Supplementary materials

Table S1 The gene-specific primers in PCR

Gene	Forward primer (5′–3′)	Reverse primer (5′–3′)	Length of PCR products/bp
cox1	5′-GGAACAGGATGAACAGTTTACCCTCC-3′	5′-TCTGAATATCGTCGAGGTATTCC-3′	930
rrnS	5′-GTAAAYCTACTTTGTTACGACTT-3′	5′-GTGCCAGCAAYCGCGGTTATAC-3′	545

Table S2 Organization of *Stenopsocus immaculatus* mitochondrial genome

Gene	Direction	Location	Size	Anticodon	Codon		Intergenic nucleotides
					Start	Stop	
trnI	F	1–66	66	30–32 GAT			
trnM	F	399–464	66	432–434 CAT			332
trnC	R	464–525	62	493–495 GAT			– 1
trnQ	R	557–621	65	590–592 TTG			31
nad2	F	636–1634	999		ATT	TAG	14
trnW	F	1633–1695	63	1663–1665 TCA			– 2
trnY	R	1696–1762	67	1730–1732 GTA			0
cox1	F	1760–3295	1536		ATT	TAA	– 3
trnL2	F	3291–3353	63	3320–3322 TAA			– 5
cox2	F	3355–4041	687		ATG	TAA	1
trnK	F	4043–4108	66	4074–4076 CTT			1
trnD	F	4109–4173	65	4141–4143 GTC			0
atp8	F	4174–4332	159		ATT	TAA	0
atp6	F	4326–5006	681		ATG	TAA	– 7
cox3	F	5006–5789	784		ATG	T-	– 1
trnG	F	5790–5851	62	5820–5822 TCC			0
trnA	F	5855–5921	64	5884–5886 TGC			3
trnR	F	5921–5985	65	5949–5951 TCG			– 1
trnF	R	5982–6046	65	6013–6015 GAA			– 4
nad5	R	6047–7763	1717		ATT	T-	0
nad3	F	7794–8150	357		ATA	TAA	30
trnN	F	8153–8217	65	8183–8185 GTT			2
trnE	F	8222–8286	65	8253–8255 TTC			4
trnS1	F	8284–8346	63	8316–8318 TCT			– 3
trnH	R	8356–8417	69	8385–8387 GTG			9
nad4	R	8418–9755	1338		ATG	TAA	0
nad4L	R	9749–10039	291		ATT	TAA	– 7
trnT	F	10041–10103	63	10072–10074 TGT			1
trnP	R	10103–10165	63	10133–10135 TGG			– 1
nad6	F	10167–10673	507		ATT	TAA	1
cytb	F	10673–11815	1143		ATG	TAA	– 1
trnS2	F	11814–11882	69	11845–11847 TGA			– 2
nad1	R	11905–12834	930		ATA	TAA	22
trnL1	R	12850–12910	61	12879–12881 TAG			15
rrnL	R	12911–14142	1232				0
trnV	R	14143–14207	65	14175–14177 TAC			0
rrnS	R	14208–14971	764				0
control region		14972–16691	1720				0

Note: A minus intergenic nucleotide means an overlap.

Table S3 Codon usage of *Stenopsocus immaculatus* mitochondrial genome

Amino acid	Codon	Total	RSCU	Amino acid	Codon	Total	RSCU
Phe	UUU (F)	249	1.86	Ser	UCU (S)	101	3.17
	UUC (F)	18	0.14		UCC (S)	10	0.31
Leu	UUA (L)	328	4.49	Ser(s)	UCA (S)	49	1.55
	UUG (L)	37	0.5		UCG (S)	2	0.05
	CUU (L)	40	0.55		AGU (S)	27	0.84
	CUC (L)	3	0.03		AGC (S)	3	0.08
	CUA (L)	28	0.38		AGA (S)	81	3.8
	CUG (L)	3	0.05		AGG (S)	7	0.31
Ile	AUU (I)	314	1.88	Thr	ACU (T)	75	1.82
	AUC (I)	15	0.09		ACC (T)	9	0.22
Met	AUA (M)	173	1.03		ACA (T)	76	1.84
	AUG (M)	16	1		ACG (T)	5	0.12
Val	GUU (V)	88	2.2	Ala	GCU (A)	77	2.42
	GUC (V)	6	0.15		GCC (A)	8	0.26
	GUA (V)	58	1.43		GCA (A)	38	1.21
	GUG (V)	9	0.23		GCG (A)	3	0.11
Tyr	UAU (Y)	116	1.63	Cys	UGU (C)	24	1.71
	UAC (Y)	27	0.37		UGC (C)	4	0.29
Stop	UAA (*)	8	0.33	Trp	UGA (W)	60	2.63
	UAG (*)	1	0.04		UGG (W)	16	1
His	CAU (H)	48	1.7	Arg	CGU (R)	14	0.67
	CAC (H)	8	0.3		CGC (R)	1	0.04
Gln	CAA (Q)	54	1.94		CGA (R)	18	0.86
	CAG (Q)	2	0.06		CGG (R)	7	0.31
Asn	AAU (N)	155	1.76	Pro	CCU (P)	60	2.4
	AAC (N)	21	0.24		CCC (P)	6	0.23
Lys	AAA (K)	78	1.83		CCA (P)	34	1.37
	AAG (K)	8	0.17		CCG (P)	0	0
Asp	GAU (D)	38	1.67	Gly	GGU (G)	46	1.14
	GAC (D)	8	0.33		GGC (G)	5	0.12
Glu	GAA (E)	56	1.79		GGA (G)	64	1.6
	GAG (E)	7	0.21		GGG (G)	46	1.14

