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Invertebrate Systematics

Supplementary Material

Multilocus and mitogenomic phylogenetic analyses reveal a new genus and species of freshwater mussel (Bivalvia: Unionidae) from Guangxi, China

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Table S1. List of sequences used in genetic distances.

Species	*COI* GenBank accession number	Locality	Voucher number	Reference
Obovalis omiensis	MT020684	Japan	MHS MPo-okA	Lopes-Lima et al., 2020
Obovalis omiensis	LC518995	Japan: Gifu	Oo14-01 m	Sano et al., 2020
Obovalis omiensis	LC518996	Japan: Kyoto	Oo16-01SUTO	Sano et al., 2020
Obovalis omiensis	LC518997	Japan: Shiga	Oo-u1	Sano et al., 2020
Ptychorhynchus pfisteri	MG463036	China: Jiangxi, Gan River	16_NCU_XPWU_SU127	Huang et al., 2019
Ptychorhynchus pfisteri	MG463034	China: Jiangxi, Gan River	16_NCU_XPWU_SU126	Huang et al., 2019
Ptychorhynchus pfisteri	MG463035	China: Hunan, Xiangyin	16_NCU_XPWU_SU125	Huang et al., 2019
Ptychorhynchus pfisteri	MG933729	Dongting Lake, China	NCUBM 20180243	Wu et al., 2018
Ptychorhynchus pfisteri	MG933730	Dongting Lake, China	NCUBM 20180244	Wu et al., 2018
Ptychorhynchus pfisteri	KY067440	China	personal:Xiaoping Wu:01-PPF-2013	Zhou et al., 2016
Parvasolenaia rivularis	MG463100	China: Jiangxi, Gan River	16_NCU_XPWU_SU189	Huang et al., 2019
Parvasolenaia rivularis	MG463101	China: Jiangxi, Gan River	16_NCU_XPWU_SU190	Huang et al., 2019
Parvasolenaia rivularis	MG463098	China: Jiangxi, Gan River	16_NCU_XPWU_SU191	Huang et al., 2019
Parvasolenaia rivularis	MG463103	China: Jiangxi, Gan River	16_NCU_XPWU_SU192	Huang et al., 2019
Parvasolenaia rivularis	MG463102	China: Jiangxi, Gan River	16_NCU_XPWU_SU193	Huang et al., 2019
Parvasolenaia rivularis	MG463099	China: Jiangxi, Gan River	16_NCU_XPWU_SU194	Huang et al., 2019
Parvasolenaia rivularis	MG463104	China: Jiangxi, Gan River	16_NCU_XPWU_SU195	Huang et al., 2019
Koreosolenaia sitgyensis	MT020682	South Korea	NCSM 113454	Lopes-Lima et al., 2020
Koreosolenaia sitgyensis	MT020683	South Korea	NNIBR IV28172	Lopes-Lima et al., 2020
Postolata guangxiensis	OP009379	China: Guangxi, Guilin, Luo Qing River	22_NCU_XPWU_PGF01	This study
Postolata guangxiensis	OP009380	China: Guangxi, Guilin, Luo Qing River	22_NCU_XPWU_PGF02	This study
Postolata guangxiensis	OP009381	China: Guangxi, Guilin, Luo Qing River	22_NCU_XPWU_PGF03	This study

Species	*COI* GenBank accession number	Locality	Voucher number	Reference
Postolata guangxiensis	OP009382	China: Guangxi, Guilin, Luo Qing River	22_NCU_XPWU_PGM04	This study
Postolata guangxiensis	OP009383	China: Guangxi, Guilin, Luo Qing River	22_NCU_XPWU_PGM05	This study
Postolata guangxiensis	OP009384	China: Guangxi, Guilin, Luo Qing River	22_NCU_XPWU_PGM06	This study
Postolata guangxiensis	OP009385	China: Guangxi, Guilin, Luo Qing River	22_NCU_XPWU_PGM07	This study

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Sano I, Saito T, Miyazaki JI, Shirai A, Uechi T, Kondo T, Chiba S (2020) Evolutionary History and Diversity of Unionoid Mussels (Mollusca: Bivalvia) in the Japanese Archipelago. *Plankton & Benthos Research* **15**(2), 97-111.

