



## Supplement

The following supplementary materials are available for this article: Ju, Y.-M., Kuo, P.-H., Wu, J.-H., Hsu, K.-C. 2025 Cryptic diversity of *Rhinogobius rubromaculatus* species complex (Gobiidae) in Taiwan: mitogenomes reveal their evolutionary history. *Taiwania* 70(2): 343-352. doi: 10.6165/tai.2024.70.343

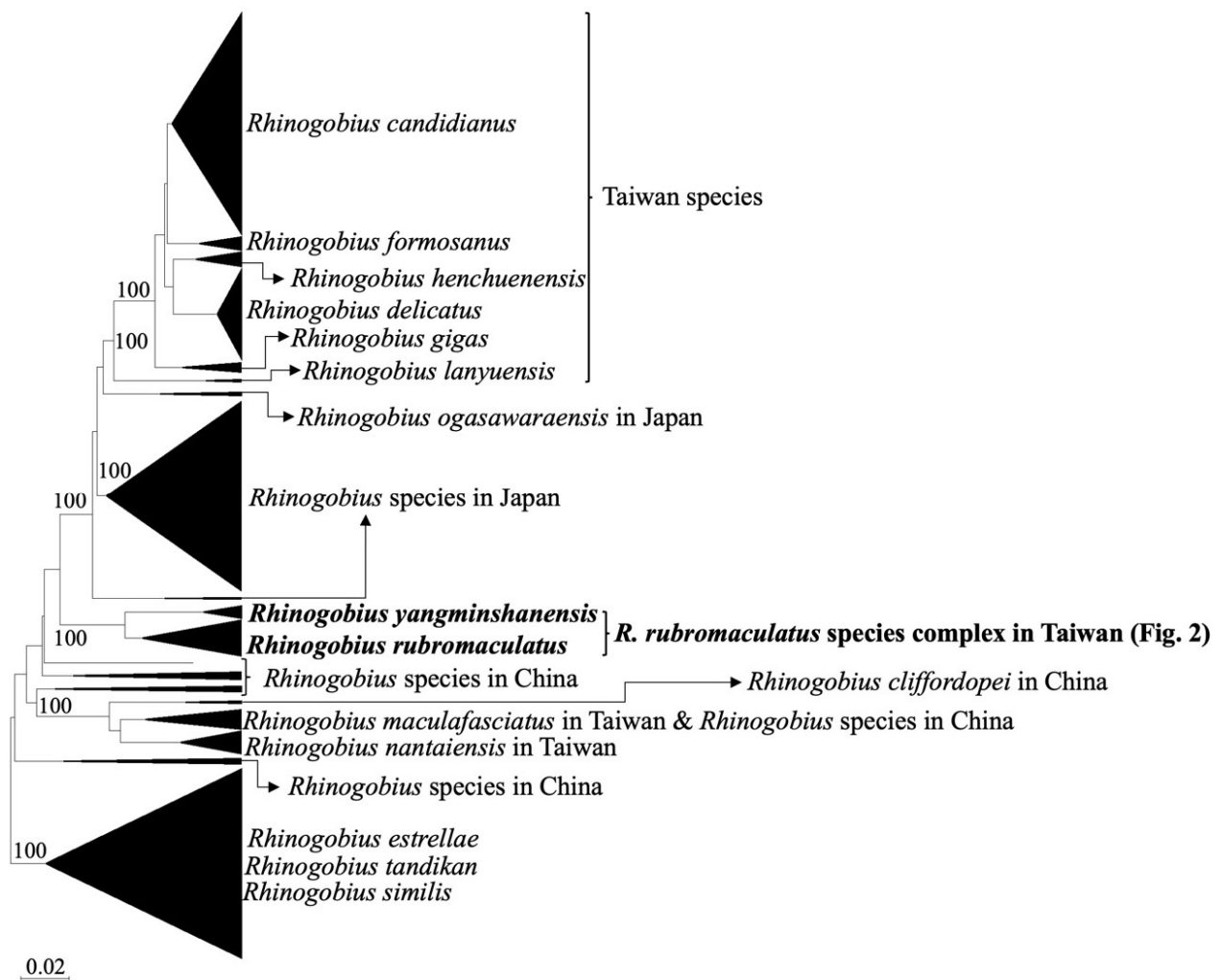
**Table S1.** Characteristics of the four newly determined *Rhinogobius* mitogenomes.