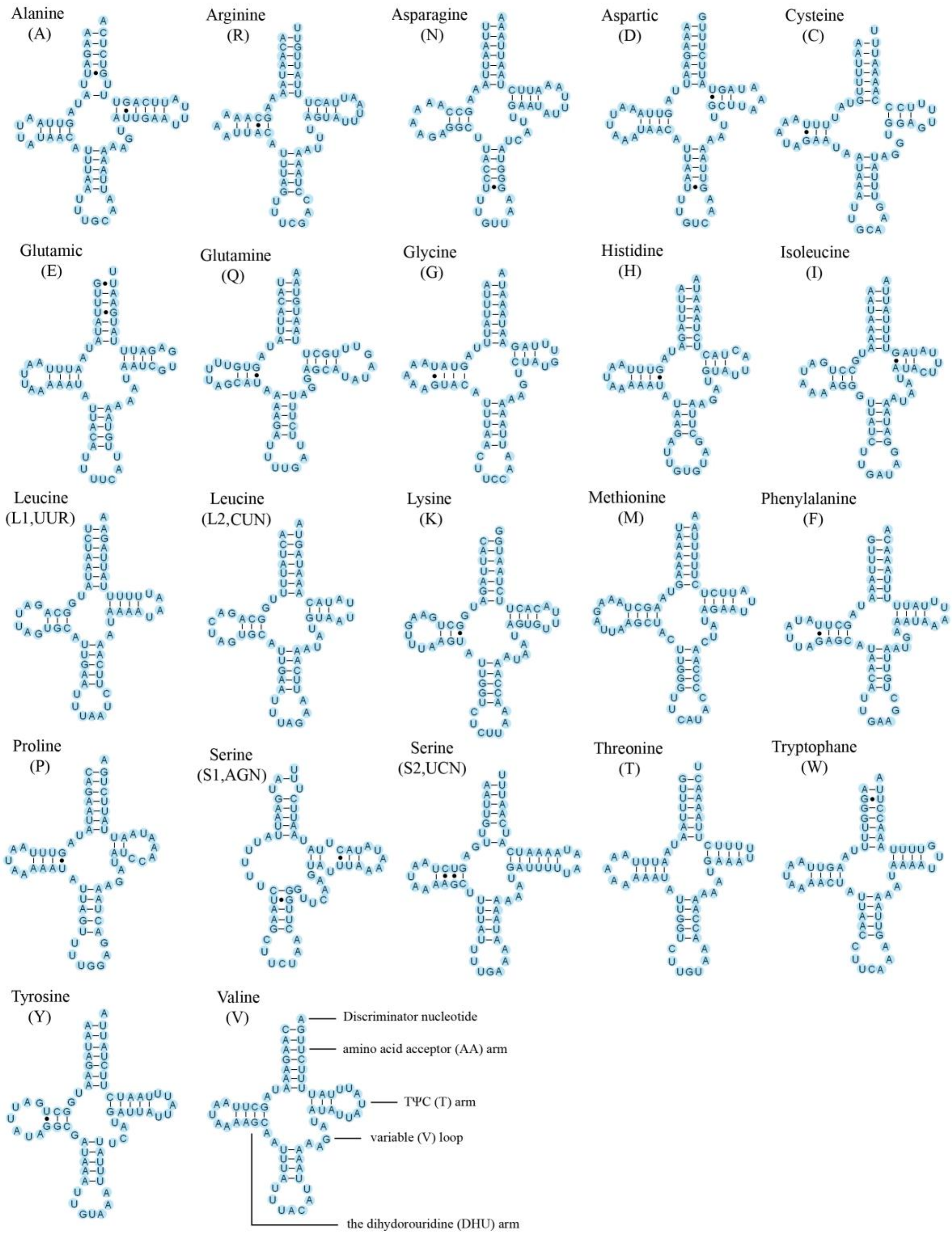

Fig. S1 Inferred secondary structure of the mitochondrial tRNAs of the narrow barklice *Stenopsocus immaculatus*. tRNAs are labeled with the abbreviations of their corresponding amino acids. Lines indicate Watson-Crick bonds; dots indicate GU or other non-classical pairs.