

Mitochondrial genetic variation reveals phylogeographic structure and cryptic diversity in *Trioza erytreae*

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Supplementary tables

Table S1. List of the 13 complete mitochondrial sequences used in the phylogenetic reconstruction of the family Triozidae (Hemiptera) with common name, broad geographic distribution, GenBank accession number and bibliographic reference. *Aphis gossypii* and *Schizaphis graminum* (Hemiptera: Aphididae) were used as outgroups.

Species	Family	Distribution	Common name	GenBank	Reference	Size (bp)
<i>Aacanthocnema dobsoni</i>	Triozidae	Australia	-	NC_038132.1	Percy et al 2018	15,179
<i>Bactericera cockerelli</i>	Triozidae	North America, Central America, Oceania	Potato psyllid	NC_030055	Wu et al 2016	15,220
<i>Leptynoptera sulfureae</i>	Triozidae	Cocos (Keeling Islands, Indian Ocean Islands)	-	NC_038136.1	Percy et al 2018	14,825
<i>Paratrioza sinica</i>	Triozidae	Asia	-	NC_024577	Zhang et al 2014	14,863
<i>Pariaconus pele</i>	Triozidae	Hawaiian islands	-	NC_038138.1	Percy et al 2018	15,080
<i>Trioza anthrisci</i>	Triozidae	Iceland, Nordic countries	-	NC_038141.1	Percy et al 2018	14,918
<i>Trioza erytreae</i> (Uganda)	Triozidae	Africa, Asia, Europe	African citrus triozid	MT416549	This study	15,095
<i>Trioza erytreae</i> (South Africa)	Triozidae	Africa, Asia, Europe	African citrus triozid	MT416550	This study	15,098
<i>Trioza erytreae</i> (Ethiopia)	Triozidae	Africa, Asia, Europe	African citrus triozid	MT416551	This study	15,095
<i>Trioza remota</i>	Triozidae	Europe	-	NC_038143.1	Percy et al 2018	14,950
<i>Trioza urticae</i>	Triozidae	Europe	-	NC_038113.1	Percy et al 2018	15,185
<i>Aphis gossypii</i>	Aphididae	Asia, Africa, North America, Central America, South	Cotton aphid	NC_024581	Zhang et al 2014	15,869
<i>Schizaphis graminum</i>	Aphididae	Asia, Africa, North America, Central America, South	Wheat aphid	NC_006158	Thao et al 2004	15,721

Table S2. Nucleotide composition of the complete mitochondrial sequence of three *Trioza erytreae* specimens collected in Ethiopia, Uganda, and South Africa. AT-skew = (A - T)/(A + T); CG-skew = (G - C)/(G + C).