Wu RW, Liu YT, Wang S, Liu XJ, Zanatta DT, Roe KJ, Song XL, An CT, Wu XP (2018) Testing the utility of DNA barcodes and a preliminary phylogenetic framework for Chinese freshwater mussels (Bivalvia: Unionidae) from the middle and lower Yangtze River. *PLoS One* **13**(8), e0200956.

Huang XC, Su JH, Ouyang JX, Ouyang S, Zhou CH, Wu XP (2019) Towards a global phylogeny of freshwater mussels (Bivalvia: Unionida): Species delimitation of Chinese taxa, mitochondrial phylogenomics, and diversification patterns. *Molecular Phylogenetics and Evolution* **130**, 45-59.

Zhou CH, Ouyang S, Wu XP, Ding MH (2016) The complete maternal mitochondrial genome of rare Chinese freshwater mussel Lepidodesma languilati (Bivalvia: Unionidae: Unioninae). *Mitochondrial DNA – A. DNA Mapping, Sequencing, and Analysis* **27**(6), 4615-4616.

Table S2. Partitioning strategies for the three-gene dataset (from MEGA X) and the mitogenome dataset (from PartitionFinder2) according to AICc.

Dataset	Subset	Best Model	Partition scheme
three-gene	1	TN93+G+I	COX1_codon1
	2	TN93	COX1_codon2
	3	GTR+ G	COX1_codon3
	4	GTR +G+I	16S
	5	GTR +G+I	28S
mitogenome	1	GTR+I+G	COX2_codon1, ND4L_codon1, ND4_codon1, ND5_codon1, ATP6_codon1, ND3_codon1
	2	GTR+I+G	ND4_codon2, ATP6_codon2, ND4L_codon2, ND3_codon2, ND5_codon2, COX3_codon1, COX2_codon2
	3	GTR+I+G	ATP6_codon3, ND3_codon3, ND5_codon3, ND4_codon3
	4	GTR+I+G	COX1_codon1, COX1_codon2, COX3_codon2
	5	GTR+I+G	COX1_codon3, COX2_codon3, COX3_codon3, ND4L_codon3
	6	SYM+I+G	ND1_codon1, CYTB_codon1
	7	GTR+I+G	ND6_codon2, ND2_codon2, ND1_codon2, CYTB_codon2
	8	GTR+I+G	ND2_codon3, CYTB_codon3, ND6_codon3, ND1_codon3
	9	GTR+I+G	ND6_codon1, ND2_codon1
	10	GTR+I+G	12S, 16S

Table S3. Characteristics of F-type mitochondrial genome of *Postolata guangxiensis.*

Gene	position		Size (bp)	Codon		Anti-codon	Strand
	start	stop		start	stop		
COI	1	1545	1545	TTG	TAA		H
COIII	1568	2347	780	ATG	TAG		H
ATP6	2361	3068	708	ATG	TAG		H
tRNA^{Asp}	3080	3143	64			CUG	H
ATP8	3144	3335	192	GTG	TAG		H
ND4L	3341	3637	297	ATG	TAG		H
ND4	3630	4979	1350	ATT	TAA		H
ND6	5026	5517	492	ATT	TAA		L
tRNA^{Gly}	5518	5578	61			CCU	L
ND1	5586	6482	897	ATC	TAA		L
tRNA^{Leu}	6483	6545	63			AAU	L
tRNA^{Val}	6546	6610	65			CAU	L
tRNA^{Ile}	6613	6676	64			UAG	L
tRNA^{Cys}	6682	6749	68			ACG	L
tRNA^{Gln}	6770	6834	65			GUU	L
ND5	7098	8831	1734	ATG	TAG		H
tRNA^{Phe}	8873	8939	67			AAG	L
Cytb	8953	10101	1149	ATT	TAA		L
tRNA^{Pro}	10102	10166	65			GGU	L
tRNA^{Asn}	10176	10241	66			UUG	L
tRNA^{Leu}	10244	10304	61			GAU	L
rrnL	10305	11602	1298				L
tRNA^{Tyr}	11603	11662	60			AUG	L
tRNA^{Thr}	11667	11731	65			UGU	L
tRNA^{Lys}	11732	11797	66			UUU	L
rrnS	11798	12644	847				L
tRNA^{Arg}	12645	12707	63			GCU	L
tRNA^{Trp}	12714	12777	64			ACU	L
F-*orf*	12815	13075	261	ATC	TAA		L
tRNA^{Glu}	13088	13152	65			CUU	L
tRNA^{Ser}	13162	13225	64			AGU	L
tRNA^{Ala}	13232	13304	73			CGU	L
ND3	13441	13797	357	ATG	TAA		H
tRNA^{Met}	13870	13934	65			UAC	L
ND2	13935	14897	963	ATG	TAA		L
tRNA^{Ser}	14916	14985	70			UCU	L
tRNA^{His}	15098	15160	63			GUG	H
COII	15211	15891	681	ATG	TAG		H

