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Hypothesis

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Supplementary material:

Table 1: Genome properties of chosen Trypanosomatids

Name of Trypanosomatids	Number of Chromosomes	Genome Size (Mb)	Total number of CDS	Number of Analyzed CDS#	Number of Non analyzed CDS##	Overall G+C % in genome	G+C % in CDSs	Copy number of t-RNA gene	Number of t-RNA
<i>L.major</i> Friedlin	36	32.82	8167	8102	65	59.72	61.42	83	45
<i>L.infantum</i> JPCM5	36	32.12	7994	7932	62	59.45	61.45	66	43
<i>L.braziliensis</i> MHOM	35	37.28	7895	7834	61	57.59	59.55	66	44
<i>T.brucei</i> 927	11	26.08	8712	8663	49	46.43	50.23	64	44
<i>T.cruzi</i> CL Brener	41	89.61	9042	8990	52	56.93 [@]	52.46	115	45

@-This value is very high as compared to *T.brucei* due to presence of very large number of N (Unidentified) nucleotides at the telomeric region; #-Less than ten thousand length; ##-More than ten thousand.

Table 2: Codon frequency table and the cognate copy number of t-RNA in Trypanosomatids

Amino Acids (AA)	Symble of AA	Codons	<i>L.major</i> Friedlin				<i>L.infantum</i> JPCM5				<i>L.braziliensis</i> MHOM				<i>T.brucei</i> 927				<i>T.cruzi</i> CL Brener			
			Frequency per thousand	t-RNA	Case	Dominant Codon	Frequency per thousand	t-RNA	Case	Dominant Codon	Frequency per thousand	t-RNA	Case	Dominant Codon	Frequency per thousand	t-RNA	Case	Dominant Codon	Frequency per thousand	t-RNA	Case	Dominant Codon
Phe	F	TTT/TTC	11.47/21	0/2	1a	TTC	11.49/20.78	0/2	1a	TTC	12.95/19.97	0/1	1a	TTC	24.03/17.09	0/2	1a	-	27.19/10.44	0/4	1a	TTT
Leu	L	TTA/TTG	1.7/10.78	2/1	2a	CTC	1.72/10.68	1/1	2a	CTC	2.6/11.47	1/0	2a	CTC	10.55/19.53	1/0	2a	TTG	7.98/22.5	2/2	2a	TTG
		CTT/ CTC	11.24/25.17	3/0	1b	CTG	11.33/24.93	1/0	1b	CTG	12.75/24.88	2/0	1b	CTG	22.02/15.56	2/0	1b	CIT	23.35/13.66	4/0	1b	CTT
		CTA/ CTG	4.64/37.21	1/2	-		4.66/36.38	1/2	-		5.91/34.45	1/2	-		7.76/17.36	1/1	2a		5.11/23.63	2/2	2a	CTG
Ile	I	CTG/CTC	37.21/25.17	2/0	3a		36.38/24.93	2/0	3a		34.45/24.88	2/0	3a		17.36/15.56	1/0	3a		23.63/13.66	2/0	3a	
		ATT/ ATC	9.33/21.26	3/0	1b	ATC	9.53/20.97	1/0	1b	ATC	11.55/19.94	2/0	1b	ATC	19.48/11.6	2/0	1b	ATT	20.79/10.75	4/0	1b	ATT
		ATA/ATC	2.88/21.26	1/0	3c		2.89/20.97	1/0	3c		3.55/19.94	1/0	3c		10.37/11.6	1/0	3c		6.59/10.75	3/0	3c	
Val	V	GTT/ GTC	9/19.53	2/0	1b	GTG	8.9/19.53	3/0	1b	GTG	10.05/18.51	2/0	1b	GTG	22.82/11.4	2/0	1b	GTG	19.04/12.73	2/0	1b	GTG
		GTA/ GTG	5.61/38.57	1/2	-		5.65/37.52	1/2	-		7.39/36.98	1/1	2a		12.36/28.05	1/1	2a		8.33/33.91	2/4	2a	
		GTT/GTG	9/38.57	2/2	3b		8.9/37.52	3/2	3b		10.05/36.98	2/1	3b		22.82/28.05	2/1	3b		19.04/33.91	2/4	-	
Ser	S	GTG/GTC	38.57/19.53	2/0	3a		37.52/19.53	2/0	3a		36.98/18.51	1/0	3a		28.05/11.4	1/0	3a		33.91/12.73	4/0	3a	
		TCT/ ICC	9.5/15.57	1/0	1b	AGC	9.6/15.66	1/0	1b	AGC	10.57/15.26	1/0	1b	AGC	12.82/12.69	1/0	1b	-	13.92/14.01	2/0	1b	-
		TCA/ TCG	6.56/19.42	1/1	2a	TCG	6.67/19.29	1/1	2a	TCG	8.4/17.48	1/0	2a	TCG	13.13/11.32	1/1	-		12.21/12.69	2/2	-	
		TCG/TCC	19.42/15.57	1/0	3a		19.29/15.66	1/0	3a		17.48/15.26	0/0	-		11.32/12.69	1/0	3a		12.69/14.01	2/0	3a	
		AGT/ AGC	6.8/23.34	0/2	1a		6.69/23.52	0/2	1a		8.44/22.11	0/2	1a		14.2/12.96	0/2	1a		12.53/13.5	0/2	1a	
Pro	P	CCT/ CCC	8.27/12.34	2/0	1b	CCG	8.61/12.25	2/0	1b	CCG	9.25/12.24	1/0	1b	CCG	11.51/11.91	1/0	1b	-	10.17/10.55	2/0	1b	-
		CCA/ CCG	9.61/24.36	1/2	-		9.77/24.56	1/2	-		11.68/20.88	1/2	-		13.86/11.79	1/1	-		13.75/14.82	2/2	-	