<i>Trioza erytreae</i> Ethiopia										
Region	A%	C%	G%	T%	A+T%	G+C%	AT-skew	GC-skew	bp	% (size)
COI	32.8	12.1	12.3	42.8	75.6	24.4	-0.13	0.01	1533	10.16
COII	36.6	14.0	9.8	39.6	76.2	23.8	-0.04	-0.18	664	4.40
ATP8	47.1	10.5	3.9	38.6	85.7	14.4	0.10	-0.46	153	1.01
ATP6	38.4	12.0	7.7	41.9	80.3	19.7	-0.04	-0.22	675	4.47
COIII	36.5	11.1	9.2	43.2	79.7	20.3	-0.08	-0.09	783	5.19
ND3	40.5	9.7	7.7	42.2	82.7	17.4	-0.02	-0.11	351	2.33
ND5	45.4	11.8	8.6	34.2	79.6	20.4	0.14	-0.16	1618	10.72
ND4	45.5	13.3	7.5	33.8	79.3	20.8	0.15	-0.28	1245	8.25
ND4L	51.4	10.8	5.9	31.9	83.3	16.7	0.23	-0.29	288	1.91
ND6	37.5	9.6	6.7	46.3	83.8	16.3	-0.11	-0.18	480	3.18
CYTB	33.9	12.4	9.6	44.0	77.9	22.0	-0.13	-0.13	1143	7.57
ND1	49.3	12.3	8.5	29.8	79.1	20.8	0.25	-0.18	918	6.08
16s rRNA	41.1	13.9	6.2	38.8	79.9	20.1	0.03	-0.38	1146	7.59
12s rRNA	39.3	12.8	7.9	40.0	79.3	20.7	-0.01	-0.24	685	4.54
ND2	37.6	10.5	6.5	45.4	83.0	17.0	-0.09	-0.24	969	6.42
PCGs	40.1	11.9	8.7	39.3	79.4	20.6	0.01	-0.16	10820	71.68
tRNAs	41.5	11.6	9.4	37.5	79.0	21.0	0.05	-0.10	1365	9.04
rRNAs	40.4	13.5	6.8	39.3	79.7	20.3	0.01	-0.33	1831	12.13
AT-rich region	44.7	6.1	5.1	44.0	88.7	11.2	0.01	-0.09	993	6.58
Complete mtDNA	40.6	11.7	8.3	39.4	80.0	20.0	0.02	-0.17	15095	100.00
<i>Trioza erytreae</i> South Africa										
Region	A%	C%	G%	T%	A+T%	G+C%	AT-skew	GC-skew	bp	% (size)
COI	32.9	12.2	12.4	42.5	75.4	24.6	-0.13	0.01	1533	10.16
COII	37.2	13.1	9.8	39.8	77.0	22.9	-0.03	-0.14	664	4.40
ATP8	48.4	9.2	2.0	40.5	88.9	11.2	0.09	-0.64	153	1.01
ATP6	38.5	12.0	7.6	41.9	80.4	19.6	-0.04	-0.22	675	4.47
COIII	36.4	10.9	9.3	43.4	79.8	20.2	-0.09	-0.08	783	5.19
ND3	40.5	9.1	8.0	42.5	83.0	17.1	-0.02	-0.06	351	2.33
ND5	45.4	11.4	8.3	34.8	80.2	19.7	0.13	-0.16	1618	10.72
ND4	45.4	13.2	7.6	33.8	79.2	20.8	0.15	-0.27	1245	8.25
ND4L	52.1	11.5	5.6	30.9	83.0	17.1	0.26	-0.35	288	1.91
ND6	37.1	9.8	6.9	46.3	83.4	16.7	-0.11	-0.17	480	3.18
CYTB	33.5	13.0	10.0	43.4	76.9	23.0	-0.13	-0.13	1143	7.57
ND1	49.3	12.5	8.3	29.9	79.2	20.8	0.24	-0.20	923	6.11
16s rRNA	41.0	13.7	6.1	39.2	80.2	19.8	0.02	-0.38	1148	7.61
12s rRNA	39.4	12.8	7.7	40.0	79.4	20.5	-0.01	-0.25	685	4.54
ND2	38.0	10.6	6.1	45.3	83.3	16.7	-0.09	-0.27	969	6.42
PCGs	40.1	11.8	8.7	39.3	79.4	20.5	0.01	-0.15	10825	71.71
tRNAs	41.3	11.4	9.5	37.9	79.2	20.9	0.04	-0.09	1365	9.04
rRNAs	40.4	13.4	6.7	39.5	79.9	20.1	0.01	-0.33	1831	12.13
AT-rich region	44.6	5.8	5.8	43.8	88.4	11.6	0.01	0.00	993	6.58
Complete mtDNA	40.6	11.6	8.3	39.5	80.1	19.9	0.01	-0.17	15095	100.00
<i>Trioza erytreae</i> Uganda										
Region	A%	C%	G%	T%	A+T%	G+C%	AT-skew	GC-skew	bp	% (size)
COI	32.8	12.1	12.3	42.8	75.6	24.4	-0.13	0.01	1533	10.16
COII	36.4	14.0	9.9	39.6	76.0	23.9	-0.04	-0.17	664	4.40
ATP8	47.1	10.5	3.9	38.6	85.7	14.4	0.10	-0.46	153	1.01
ATP6	38.7	12.0	7.4	41.9	80.6	19.4	-0.04	-0.24	675	4.47
COIII	36.5	11.0	9.2	43.2	79.7	20.2	-0.08	-0.09	783	5.19
ND3	40.5	9.7	7.7	42.2	82.7	17.4	-0.02	-0.11	351	2.33
ND5	45.4	11.8	8.7	34.2	79.6	20.5	0.14	-0.15	1618	10.72
ND4	45.5	13.3	7.5	33.7	79.2	20.8	0.15	-0.28	1245	8.25
ND4L	51.1	10.6	6.4	31.9	83.0	17.0	0.23	-0.25	288	1.91
ND6	37.5	9.6	6.7	46.3	83.8	16.3	-0.11	-0.18	480	3.18
CYTB	33.9	12.5	9.6	43.9	77.8	22.1	-0.13	-0.13	1143	7.57
ND1	49.0	12.2	8.8	30.0	79.0	21.0	0.24	-0.16	923	6.11
16s rRNA	41.0	13.9	6.3	38.8	79.8	20.2	0.03	-0.38	1146	7.59
12s rRNA	39.3	12.8	7.9	40.0	79.3	20.7	-0.01	-0.24	685	4.54
ND2	37.4	10.6	6.6	45.4	82.8	17.2	-0.10	-0.23	965	6.39
PCGs	40.0	11.9	8.8	39.3	79.3	20.7	0.01	-0.15	10821	71.69
tRNAs	41.4	11.6	9.5	37.5	78.9	21.1	0.05	-0.10	1365	9.04
rRNAs	40.4	13.5	6.9	39.3	79.7	20.4	0.01	-0.32	1831	12.13
AT-rich region	44.6	6.1	5.1	44.0	88.6	11.2	0.01	-0.09	993	6.58
Complete mtDNA	40.5	11.7	8.4	39.4	79.9	20.1	0.01	-0.16	15095	100.00