Table S4. Shell measurements of *Postolata guangxiensis*.

Status of specimen	Specimen voucher	Sex	Shell length (mm)	Shell width (mm)	Shell height (mm)
Holotype	22_NCU_XPWU_PGF01	Female	57.32	22.61	38.45
Paratype	22_NCU_XPWU_PGF02	Female	55.30	21.80	35.54
Paratype	22_NCU_XPWU_PGF03	Female	53.55	20.58	35.80
Paratype	22_NCU_XPWU_PGM04	Male	57.55	22.35	37.51
Paratype	22_NCU_XPWU_PGM05	Male	55.87	21.00	37.36
Paratype	22_NCU_XPWU_PGM06	Male	54.24	19.64	34.75
Paratype	22_NCU_XPWU_PGM07	Male	45.99	16.72	29.20
Paratype	22_NCU_XPWU_PGM08	Male	56.39	21.34	35.55
Paratype	22_NCU_XPWU_PGM09	Male	59.44	22.44	39.12
Paratype	22_NCU_XPWU_PGF10	Female	51.51	20.93	31.14
Paratype	22_NCU_XPWU_PGM11	Male	50.13	20.47	32.94
Paratype	22_NCU_XPWU_PGF12	Female	59.35	20.97	35.98
Paratype	22_NCU_XPWU_PGM13	Male	53.87	19.59	34.83
Paratype	22_NCU_XPWU_PGM14	Male	60.82	20.95	40.33
Paratype	22_NCU_XPWU_PGM15	Male	45.31	18.09	28.86
Paratype	22_NCU_XPWU_PGM16	Male	57.05	21.48	38.63
Paratype	22_NCU_XPWU_PGM17	Male	52.73	21.38	36.53
Paratype	22_NCU_XPWU_PGM18	Male	49.43	20.51	32.94

