Comparative genomics of protozoa and bacteria

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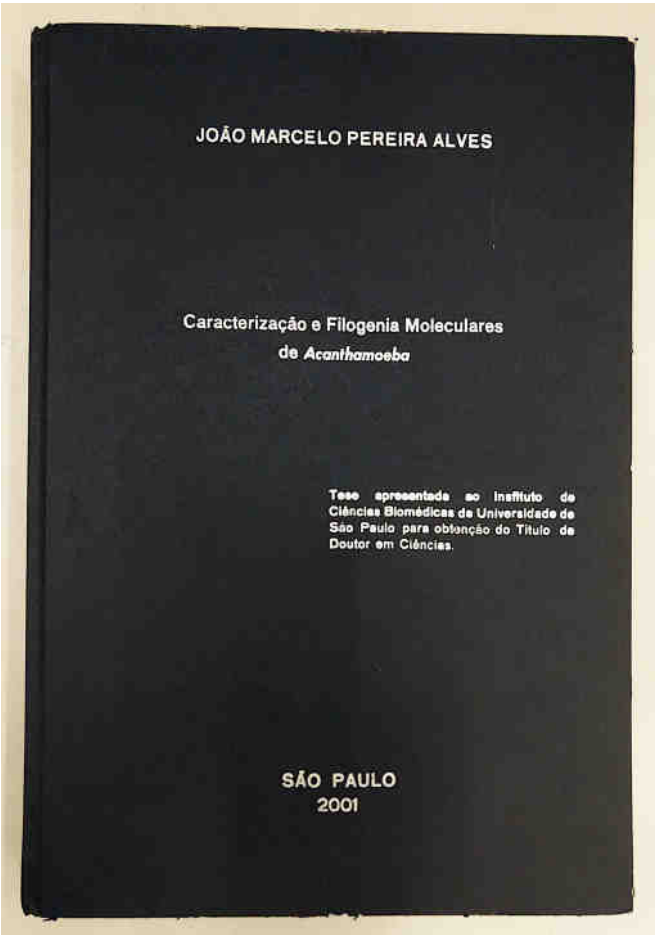
GENOME20+2

21/11/2022

MS 1996-1998; PhD 1998-2001; TT5 2012-2013; JP 2013-2018

I was impacted by the FAPESP genome project way before I myself started working on genomes...

Many thanks to Luiz R. Nunes



(my PhD thesis)

Protozoogenomics

- We study **protozoans** (and other organisms as well)

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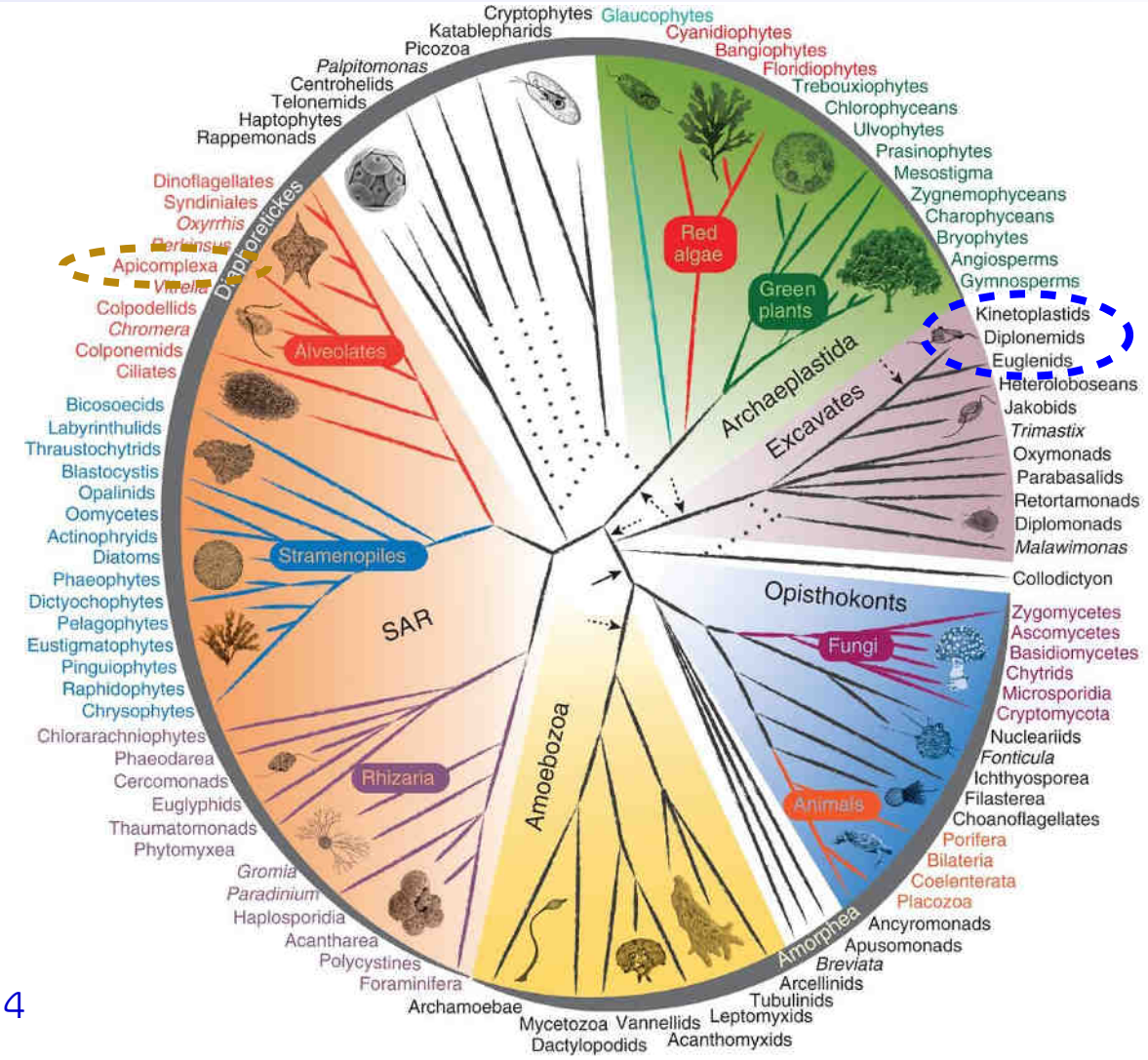
- We use high-throughput **genomic** methods