Table S3. Pairwise comparison of three *Trioza erytreae* specimens collected in Ethiopia (TE-ETH), Uganda (TE-UG), and South Africa (TE-SA) given as the number of single nucleotide polymorphisms (SNPs) and non-synonymous amino acid substitutions (NS) in the complete complement of 13 mitochondrial protein coding genes.

Gene	Length (bp)	TE-UG vs TE-SA				TE-ETH vs SA-TE				TE-ETH vs TE-UG			
		SNPs	%	NS	%	SNPs	%	NS	%	SNPs	%	NS	%
ATP6	674	15	1.76	6	0.89	15	1.76	5	0.74	2	0.21	1	0.15
ATP8	153	7	2.56	3	1.96	7	2.56	3	1.96	0	0.00	0	0.00
COI	1533	28	2.80	0	0.00	30	2.71	0	0.00	2	0.09	0	0.00
COII	664	20	2.94	3	0.45	19	2.83	3	0.45	1	0.33	0	0.00
COIII	783	29	2.81	10	1.28	28	2.73	9	1.15	3	0.00	1	0.13
CYTB	1143	32	3.58	5	0.44	31	3.52	5	0.44	1	0.12	0	0.00
ND1	918	27	1.83	6	0.65	26	1.96	7	0.76	3	0.13	1	0.11
ND2	968	17	3.01	5	0.52	17	2.86	6	0.62	2	0.15	1	0.10
ND3	351	9	2.71	3	0.85	9	2.71	3	0.85	0	0.00	0	0.00
ND4	1245	35	4.58	4	0.32	34	4.58	4	0.32	0	0.00	0	0.00
ND4L	288	1	2.08	6	2.08	1	2.08	0	0.00	0	0.00	0	0.00
ND5	1618	58	3.70	16	0.99	57	3.58	16	0.99	2	0.38	0	0.00
ND6	480	13	2.23	5	1.04	13	2.23	6	1.25	0	0.30	0	0.00
Total		291		72		287		67		16		4	

Table S4. List of publicly available and new cytochrome c subunit 1 (*COI*) sequences (n = 89) reported as *Trioza erytreae* (Hemiptera: Triozidae), and used for the construction of median-joining network, neighbor-joining tree, and estimates of genetic distances and genetic diversity.

