

Table S1. Gene or element features of the mitochondrial genomes of *Exostoma tibetanium* and *Exostoma tenuicaudatum*.

Gene	Strand	Location		Size (bp)		Start codon		Stop codon		Anticodon		IGN	
		ti	te	ti	te	ti	te	ti	te	ti	te	ti	te
<i>tRNA-Phe</i>	+	1–69	1–69	69	69					GAA	GAA		
<i>12SrRNA</i>	+	71–1024	71–1025	954	955							1	1
<i>tRNA-Val</i>	+	1025–1096	1026–1097	72	72					TAC	TAC	0	0
<i>16SrRNA</i>	+	1118–2768	1119–2770	1651	1652							21	21
<i>tRNA-Leu¹</i>	+	2767–2841	2769–2843	75	75					TAA	TAA	–2	–2
<i>ND1</i>	+	2844–3815	2847–3818	972	972	ATG	ATG	TAA	TAA			2	3
<i>tRNA-Ile</i>	+	3821–3892	3824–3895	72	72					GAT	GAT	5	5
<i>tRNA-Gln</i>	–	3892–3962	3895–3965	71	71					TTG	TTG	–1	–1
<i>tRNA-Met</i>	+	3962–4032	3965–4035	71	71					CAT	CAT	–1	–1
<i>ND2</i>	+	4033–5079	4039–5085	1047	1047	ATG	ATG	TAG	TAG			0	3
<i>tRNA-Trp</i>	+	5080–5151	5086–5155	72	70					TCA	TCA	0	0
<i>tRNA-Ala</i>	–	5154–5222	5158–5226	69	69					TGC	TGC	2	2
<i>tRNA-Asn</i>	–	5224–5296	5228–5300	73	73					GTT	GTT	1	1
<i>OL</i>	–	5299–5328	5303–5332	30	30							2	2
<i>tRNA-Cys</i>	–	5329–5394	5333–5398	67	67					GCA	GCA	0	0
<i>tRNA-Tyr</i>	–	5395–5465	5399–5469	71	71					GTA	GTA	0	0
<i>COX1</i>	+	5467–7017	5471–7021	1551	1551	GTG	GTG	TAA	TAA			1	1
<i>tRNA-Ser¹</i>	–	7018–7088	7022–7092	71	71					TGA	TGA	0	0
<i>tRNA-Asp</i>	+	7093–7162	7097–7166	70	70					GTC	GTC	4	4
<i>COX2</i>	+	7177–7867	7181–7871	691	691	ATG	ATG	T	T			14	14
<i>tRNA-Lys</i>	+	7868–7942	7872–7946	75	75					TTT	TTT	0	0
<i>ATP8</i>	+	7943–8110	7948–8115	168	168	ATG	ATG	TAA	TAA			0	1
<i>ATP6</i>	+	8101–8784	8106–8789	684	684	ATG	ATG	TAA	TAA			–10	–10
<i>COX3</i>	+	8784–9568	8789–9573	785	785	ATG	ATG	TA	TA			–1	–1
<i>tRNA-Gly</i>	+	9569–9635	9574–9642	67	69					TCC	TCC	0	0
<i>ND3</i>	+	9636–9986	9643–9993	351	351	ATG	ATG	TAG	TAG			0	0
<i>tRNA-Arg</i>	+	9987–10056	9994–10062	70	69					TCG	TCG	0	0
<i>ND4L</i>	+	10057–10353	10063–10359	297	297	ATG	ATG	TAA	TAA			0	0
<i>ND4</i>	+	10347–11727	10353–11733	1381	1381	ATG	ATG	T	T			–7	–7
<i>tRNA-His</i>	+	11728–11797	11734–11803	70	70					GTG	GTG	0	0
<i>tRNA-Ser²</i>	+	11798–11864	11804–11870	67	67					GCT	GCT	0	0
<i>tRNA-Leu²</i>	+	11871–11942	11875–11946	72	72					TAG	TAG	6	4
<i>ND5</i>	+	11943–13769	11947–13773	1827	1827	ATG	ATG	TAA	TAA			0	0
<i>ND6</i>	–	13765–14283	13770–14288	519	519	ATG	ATG	AGA	TAA			–5	–1
<i>tRNA-Glu</i>	–	14284–14352	14289–14357	69	69					TTC	TTC	–3	0
<i>CYTb</i>	+	14355–15492	14360–15497	1138	1138	ATG	ATG	T	T			2	2
<i>tRNA-Thr</i>	+	15493–15564	15498–15569	72	72					TGT	TGT	0	0
<i>tRNA-Pro</i>	–	15563–15632	15568–15637	70	70					TGG	TGG	–2	–2
<i>D-loop</i>	+	15633–16528	15638–16533	896	896							0	0