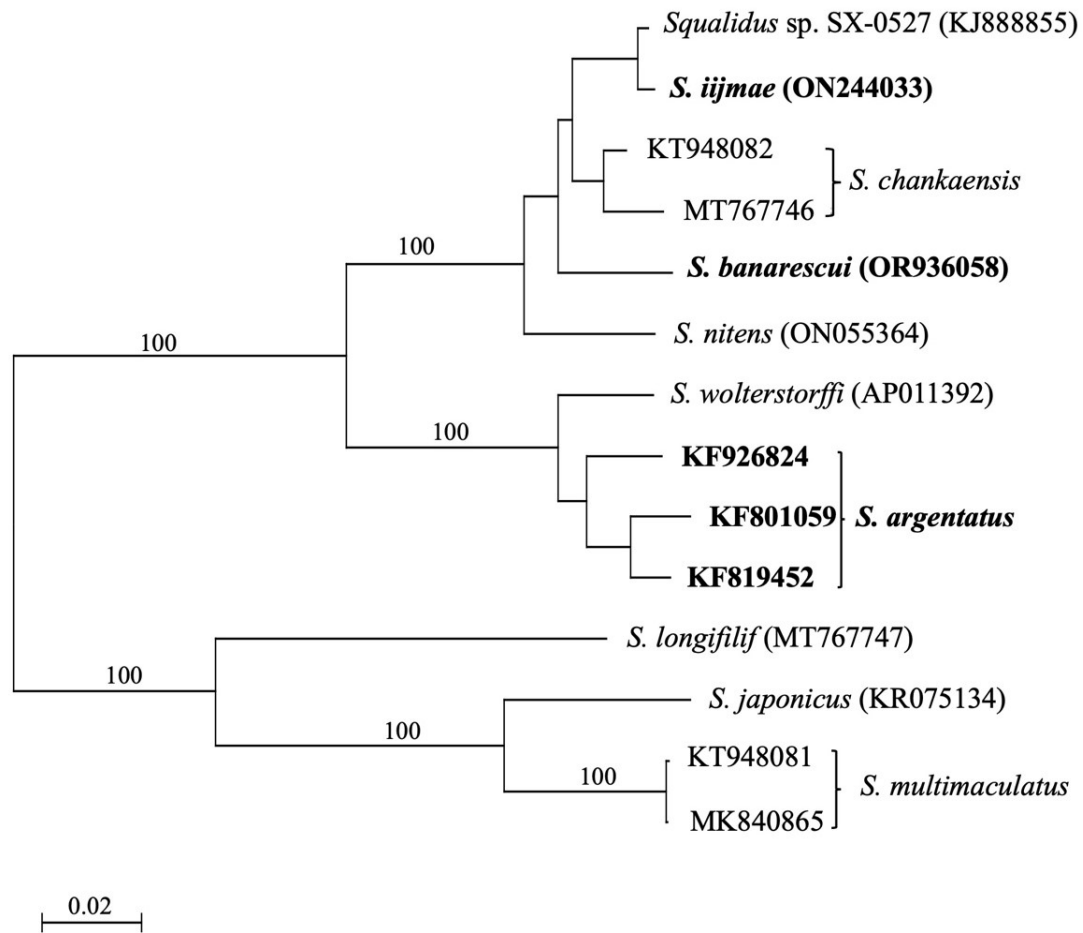
Gene	Position		Codons		Strand	Intergenic nucleotides
	From	To	Start	Stop		
tRNA <sup>Phe</sup>	1/1/1/1	68/68/68/68			H	0/0/0/0
12S rRNA	69/69/69/69	1029/1025/1023/1018			H	0/0/0/0
tRNA <sup>Val</sup>	1030/1026/1024/1019	1101/1097/1095/1090			H	0/0/0/0
16S rRNA	1102/1098/1096/1091	2783/2776/2775/2770			H	0/0/0/0
tRNA <sup>Leu</sup>	2784/2777/2776/2771	2858/2851/2850/2845			H	0/0/0/0
ND1	2859/2852/2851/2846/	3833/3824/3825/3820	ATG	TAA	H	3/3/3/3
tRNA <sup>Ile</sup>	3837/3828/3829/3824	3906/3897/3898/3893			H	-1/-1/-1/-1
tRNA <sup>Gln</sup>	3906/3897/3898/3893	3976/3967/3968/3963			L	-1/-1/-1/-1
tRNA <sup>Met</sup>	3976/3967/3968/3963	4044/4035/4036/4031			H	0/0/0/0
ND2	4045/4036/4037/4032	5091/5082/5083/5078	ATG	TAA	H	1/1/0/2
tRNA <sup>Trp</sup>	5093/5084/5084/5081	5163/5154/5155/5152			H	2/2/2/2
tRNA <sup>Ala</sup>	5166/5157/5158/5155	5235/5226/5227/5223			L	1/1/1/1
tRNA <sup>Asn</sup>	5237/5228/5229/5225	5309/5300/5301/5297			L	0/0/0/0
O <sub>L</sub>	5310/5301/5302/5298	5341/5331/5333/5329			L	0/0/0/0
tRNA <sup>Cys</sup>	5342/5332/5334/5330	5406/5397/5398/5394			L	0/0/0/0
tRNA <sup>Tyr</sup>	5407/5398/5399/5395	5476/5467/5468/5464			L	1/1/1/1
COI	5478/5469/5470/5466	7031/7022/7023/7019	GTG	TAA	H	0/0/0/0
tRNA <sup>Ser</sup>	7032/7023/7024/7020	7102/7093/7094/7090			L	3/3/3/3
tRNA <sup>Asp</sup>	7106/7097/7098/7094	7177/7168/7169/7165			H	2/2/2/2