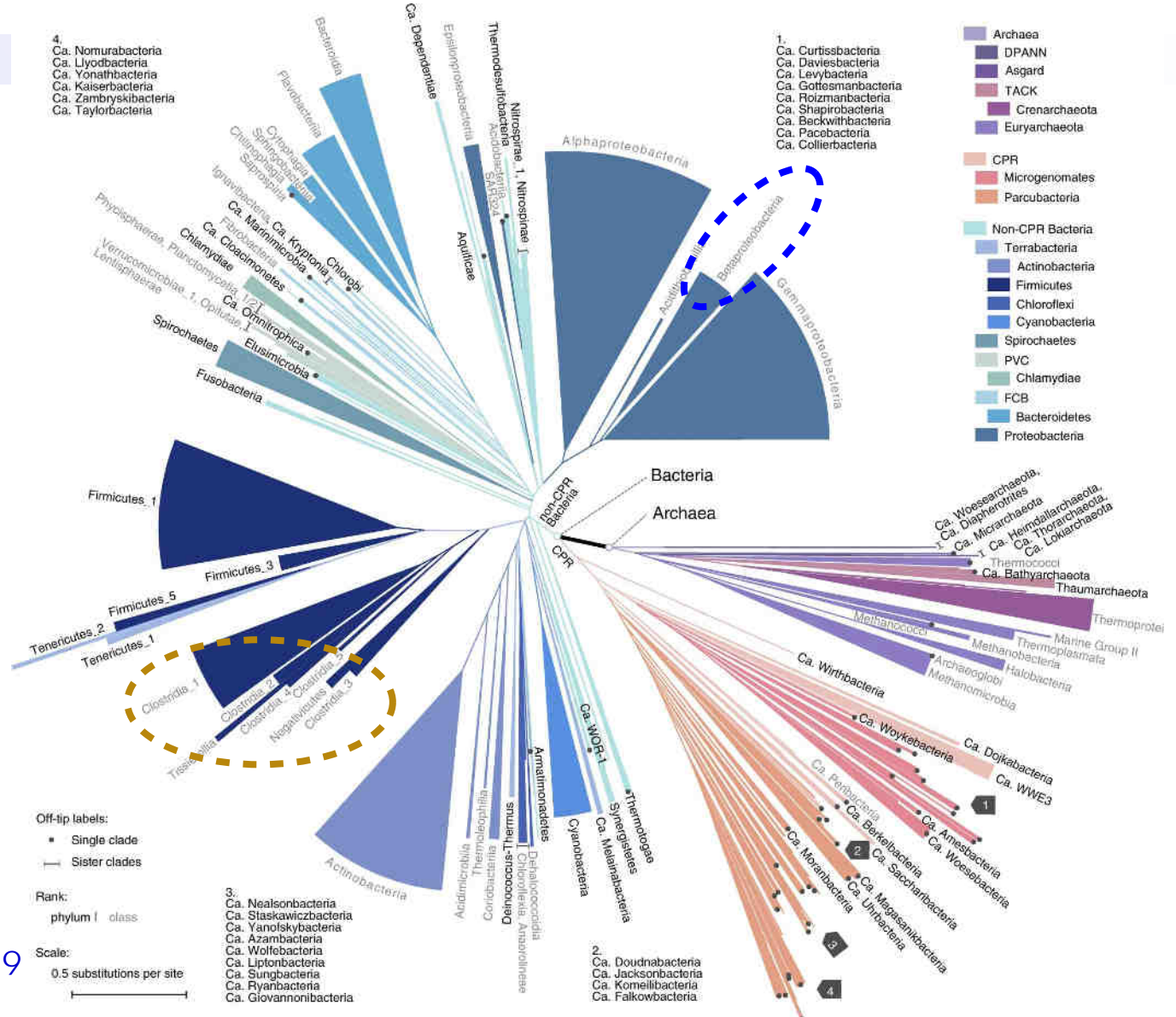
  (genomics, transcriptomics)