Country	Name	Accession	REF	Haplotype
Ethiopia	TE-ETH	Upon acceptance	This study	Hap 7
Kenya	Kenya citrus 01	KY754595.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 02	KY754596.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 03	KY754597.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 04	KY754599.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 05	KY754600.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 06	KY754610.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 07	KY754613.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 08	KY754614.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 09	KY754615.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 10	KY754619.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 11	KY754620.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 12	KY754621.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 13	KY754622.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 14	KY754623.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 15	KY754624.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 16	KY754625.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 17	KY754626.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 18	KY754627.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 19	KY754628.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 20	KY754629.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 21	KY754630.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 22	KY754631.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 23	KY754632.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 24	KY754633.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 25	KY754634.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 26	KY754635.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 27	KY754641.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 28	KY754642.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 29	KY754643.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 30	KY754644.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 31	KY754645.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 32	KY754646.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 33	KY754647.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 34	KY754648.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 35	KY754649.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 36	KY754650.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 37	KY754651.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 38	KY754652.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 39	KY754653.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 40	KY754654.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 41	KY754655.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 42	KY754656.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 43	KY754611.1	Khamis et al 2017	Hap 1
Kenya	Kenya citrus 44	KY754612.1	Khamis et al 2017	Hap 2
Kenya	Kenya citrus 45	KY754598.1	Khamis et al 2017	Hap 3
Kenya	Kenya <i>Clausena anisata</i> 1	KY754616.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Clausena anisata</i> 2	KY754617.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Clausena anisata</i> 3	KY754618.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Clausena anisata</i> 4	KY754586.1	Khamis et al 2017	Hap 6
Kenya	Kenya <i>Clausena anisata</i> 5	KY754585.1	Khamis et al 2017	Hap 8
Kenya	Kenya <i>Clausena anisata</i> 6	KY754584.1	Khamis et al 2017	Hap 9
Kenya	Kenya <i>Clausena anisata</i> 7	KY754587.1	Khamis et al 2017	Hap 10
Kenya	Kenya <i>Murraya koenigii</i> 1	KY754601.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Murraya koenigii</i> 2	KY754602.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Murraya koenigii</i> 3	KY754603.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Murraya koenigii</i> 4	KY754604.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Murraya koenigii</i> 5	KY754605.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Murraya koenigii</i> 6	KY754606.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Murraya koenigii</i> 7	KY754607.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Murraya koenigii</i> 8	KY754608.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Murraya koenigii</i> 9	KY754609.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Stephania abyssinica</i> 1	KY754636.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Stephania abyssinica</i> 2	KY754637.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Stephania abyssinica</i> 3	KY754638.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Stephania abyssinica</i> 4	KY754639.1	Khamis et al 2017	Hap 1
Kenya	Kenya <i>Stephania abyssinica</i> 5	KY754640.1	Khamis et al 2017	Hap 1
Portugal	Portugal Madeira	MK285558.1	Pérez-Rodríguez et al 2019	Hap 4
South Africa	SA citrus 1	KY754589.1	Khamis et al 2017	Hap 3
South Africa	SA citrus 2	KY754591.1	Khamis et al 2017	Hap 3
South Africa	SA citrus 3	KY754592.1	Khamis et al 2017	Hap 3
South Africa	SA citrus 4	KY754593.1	Khamis et al 2017	Hap 3
South Africa	SA citrus 5	KY754590.1	Khamis et al 2017	Hap 4
South Africa	SA citrus 6	KY754594.1	Khamis et al 2017	Hap 4
South Africa	SA Nelspruit 1	MK285554.1	Pérez-Rodríguez et al 2019	Hap 5
South Africa	SA Nelspruit 2	MK285555.1	Pérez-Rodríguez et al 2019	Hap 5
South Africa	SA Pretoria 1	MK285559.1	Pérez-Rodríguez et al 2019	Hap 4
South Africa	SA Pretoria 2	MK285560.1	Pérez-Rodríguez et al 2019	Hap 5
South Africa	SA Tzaneen 1	MK285556.1	Pérez-Rodríguez et al 2019	Hap 3
South Africa	SA Tzaneen 2	MK285557.1	Pérez-Rodríguez et al 2019	Hap 5
South Africa	TE-SA	Upon acceptance	This study	Hap 5
Spain	Spain Galicia Aldan	MK285548.1	Pérez-Rodríguez et al 2019	Hap 4
Spain	Spain Galicia Areiro	MK285549.1	Pérez-Rodríguez et al 2019	Hap 4
Spain	Spain Galicia Portonovo	MK285550.1	Pérez-Rodríguez et al 2019	Hap 4
Spain	Spain Gran Canaria	MK285553.1	Pérez-Rodríguez et al 2019	Hap 4
Spain	Spain Tenerife 1	MK285551.1	Pérez-Rodríguez et al 2019	Hap 4
Spain	Spain Tenerife 2	MK285552.1	Pérez-Rodríguez et al 2019	Hap 4
Tanzania	Tanzania citrus	KY754588.1	Khamis et al 2017	Hap 1
Uganda	TE-UG	Upon acceptance	This study	Hap 7

Table S5. Estimates of minimum, maximum and average intra-specific genetic divergence in 31 species belonging to the genus *Trioza* (Hemiptera: Triozidae), calculated as percentage of pairwise distances under the Kimura 2-parameter model.