ti representing *E. tibetanium*; te representing *E. tenuicaudatum*.

Table S2. The codon counts and relative synonymous codon usages (RSCU) in the mitochondrial protein-coding genes of *Exostoma tibetanum* and *Exostoma tenuicaudatum*.

Amino acid	Codon	<i>E. tibetanum</i>		<i>E. tenuicaudatum</i>	
		Count	RSCU	Count	RSCU
<i>Phe</i>	UUU	81	0.75	92	0.85
	UUC	134	1.25	125	1.15
<i>Leu</i> ¹	UUA	98	0.92	83	0.78
	UUG	20	0.19	24	0.23
<i>Leu</i> ²	CUU	64	0.6	59	0.56
	CUC	92	0.86	98	0.92
	CUA	316	2.96	314	2.96
	CUG	51	0.48	58	0.55
<i>Ile</i>	AUU	131	0.93	133	0.92
	AUC	150	1.07	156	1.08
<i>Met</i>	AUA	139	1.54	128	1.44
	AUG	42	0.46	50	0.56
<i>Val</i>	GUU	48	0.96	46	0.92
	GUC	45	0.9	43	0.86
	GUA	78	1.55	86	1.73
	GUG	30	0.6	24	0.48
<i>Ser</i> ¹	UCU	33	0.86	35	0.98
	UCC	69	1.81	68	1.9
	UCA	73	1.91	71	1.98
	UCG	5	0.13	2	0.06
<i>Pro</i>	CCU	25	0.46	21	0.39
	CCC	105	1.94	100	1.84
	CCA	72	1.33	85	1.57
	CCG	14	0.26	11	0.2
<i>Thr</i>	ACU	42	0.5	39	0.45
	ACC	130	1.56	147	1.7
	ACA	145	1.74	147	1.7
	ACG	16	0.19	13	0.15
<i>Ala</i>	GCU	37	0.44	45	0.55
	GCC	174	2.07	151	1.85
	GCA	112	1.33	119	1.46
	GCG	14	0.17	11	0.13
<i>Tyr</i>	UAU	41	0.75	44	0.8
	UAC	68	1.25	66	1.2
<i>His</i>	CAU	26	0.47	22	0.4
	CAC	85	1.53	89	1.6
<i>Gln</i>	CAA	88	1.71	94	1.83
	CAG	15	0.29	9	0.17
<i>Asn</i>	AAU	29	0.48	39	0.6
	AAC	93	1.52	92	1.4
<i>Lys</i>	AAA	77	1.86	76	1.83
	AAG	6	0.14	7	0.17
<i>Asp</i>	GAU	18	0.53	17	0.47
	GAC	50	1.47	55	1.53
<i>Glu</i>	GAA	85	1.67	85	1.72
	GAG	17	0.33	14	0.28

<i>Cys</i>	UGU	11	0.73	6	0.43
	UGC	19	1.27	22	1.57
<i>Trp</i>	UGA	92	1.53	98	1.62
	UGG	28	0.47	23	0.38
<i>Arg</i>	CGU	3	0.17	7	0.39
	CGC	8	0.44	4	0.22
	CGA	53	2.94	53	2.94
	CGG	8	0.44	8	0.44
<i>Ser²</i>	AGU	4	0.1	3	0.08
	AGC	45	1.18	36	1
<i>Gly</i>	GGU	24	0.41	23	0.39
	GGC	76	1.29	71	1.2
	GGA	98	1.66	102	1.72
	GGG	38	0.64	41	0.69

Table S3. The differences of phylogenetic topologies inferred from concatenated protein-coding genes and single protein-coding gene for glyptosternine catfishes via Shimodaira–Hasegawa test.

