

Additional file 1: Table S1. Primers used for fragment amplification of the *G. polyophthalmus* mitogenome.

Forward	Sequence* (5'-3')	Reverse	Sequence (5'-3')
Z15	ATTAAAGCATAACHCTGAAGATGTTAAGAT	F2671	AGATAGAAACTGACCTGGAT
16SAR	CGCCTGTTTATCAAAAACAT	16SBR	CCGGTCTGAACTCAGATCACGT
ZILE	CTTGCCCTGGTTGTATGA	FCOI-70	CCHACYATNCCDGCYCARGCMCCRAA
ZCOI-1295	TNACHTTYTTYCCNCARCAYTTC	FLYS	CACCADTYTYYAGMTYAAAAG
ZATP-6310	ACHTTYACNCCHACHACNCARCTNTC	FND4-865	CCYATGTGVCYNACDGADGAGTADGC
Z10818	TTYGAAGCAGCCGCMTGATACTGACAYTT	F13413	TAGCTGCTACTCGGATTTGCACCAAGAGT
ZND6-210	GCHARNGCNRCHGARTANGCAAA	FCYTB-95	CCNARNARDGANCCRAARTTTCA
FCYTB-065	CGCTAATGACCAACCTGCGAAAG	RND6-065	GTCTTGGGTCTTGTGGCTGTTGCT
FND6-065	GAGCGTCTATGTTGCGCCAAGGT	RZ15-065	CCACTCTTTACGCCGCTTTCTGT

*Information of degenerate bases in the sequences as follows: H = A/C/T, Y=C/T, N=A/C/G/T, D=A /G /T, R=A/G, and M =A/C.

Additional file 2: Table S2. Organization of the *G. polyophthalmus* mitogenome.

Feature	Start	End	Length	IS*	Anti-codon	Start Codon	Stop Codon	Strand
<i>tRNA-Phe (F)</i>	1	68	68	0	GAA			H
<i>12S</i>	69	1018	950	0				H
<i>tRNA-Val (V)</i>	1019	1088	70	0	TAC			H
<i>16S</i>	1089	2787	1699	0				H
<i>tRNA-Leu₁ (L₁)</i>	2788	2860	73	4	TAA			H
<i>ND1</i>	2865	3842	978	2		ATG	TAA	H
<i>tRNA-Ile (I)</i>	3845	3915	71	3	GAT			H
<i>tRNA-Met (M)</i>	3919	3987	69	0	CAT			H
<i>ND2</i>	3988	5037	1050	-1		ATG	TAA	H
<i>tRNA-Trp (W)</i>	5037	5107	71	4	TCA			H
<i>tRNA-Asn (N)</i>	5112	5184	73	-4	GTT			L
<i>O_L</i>	5181	5222	42	2				H
<i>COX1</i>	5225	6778	1554	61		GTG	TAG	H
<i>COX2</i>	6840	7542	703	0		ATG	T	H
<i>tRNA-Lys (K)</i>	7543	7614	72	1	TTT			H
<i>ATP8</i>	7616	7783	168	-10		ATG	TAA	H
<i>ATP6</i>	7774	8457	684	-1		ATG	TAA	H
<i>COX3</i>	8457	9242	786	-1		ATG	TAA	H
<i>tRNA-Gly (G)</i>	9242	9312	71	0	TCC			H
<i>ND3</i>	9313	9663	351	-2		ATG	TAG	H
<i>tRNA-Arg (R)</i>	9662	9730	69	0	TCG			H
<i>ND4L</i>	9731	10027	297	-7		ATG	TAA	H
<i>ND4</i>	10021	11401	1381	0		ATG	T	H
<i>tRNA-His (H)</i>	11402	11471	70	0	GTG			H
<i>tRNA-Ser₂ (S₂)</i>	11472	11538	67	4	GCT			H
<i>tRNA-Leu₂ (L₂)</i>	11543	11615	73	0	TAG			H
<i>ND5</i>	11616	13454	1839	20		ATG	AGG	H
<i>Cytb</i>	13475	14615	1141	0		ATG	T	H
<i>tRNA-Thr (T)</i>	14616	14687	72	0	TGT			H
<i>CR1</i>	14688	15460	773	0				H
<i>tRNA-Gln (Q)</i>	15461	15531	71	1	TTG			L
<i>tRNA-Ala (A)</i>	15533	15601	69	4	TGC			L
<i>tRNA-Cys (C)</i>	15606	15671	66	0	GCA			L
<i>tRNA-Tyr (Y)</i>	15672	15742	71	8	GTA			L
<i>tRNA-Ser₁ (S₁)</i>	15751	15821	71	1	TGA			L
<i>tRNA-Asp (D)</i>	15823	15891	69	4	GTC			H
<i>ND6</i>	15896	16417	522	0		ATG	TAG	L
<i>tRNA-Glu (E)</i>	16418	16485	68	3	TTC			L
<i>tRNA-Pro (P)</i>	16489	16559	71	0	TGG			L
<i>CR2</i>	16560	18170	1611					H

*IS indicates an intergenic spacer that refers to noncoding bases between the feature on

the same line and that on the line below. Negative IS numbers indicate overlaps.

Additional file 3: Figure S1. Gene map of the *G. polyophthalmus* mitogenome.

Additional file 4: Figure S2. Aligned sequences of complete control region in 13 bothids and *Pleuronichthys cornutus*. The shaded blocks represent conserved sequences. TAS is an acronym for the terminal associated sequence. CSB is an acronym for the conserved sequence block. Abbreviations of species names are as in Fig. 3. The number 1 and 2 after the species names indicate CR1 and CR2. The bold sequences in parentheses indicate repeating motifs, and the numbers after these sequences represent the repeat copy number.