Table 1. Organization of the complete mitochondrial genome of *G. olivaceus*.

Gene	Position		Size (bp)		Codon		Intergenic nucleotide[a]	Strand
	From	To	Nucleotide	Amino acid	Initiation	stop[b]		
tRNA^{Phe}	1	68	68					H
12S rRNA	69	1017	949					H
tRNA^{Val}	1018	1088	71				1	H
16S rRNA	1090	2767	1678					H
tRNA^{Leu}(UUR)	2768	2842	75					H
ND1	2843	3817	975	324	ATG	TAA	3	H
tRNA^{Ile}	3821	3890	70				-1	H
tRNA^{Gln}	3890	3960	71				-1	L
tRNA^{Met}	3960	4028	69					H
ND2	4029	5078	1050	349	ATG	TAG	-2	H
tRNA^{Trp}	5077	5148	72				2	H
tRNA^{Ala}	5151	5219	69				2	L
tRNA^{Asn}	5222	5294	73				37	L
tRNA^{Cys}	5332	5399	68					L
tRNA^{Tyr}	5400	5470	71				1	L
COI	5472	7025	1554	517	GTG	TAA		H
tRNA^{Ser}(UCN)	7026	7096	71				3	L
tRNA^{Asp}	7100	7171	72				5	H
COII	7177	7867	691	230	ATG	T--		H
tRNA^{Lys}	7868	7943	76				1	H
ATPase8	7945	8112	168	55	ATG	TAA	-10	H
ATPase6	8103	8786	684	227	ATG	TAA	2	H
COIII	8789	9573	785	261	ATG	TA-	-1	H
tRNA^{Gly}	9573	9645	73					H
ND3	9646	9996	351	116	ATG	TAG	-2	H
tRNA^{Arg}	9995	10063	69					H
ND4L	10064	10360	297	98	ATG	TAA	-7	H
ND4	10354	11736	1383	460	GTG	TAG	-1	H
tRNA^{His}	11736	11804	69					H
tRNA^{Ser}(AGY)	11805	11872	68				1	H
tRNA^{Leu}(CUN)	11874	11946	73					H
ND5	11947	13785	1839	612	ATG	TAG	-4	H
ND6	13782	14303	522	173	ATG	TAA		L
tRNA^{Glu}	14304	14372	69				5	L
Cytb	14378	15518	1141	380	ATG	T--		H
tRNA^{Thr}	15519	15590	72					H
tRNA^{Pro}	15591	15661	71					L
Control Region	15662	16568	907					H

a Numbers correspond to the nucleotides separating adjacent genes. Negative number indicates overlapping nucleotides. b TA and T represent incomplete stop codons.

Table 2. Base composition of *G. olivaceus* mitochonondrial genome.

Gene/region	Base composition (%)				
	T	C	A	G	A+T
1st	21.73	27.19	25.12	15.96	46.85
2nd	40.46	27.81	18.05	13.67	58.51
3rd	21.52	36.66	30.26	11.56	51.78
Total	27.91	30.55	24.48	17.06	52.39
tRNA	23.53	26.22	29.94	20.32	53.47
sRNA	20.06	26.15	32.43	21.36	52.49
control region	31.09	22.93	29.77	16.21	60.86
overall	25.65	29.82	27.17	17.36	52.82