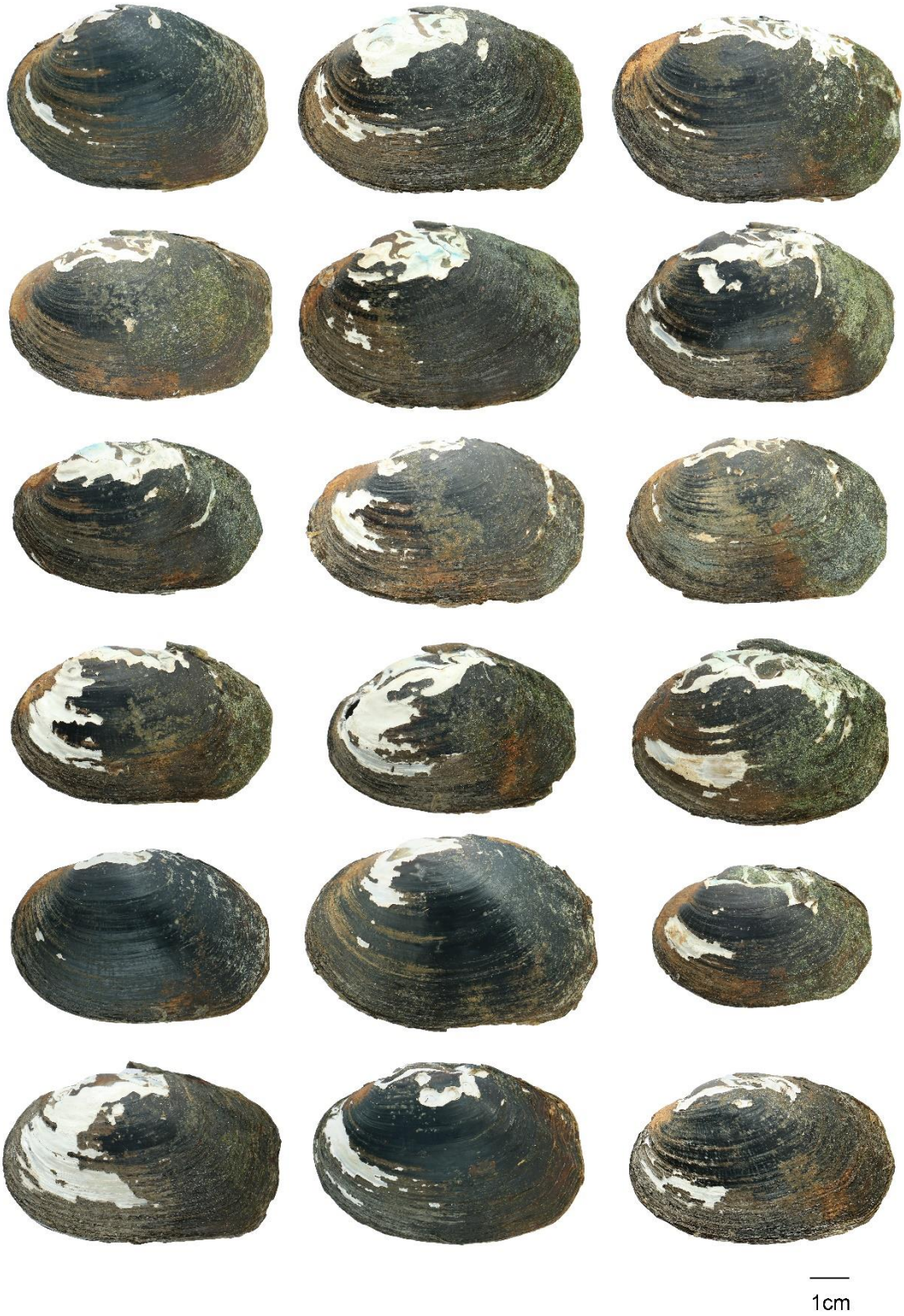

Fig. S1. Eighteen specimens of *Postolata guangxiensis* were collected from Luo Qing River, Guilin city, Guangxi, China.

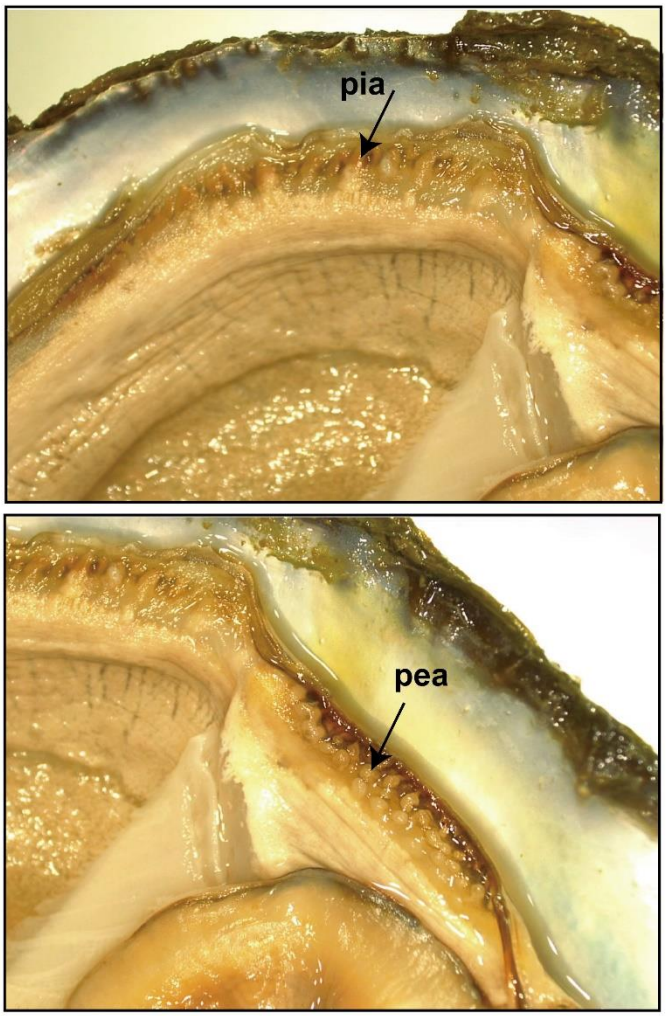

Fig. S2. Papillae of *Postolata guangxiensis*. pia, papillae of the incurrent aperture; pea, papillae of the excurrent aperture.