Species	n	bp	Min	Max	Mean	SE
<i>Trioza acuta</i>	4	395	0.00	1.54	0.80	0.300
<i>Trioza anceps</i>	2	472	14.27	14.27	14.30	1.900
<i>Trioza apicalis</i>	3	430	0.00	0.23	0.20	0.200
<i>Trioza aylmeriae</i>	5	355	0.00	0.00	0.00	0.000
<i>Trioza barrettiae</i>	3	400	0.25	1.52	1.00	0.400
<i>Trioza bifida</i>	3	395	0.00	1.02	0.50	0.200
<i>Trioza brevigenae</i>	9	658	0.00	0.00	0.00	0.000
<i>Trioza colorata</i>	4	395	0.00	1.02	0.50	0.200
<i>Trioza compressa</i>	4	395	0.00	0.51	0.30	0.200
<i>Trioza curta</i>	2	395	0.00	0.00	0.00	0.000
<i>Trioza dacrydii</i>	2	395	0.51	0.51	0.50	0.300
<i>Trioza decurvata</i>	3	395	2.06	3.92	3.10	0.700
<i>Trioza discariae</i>	4	395	0.00	0.25	0.10	0.100
<i>Trioza doryphora</i>	4	395	0.00	0.00	0.00	0.000
<i>Trioza erytreae</i>	52	535	0.00	11.71	0.90	0.200
<i>Trioza eugeniae</i>	7	395	0.00	2.33	0.90	0.300
<i>Trioza falcata</i>	4	395	0.00	1.28	0.90	0.400
<i>Trioza fasciata</i>	2	395	3.93	3.93	3.90	1.000
<i>Trioza gourlayi</i>	2	395	0.25	0.25	0.30	0.200
<i>Trioza grallata</i>	2	470	0.00	0.00	0.00	0.000
<i>Trioza hebicola</i>	2	395	0.25	0.25	0.30	0.200
<i>Trioza incrustata</i>	2	470	0.00	0.00	0.00	0.000
<i>Trioza irregularis</i>	11	395	0.00	1.28	0.60	0.200
<i>Trioza obscura</i>	3	395	0.00	1.54	1.00	0.400
<i>Trioza obunca</i>	2	472	0.00	0.00	0.00	0.000
<i>Trioza panacis</i>	4	395	0.00	0.51	0.30	0.200
<i>Trioza remota</i>	2	472	0.43	0.43	0.40	0.300
<i>Trioza subacuta</i>	5	395	0.00	0.51	0.40	0.200
<i>Trioza subvexa</i>	5	395	0.25	3.39	2.00	0.600
<i>Trioza tricornuta</i>	6	370	0.00	1.65	1.00	0.400
<i>Trioza urticae</i>	96	472	0.00	4.18	1.60	0.300

Table S6. Sample data of the tree adult specimens of the African citrus triozid *Trioza erytreae* (Hemiptera: Triozidae) collected in Ethiopia (TE-ETH), Uganda (TE-UG) and South Africa (TE-SA) on *Citrus sinensis* (L.) Osbek, and used for next-generation sequencing of the complete mitochondrial genomes.

Sample	Species	Collection date	Country	Latitude	Longitude
TE-ETH	<i>Trioza erytreae</i>	19-Nov-17	Ethiopia	11.3917	37.0741
TE-UG	<i>Trioza erytreae</i>	24-Mar-17	Uganda	-0.4964	31.5548
TE-SA	<i>Trioza erytreae</i>	10-Jul-19	South Africa	-25.4791	30.9928

Supplementary figures

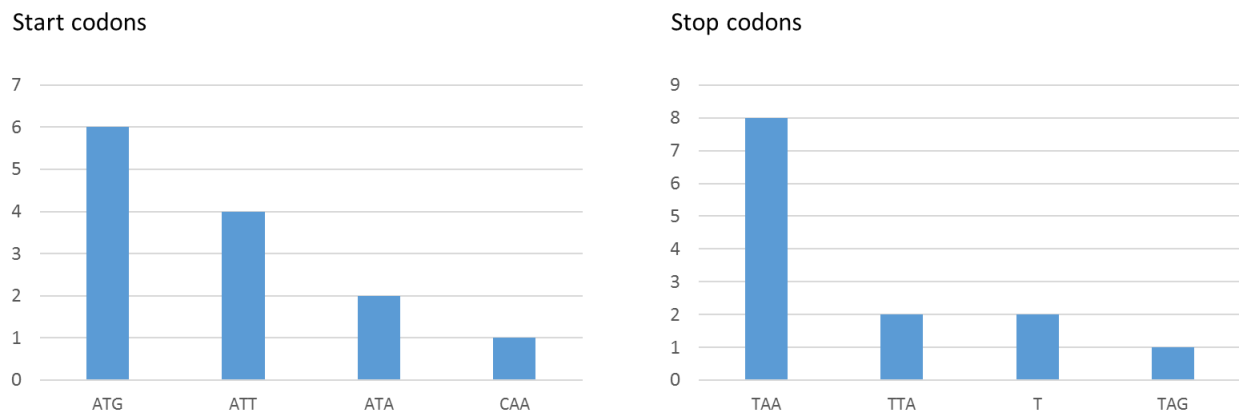


Figure S1. Start and stop codons found in the complete complement of 13 mitochondrial genes of *Trioza erytreae*.