

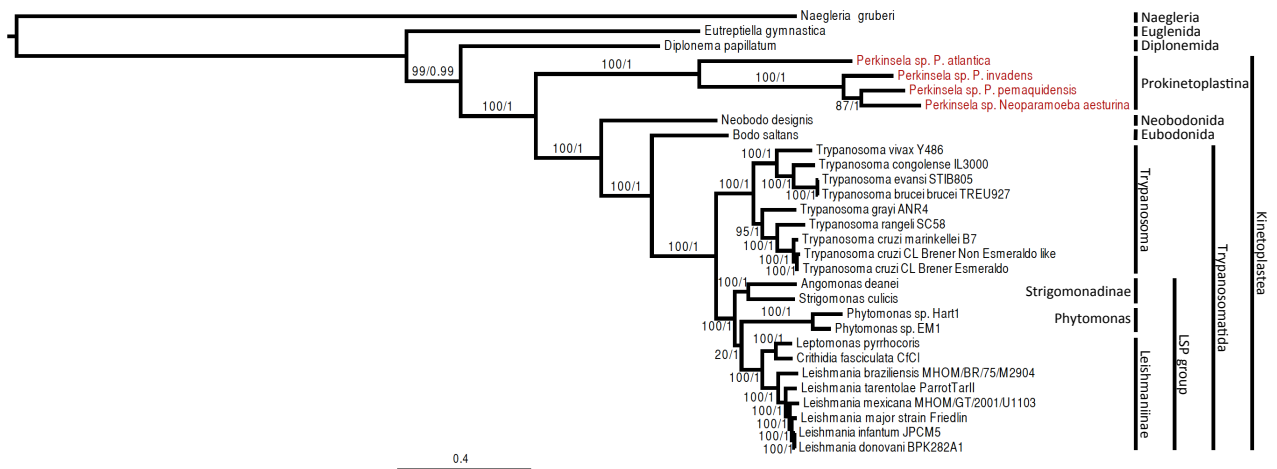


Figure S1.1: Phylogeny of Kinetoplastea based on a concatenation of 11 proteins. The tree was built using the C20 + Poisson model with Phylobayes 4.1. 1,000 bootstrap repetitions were performed using the LG4X model IQTREE and mapped onto the nodes (left) alongside posterior probabilities (right). The Prokinetoplastina, represented by *Perkinsela* spp. are highlighted red. Higher-level taxonomic classifications are indicated on the right for each group of organisms. The Kinetoplastea form a group with Diplonemida and Euglenida forming successively deeper branches when the heterolobosean *Naegleria gruberi* is used to root the tree. The Prokinetoplastina are a well-supported, early-branching group of Kinetoplastea. The bodonids branch as sister to the Trypanosomatida, while Leishmaniinae, *Phytomonas* and Strigomonadinae form a strongly supported, distinct group. The scale bar shows the inferred number of amino acid substitutions per site.

Table S1.2: Topology test results for the Kinetoplastea (Figure 1) using the LG4X model in RAxML. The groups tested are indicated on the right. For each test, the following information is provided: bp-RELL, p-KH, p-SH, c-ELW. A '+' sign indicates that the topology is not rejected, while '-' indicates rejection. Abbreviations: Ngr: *N. gruberi*, Egy: *E. gymnastica*, Dpa: *D. papillatum*, Nde: *N. designis*, Bsa: *B. saltans*, PhH: *Phytomonas* Hart1, PhE: *Phytomonas* EM1, Ade: *A. deanei*, Cfa: *C. fasciculata* CfCl, Lpy: *L. pyrrhocoris*, Scu: *S. culicis*, Lbr: *L. braziliensis* MHOMBR75M2904, Lta: *L. tarentolae* ParrotTarII, Lme: *L. Mexicana* MHOMGT2001U1103, Lma: *L. major* Friedlin, Ldo: *L. donovani* BPK282A1, Lin: *L. infantum* JPCM5, Pea: *P. atlantica*, Pei: *Perkinsela* from *Paramoeba invadens*, Nea: *N. aestuarina*, Pep: *Perkinsela* from *Paramoeba pemaquidensis*, Tgr: *T. grayi* ANR4, Tra: *T. rangeli* SC58, Tcm: *T. cruzi* marinkellei B7, TcBE: *T. cruzi* CL Brener Esmeraldo like, TcBN: *T. cruzi* CL Brener Non Esmeraldo like, Tvi: *T. vivax* Y486, Tco: *T. congolense* IL3000, TbT: *T. brucei* TREU927, TbL: *T. brucei* Lister 427, TbL: *T. brucei* gambiense DAL972, Tev: *T. evansi* STIB805.

