s) and transversion substitution(s) (v).