COII	7180/7171/7172/7168	7870/7861/7862/7858	ATG	TAA	H	0/0/0/0
tRNA <sup>Lys</sup>	7871/7862/7863/7859	7946/7937/7938/7934			H	1/1/1/1
ATP8	7948/7939/7940/7936	8112/8103/8104/8100	ATG	TAA	H	-7/-7/-7/-7
ATP6	8106/8097/8098/8094	8788/8779/8780/8776	ATG	TAA	H	0/0/0/0
COIII	8789/8780/8781/8777	9572/9563/9564/9560	ATG	TAA	H	0/0/0/0
tRNA <sup>Gly</sup>	9573/9564/9565/9561	9643/9634/9635/9631			H	0/0/0/0
ND3	9644/9635/9636/9632	9992/9983/9984/9980	ATG	TAA	H	0/0/0/0
tRNA <sup>Arg</sup>	9993/9984/9985/9981	10061/10052/10053/10047			H	0/0/0/0
ND4L	10062/10054/10054/10048	10358/10349/10350/10346	ATG	TAA	H	-7/-7/-7/-7
ND4	10352/10343/10344/10340	11732/11723/11724/11720	ATG	TAA	H	0/0/0/0
tRNA <sup>His</sup>	11733/11724/11725/11721	11801/11792/11793/11789			H	0/0/0/0
tRNA <sup>Ser</sup>	11802/11793/11794/11790	11869/11860/11861/11857			H	4/4/4/4
tRNA <sup>Leu</sup>	11874/11865/11866/11862	11946/11937/11938/11934			H	0/0/0/0
ND5	11947/11938/11939/11935	13785/13776/13777/13773	ATG	TAA	H	-4/-4/-4/-4
ND6	13782/13773/13774/13770	14303/14294/14295/14291	ATG	TAA	L	0/0/0/0
tRNA <sup>Glu</sup>	14304/14295/14296/14292	14372/14363/14364/14360			L	7/7/7/7
Cyt b	14380/14371/14372/14368	15520/15511/15512/15508	ATG	TAA	H	0/0/0/0
tRNA <sup>Thr</sup>	15521/15512/15513/15509	15592/15583/15584/15580			H	-1/-1/-1/-1
tRNA <sup>Pro</sup>	15592/15583/15584/15580	15661/15652/15653/15649			L	0/0/0/0
d-loop	15662/15653/15654/15650	16506/16497/16496/16492			H	