Trees	logL	deltaL	bp-RELL	p-KH	p-SH	c-ELW	
(Ngr,Egy,Dpa,(Nde,Bsa,((Pea,Pei,Nea,Pep),(PhE,PhH),Ade,Cfa,Lpy,Scu,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev)))	-107771.796	772.869	0.0000	0.0000	0.0000	0.0000	Test Prokinetoplastina
(Ngr,Egy,Dpa,(Nde,Bsa,((PhE,PhH),Ade,Cfa,Lpy,Scu,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Pea,Pei,Nea,Pep),Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev)))	-108059.426	1060.498	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,Dpa,(Nde,Bsa,((PhE,PhH),Ade,Cfa,Lpy,Scu,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Pea,Pei,Nea,Pep),Tvi,Tco,TbT,Tev)))	-108051.205	1052.278	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,Dpa,(Nde,Bsa,((PhE,PhH),Ade,Cfa,Lpy,Scu,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Pea,Pei,Nea,Pep),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev)))	-107772.682	773.754	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,((Pea,Pei,Nea,Pep),(Dpa,(Nde,Bsa,((PhE,PhH),Ade,Cfa,Lpy,Scu,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107026.713	27.786	0.0080	0.0420	0.8730	0.0022	
(Ngr,((Pea,Pei,Nea,Pep),(Egy,Dpa,(Nde,Bsa,((PhE,PhH),Ade,Cfa,Lpy,Scu,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107082.217	83.29	0.0000	0.0010	0.4000	0.0000	
(Ngr,Egy,Dpa,(Nde,((Pea,Pei,Nea,Pep),Bsa,((PhE,PhH),Ade,Cfa,Lpy,Scu,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107155.537	156.61	0.0000	0.0000	0.0490	0.0000	Test Phytomonas
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),Nde,Bsa,((Ade,Scu),((PhE,PhH),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107028.707	29.779	0.0160	0.1180	0.8590	0.0006	
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),((PhE,PhH),Nde,Bsa,((Ade,Scu),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107618.093	619.166	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),Nde,(Bsa,PhE,PhH),((Ade,Scu),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107449.631	450.704	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),(Nde,PhE,PhH),Bsa,((Ade,Scu),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107736.643	737.715	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),Nde,Bsa,((Ade,Scu),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),((PhE,PhH),Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107149.315	150.388	0.0000	0.0000	0.0550	0.0000	
(Ngr,Egy,Dpa,(((PhE,PhH),Pea,Pei,Nea,Pep),Nde,Bsa,((Ade,Scu),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107879.349	880.422	0.0000	0.0000	0.0000	0.0000	Test Strigomonidae
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),Nde,Bsa,((PhE,PhH),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Ade,Scu),Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107223.188	224.261	0.0000	0.0000	0.0040	0.0000	
(Ngr,Egy,Dpa,((Ade,Scu),Pea,Pei,Nea,Pep),Nde,Bsa,((PhE,PhH),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-108017.616	1018.688	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),Nde,((Ade,Scu),Bsa,((PhE,PhH),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107591.189	592.261	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),((Ade,Scu),Nde,Bsa,((PhE,PhH),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin)),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107875.603	876.676	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),Cfa,Lpy,Lbr,Lta,Lme,Lma,Ldo,Lin),(Nde,Bsa,((Ade,Scu),((PhE,PhH),Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107900.434	901.507	0.0000	0.0000	0.0000	0.0000	
(Ngr,Egy,Dpa,(Pea,Pei,Nea,Pep),Nde,Bsa,((PhE,PhH),Ade,Scu),((Lpy,Cfa,Lbr,Lta,Lme,Lma,Ldo,Lin),(Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107274.14	275.213	0.0000	0.0000	0.0020	0.0000	Test Leishmani
(Ngr,Egy,Dpa,((Pea,Pei,Nea,Pep),Nde,Bsa,(Lpy,Cfa,Lbr,Lta,Lme,Lma,Ldo,Lin)),((PhE,PhH),Ade,Scu),((Tgr,Tra,Tcm,TcBE,TcBN),(Tvi,Tco,TbT,Tev))))	-107275.172	276.245	0.0000	0.0000	0.0000	0.0000	
No constraint	-106998.927	0	0.0240	0.5050	1.0000	0.0013	