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Thr	T	CCG/CCC	24.36/12.34	2/0	3a		24.56/12.3	2/0	3a		20.88/12.24	2/0	3a		11.79/11.91	1/0	3a		14.82/10.55	2/0	3a		
		ACT/ACC	6.6/17.5	3/0	1b	ACG		6.73/17.19	0/0	-	ACG		8.88/17.79	0/0	-	ACG		12.66/11.86	1/0	1b		9.92/11.68	2/0
Ala	A	ACA/ACG	9.8/24	1/2	-		9.61/24.01	1/2	-		11.83/21.66	1/2	-		17.04/14.58	1/1	-		16.29/19.74	2/2	-		
		ACG/ACC	24/17.5	2/0	3a		24.01/17.19	2/0	3a		21.66/17.79	2/0	3a		14.58/11.86	1/0	3a		19.74/11.68	2/0	3a		
		GCT/GCC	17.2/34.6	2/0	1b	GCG		17.35/35.26	2/0	1b	GCG		18.54/30.92	2/0	1b	GCG		19.71/17.62	2/0	1b		16.35/21.75	2/0
Tyr	Y	GCA/GCG	18.23/41.42	1/2	-		18.56/41.31	1/0	2a		19.83/35.5	1/1	2a		21.92/19.94	1/2	2b		21.33/27	1/2	-		
		GCT/GCG	17.2/41.42	2/2	3b		17.35/41.31	2/0	3b		18.54/35.5	2/1	3b		19.71/19.94	2/2	-		16.35/27	2/2	3b		
His	H	TAT/TAC	4.44/22.27	0/3	1a	TAC	4.43/22.15	0/1	1a	TAC	5.3/21.97	0/1	1a	TAC	12.34/14.64	0/2	1a		9.4/14.65	0/2	1a	-	
Gln	Q	CAT/CAC	6.32/20.37	0/2	1a	CAC	6.46/20.27	0/2	1a	CAC	7.07/20.04	1/1	1b	CAC	11.79/13.61	0/1	1a		12.24/12.79	0/4	1a	-	
		CAA/CAG	7.36/32.64	1/3	-	CAG	7.56/32.49	1/3	-	CAG	8.52/31.7	1/2	2a	CAG	16.71/19.93	1/2	-	-	14.7/22.9	1/4	2b	-	
Asn	N	AAT/AAC	5.86/22.52	0/3	1a	AAC	5.91/22.35	0/1	2a	AAC	7.45/22.1	0/3	2a	AAC	17.5/18.91	0/2	2a		18.33/16.99	0/4	2a	-	
Lys	K	AAA/AAG	6.14/33.91	1/3	-	AAG	6.44/33.75	1/3	-	AAG	7.37/33.1	1/3	-	AAG	22.25/27.75	1/3	2b		18.46/26.23	2/4	-	-	
Asp	D	GAT/GAC	14.82/33.79	0/3	1a	GAC	15/33.59	0/2	1a	GAC	15.98/31.99	0/4	1a	GAC	26.1/21.15	0/2	1a		25.94/22.76	0/2	1a	-	
Glu	E	GAA/GAG	11.43/49.18	1/2	2a	GAG	11.78/49.11	1/1	2a	GAC	12.87/47.87	1/2	2a	GAC	30.07/35.64	1/2	2b		28.73/43.15	2/4	-	-	
Cys	C	TGT/TGC	4.28/15.48	0/1	1a	TGC	4.1/15.46	0/1	1a	TGC	5.17/14.55	0/1	1a	TGC	11.97/11.82	0/2	1a		9.33/11.11	0/2	1a	-	
Arg	R	CGT/CGC	10.74/32.98	4/0	1b	CGC	10.64/33.33	4/0	1b	CGC	11.63/30.28	2/1	1b	CGC	15.81/15.75	3/0	1b	CGT	17.1/15.37	4/0	1b	CGT	
Gly	G	CGA/CGG	6.89/12.74	1/1	2a		7.25/12.83	1/1	2a		7.81/11.58	1/1	2a		9.08/12.34	1/1	2a		9.84/12.93	2/2	-		
		AGA/AGG	2.49/5.27	1/1	-		2.64/5.33	1/1	-		3.12/5.97	1/1	-		7.1/10.21	1/1	-		6.22/9.4	2/2	-		
		GGT/GGC	12.6/33.79	0/4	1b	GGC	12.13/34.25	0/2	1b	GGC	13.95/29.78	0/1	1b	GGC	21.59/14.69	0/3	1b	GCT	17.15/19.65	0/4	1b	-	
Met	M	GGA/GGG	6.27/11.3	1/1	-		6.51/11.26	1/1	-		7.29/11.57	1/1	-		15.36/14.06	1/1	-		14.15/15.53	2/2	-		
Trp	W	ATG	25.36	4	-		25.22	4	-		25.53	5	-		25.05	3	-		25.03	6	-		
		TGG	11.32	1	-		11.22	1	-		11.41	1	-		11.57	1	-		11.7	2	-		