The order of the four populations in the table is as follows: RY1, RY2, RRa and RRb (Fig. 2).

**Table S2.** Nucleotide compositions of 13 PCGs in lineages RY1, RY2, RRa and RRb (Fig. 2).

	AT%				AT skew				GC skew			
	RY1	RY2	RRa	RRb	RY1	RY2	RRa	RRb	RY1	RY2	RRa	RRb
ND1	51.1	51.3	51.4	50.6	-0.0966	-0.1033	-0.0876	-0.1067	-0.3610	-0.3641	-0.3886	-0.3684
ND2	51.2	51.7	52.8	50.7	-0.0397	-0.0406	-0.0195	-0.0493	-0.4490	-0.4813	-0.5038	-0.4777
COI	52.7	52.9	54.2	52.0	-0.1005	-0.1115	-0.0787	-0.1192	-0.1954	-0.1889	-0.2218	-0.1833
COII	53.3	53.5	54.3	53.1	0.0319	0.0299	0.0491	0.0358	-0.2820	-0.2801	-0.2974	-0.3006
ATP8	54.6	56.0	57.0	52.5	0.0220	0.00679	0.1053	0.0629	-0.4140	-0.5136	-0.5488	-0.4645
ATP6	52.7	51.5	52.1	50.5	-0.0967	-0.1029	-0.0869	-0.0738	-0.1237	-0.4103	-0.4466	-0.4214
COIII	51.7	52.0	52.0	51.1	-0.0730	-0.1135	-0.0506	-0.0802	-0.2868	-0.2776	-0.2949	-0.2693
ND3	49.0	47.9	50.0	49.5	-0.2530	-0.2818	-0.1967	-0.2606	-0.3490	-0.3409	-0.3701	-0.3069
ND4L	47.5	47.1	50.5	45.8	-0.0596	-0.1295	-0.1049	-0.1484	-0.4220	-0.3636	-0.4424	-0.3911
ND4	52.6	52.8	52.5	51.0	-0.0291	-0.0416	-0.0139	-0.0470	-0.3839	-0.3728	-0.3992	-0.3591
ND5	54.0	54.1	55.4	53.6	-0.0203	-0.0246	0.0096	-0.0111	-0.3768	-0.3799	-0.4488	-0.3909
ND6	50.4	48.5	50.6	49.0	-0.4890	-0.4927	-0.5454	-0.5064	-0.4912	-0.1196	-0.5425	-0.4793
Cyt b	52.8	53.2	54.4	53.7	-0.1167	-0.1127	-0.0826	-0.1135	-0.3017	-0.3076	-0.3562	-0.3275

**Fig. S1.** The maximum likelihood tree of the mtDNA cytochrome *b* sequences of *Rhinogobius* species, including all sequences in the present study and GenBank. The number at the nodes are bootstrap values. The most appropriate nucleotide substitution model was TrN (Tamura-Nei).



**Fig. S2.** The maximum likelihood tree of the complete mitogenomes of the genus *Squalidus*. The most appropriate nucleotide substitution model was GTR (General Time Reversible). The number at the nodes are bootstrap values.