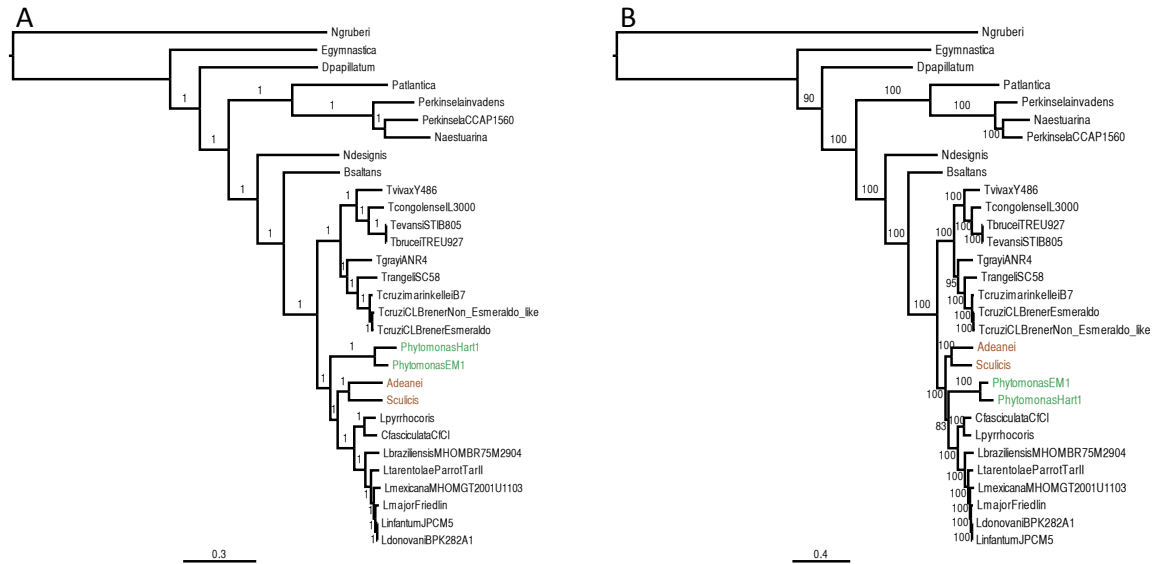


Figure S1.3: (A) Phylogenetic tree of Kinetoplastea and related lineages constructed using phylobayes with the LG model. (B) Phylogenetic tree using IQTREE and the ultrafast bootstrap method with the C20 model. The *Phytomonas* spp. is highlighted in green, while Strigomanidae is colored in brown. Scale bar indicates the inferred number of substitutions per amino acid site.

Table S1.4: Percentage of missing data for each organism in the alignment used to construct the Kinetoplastea evolution tree.

	Gaps
A. deanei	2.67%
B. saltans	25.10%
C. fasciculata CfCI	14.35%
D. papillatum	42.49%
E. gymnastica	12.27%
L. braziliensis MHOMBR75M2904	0.57%
L. donovani BPK282A1	0.53%
L. infantum JPCM5	0.53%
L. major Friedlin	0.53%
L. mexicana MHOMGT2001U1103	0.53%
L. pyrrhocoris	0.00%
L. tarentolae Parrot TarII	0.00%
N. aestuarina	10.73%
N. designis	9.53%
N. gruberi	24.09%
P. atlantica	47.63%
Perkinsela CCAP1560/4	1.11%
Perkinsela invadens	0.89%
Phytomonas EM1	15.36%
Phytomonas Hart1	13.77%
S. culicis	5.97%
T. brucei TREU927	0.04%
T. congolense IL 3000	20.71%
T. cruzi CL Brener Esmeraldo	22.04%
T. cruzi CL Brener Non Esmeraldo like	15.89%
T. cruzi marinkellei B7	7.55%
T. evansi STIB805	0.04%
T. grayi ANR4	2.89%
T. rangeli SC58	7.91%
T. vivax Y486	3.42%