1a: T ending codon encoded by the t-RNA of C ending codon (pyrimidine - pyrimidine); 1b: C ending codon encoded by the t-RNA of T ending codon (pyrimidine - pyrimidine); 2a: G ending codon encoded by the t-RNA of A ending codon (purine - purine); 2b: A ending codon encoded by the t-RNA of G ending codon (purine - purine); 3a: C ending codon encoded by the t-RNA of G ending codon (purine - pyrimidine); 3b: G ending codon encoded by the t-RNA of T ending codon (pyrimidine - purine); 3c: C ending codon encoded by the t-RNA of A ending codon (purine - pyrimidine)

Table 3: Table of amino acid frequency on the basis of their properties

	Amino Acid Properties	<i>L.major</i> Friedlin	<i>L.infantum</i> JPCM5	<i>L.braziliensis</i> MHOM	<i>T.brucei</i> 927	<i>T.cruzi</i> CL Brenner
For all CDSs	Hydrophobic	404.25	402.46	401.95	392.77	393.22
	Hydrophilic	454.59	455.7	458.87	464.96	470.56
	Special	138.3	138.9	136.36	138.56	136.22
For essential Genes	Hydrophobic	420.35	404.5	401.1	382.4	394.62
	Hydrophilic	446.67	448.0	461.79	471.41	472.29
	Special	142.18	145.08	135.94	139.75	131.13

Hydrophobic - LMIVWAFY; Hydrophilic - DEKRHSTNQ; Special - GCP