Gene	Size (bp)	ln <i>L</i>	Diff ln <i>L</i>	<i>P</i> -value
13PCGs	11379	−99899.8	0	0.9638
<i>ND1</i>	972	−119706	19806.228	0.0000
<i>ND2</i>	1044	−103874.9	3975.136	0.0000
<i>COX1</i>	1545	−117950.4	18050.58	0.0000
<i>COX2</i>	690	−106545	6645.191	0.0000
<i>ATP8</i>	165	−126735.7	26835.891	0.0000
<i>ATP6</i>	681	−106094.6	6194.823	0.0000
<i>COX3</i>	783	−109676.5	9776.72	0.0000
<i>ND3</i>	348	−108157.9	8258.074	0.0000
<i>ND4L</i>	294	−116608.9	16709.058	0.0000
<i>ND4</i>	1380	−124910.1	25010.258	0.0000
<i>ND5</i>	1824	−123050.7	23150.907	0.0000
<i>ND6</i>	516	−123570.9	23671.09	0.0000
<i>CYTB</i>	1137	−123448.8	23549.033	0.0000

Table S4. Estimation of dN, dS, and ω values for protein-coding genes of three *Exostoma* species.

genes	<i>Exostoma tibetanum</i>			<i>Exostoma tenuicaudatum</i>			<i>Exostoma gaoligongense</i>		
	dN	dS	ω	dN	dS	ω	dN	dS	ω
<i>ND1</i>	0.0073	0.1699	0.0428	0.0148	0.2955	0.0500	0.0121	0.2630	0.0458
<i>ND2</i>	0.0255	0.2703	0.0944	0.0182	0.2618	0.0696	0.0252	0.2508	0.1004
<i>COX1</i>	0.0000	0.0000	0.0384	0.0000	0.0000	0.0607	0.0027	0.2317	0.0118
<i>COX2</i>	0.0000	0.1621	0.0001	0.0000	0.1660	0.0001	0.0041	0.2689	0.0151
<i>ATP8</i>	0.0238	0.1760	0.1350	0.0262	0.1736	0.1510	0.0711	0.1248	0.5699
<i>ATP6</i>	0.0172	0.1475	0.1164	0.0124	0.2307	0.0538	0.0378	0.2303	0.1640
<i>COX3</i>	0.0062	0.1504	0.0409	0.0095	0.1401	0.0677	0.0135	0.4521	0.0299
<i>ND3</i>	0.0352	0.2381	0.1480	0.0188	0.4230	0.0445	0.0353	0.5198	0.0678
<i>ND4L</i>	0.0169	0.0553	0.3046	0.0107	0.1357	0.0791	0.0206	0.2587	0.0795
<i>ND4</i>	0.0132	0.3067	0.0430	0.0102	0.3062	0.0333	0.0101	0.2691	0.0374
<i>ND5</i>	0.0195	0.2450	0.0797	0.0239	0.2078	0.1149	0.0286	0.2128	0.1343
<i>ND6</i>	0.0165	0.2015	0.0819	0.0227	0.2141	0.1059	0.0371	0.2341	0.1587
<i>CYTB</i>	0.0156	0.1519	0.1027	0.0119	0.3581	0.0333	0.0220	0.3373	0.0653
13 PCGs	0.0132	0.1505	0.0880	0.0128	0.1761	0.0726	0.0189	0.2406	0.0784