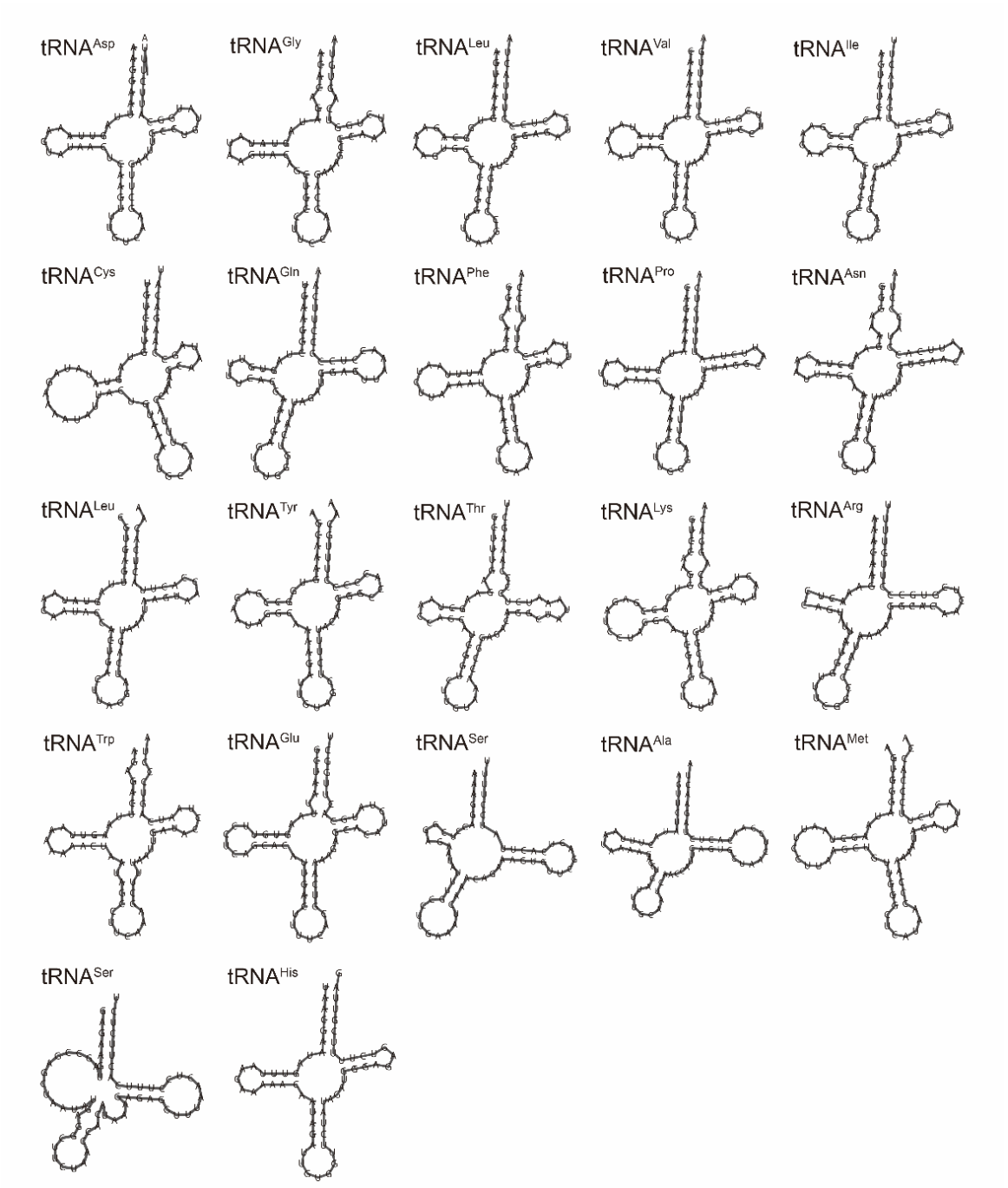

Fig. S3. Inferred secondary structures of 22 tRNA genes in *Postolata guangxiensis*.