

GENE	START CODON	START LOC	STOP CODON	STOP LOC	LENGTH (bps)				
nad5	atg	0	taa	3551	3551				
nad1	atg	966	tag	1949	984				
nad3	atg	1959	taa	2315	357				
trnW(tga)		3573		3642					
nad2	atg	4009	tag	5148	1140				
12s		5327		6319	993				
cox2	atg	6366	tag	7115	750				
nad4	atg	7182	taa	8657	1476				
nad6	ata (ttg?)	8750	taa	9310	561				
cytb	atg	9356	tag	10493	1138(?)				
trnM(atg)		10623		10693					
16s		11166		12867	1702				
cox3	atg	12950	taa	13738	789				
cox1_a	ata	13782	tag	14578	797				
cox1_b		15505		16354	850				
nad4l	atg	16412	taa	16711	300				
atp8	atg	16747	tag	16959	213				
atp6	atg	17000	taa	17698	699				

Title: *R. daphneae* gene table

Caption: List of the start and stop codons, start and stop loci, and lengths of each of the 13 protein-coding genes used in our analysis of *Relicanthus daphneae*.

```

      g
    a-t
    g-c
    g-c
    a-t
    g-c
    g-c
    t.t      tg
      t      cacc a
aa      a      !!!!! a
a  tcgg      gtggg c
g  + !!      t      tt
t  gacc      g
  a      g      a
      t-aa
      t-a
      a-t
      g-c
      t-a
      c      a
      t      a
      tca

```

```

      c
      a-t
      t+g
      t-a
      g.a
      c-g
      a-t
      t-a          tg
cg      ggcgc  a
gc      !ll+l  t
t        ccggg  t
c        c      gt
gt       a
ca       a
      g-ccc
      t-a
      t+g
      c-g
      g-c
      t-a
      g  a
      t  a
      gtg

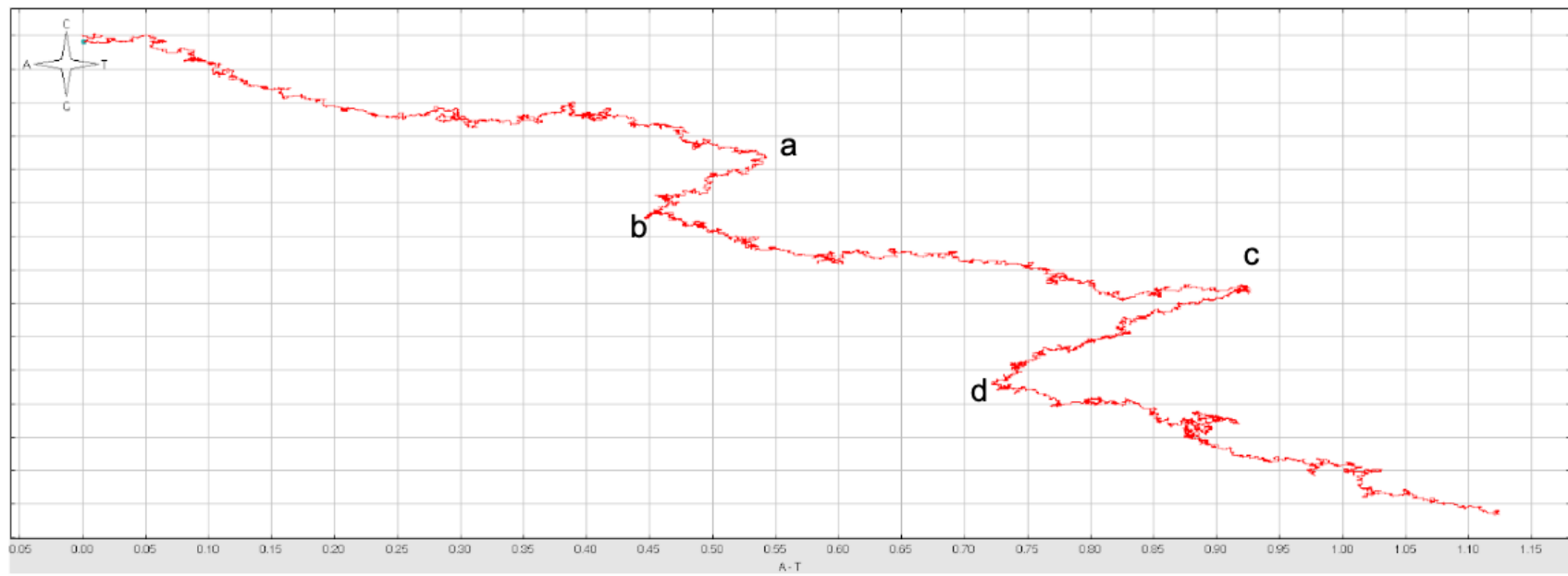
```

```

a
g-c
t-a
a-t
g-c
a-t
g-c          tc
t      cgtcc a
aa      a      !+!!! a
c  tcag      gtagg c
g  !!!!      t      tt
g  agtc      a
ta      a      a
c-gt
c-g
a-t
g-c
a-t
c      a
t      g
cat

```

Caption: Display of all three tRNA structures identified in the mitogenome of *Relicanthus*.



- a. 5187 (nad2 ~ 12S)
- b. 6303 (12S ~ cox2)
- c. 11387 (mid 16S)
- d. 14563 (mid cox1)

Title: *R. daphneae* DNA walk

Caption: The DNA walk visualizes the A/T (x-axis) and G/C (y-axis) skew along the Relicanthus mitogenome.

Title: Maximum composite likelihood analysis on *Relicanthus* and actinurians

Caption: A maximum composite likelihood analysis was used to generate pairwise distance scores between all actinurian taxa and *Relicanthus*. Scores generated from comparisons between *Relicanthus* and actinurians are highlighted in yellow.

Title: Table of acridian species included in this study, including *Relicantia*

Caption: List of taxonomic, GenBank accession, voucher location, and gene loci information for taxa included in this study. Abbreviations: AMNH, American Museum of Natural History; FMNH, Field Museum of Natural History; NMNH, National Museum of Natural History. (1), (2), and (3), for information for these taxa see Emblem et al. (2014), Fox et al. (2015), Chi and Johansen (2017), respectively; (4) Unpublished research, only GenBank accession number and information available.