Protozoogenomics

- We study **protozoans** (and other organisms as well)
- We use high-throughput **genomic** methods (genomics, transcriptomics)
- And, of course, plenty of **bioinformatics**

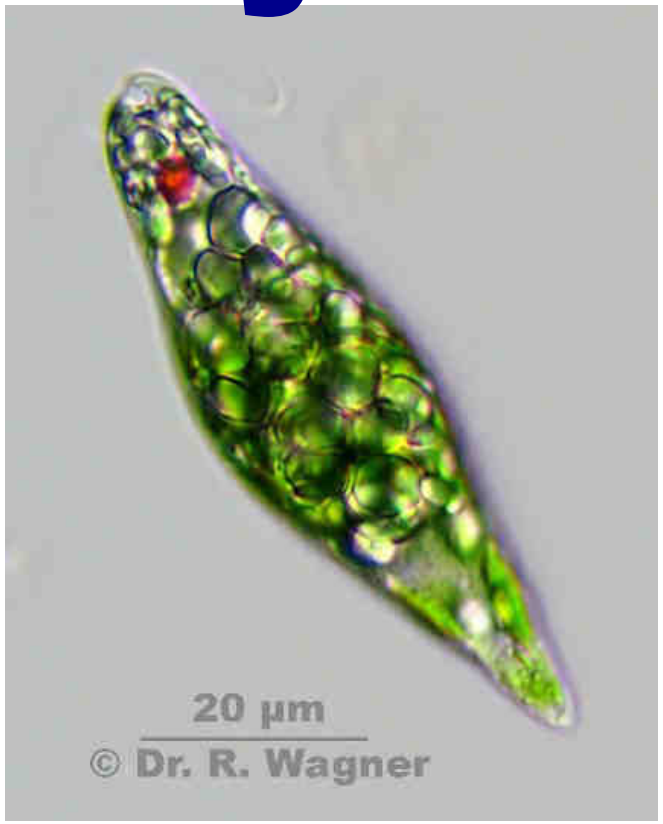


From: Burki, F., 2014

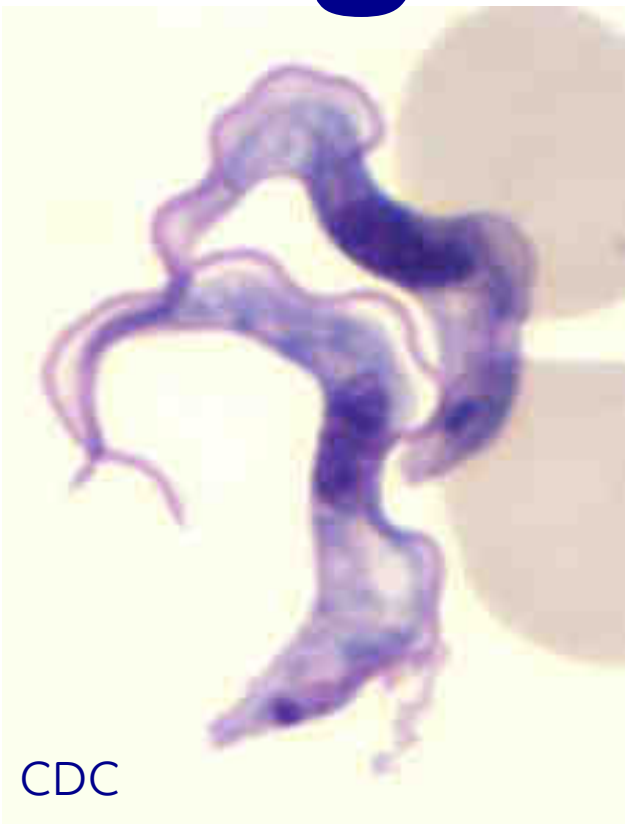


From: Xhu, Q. et al., 2019

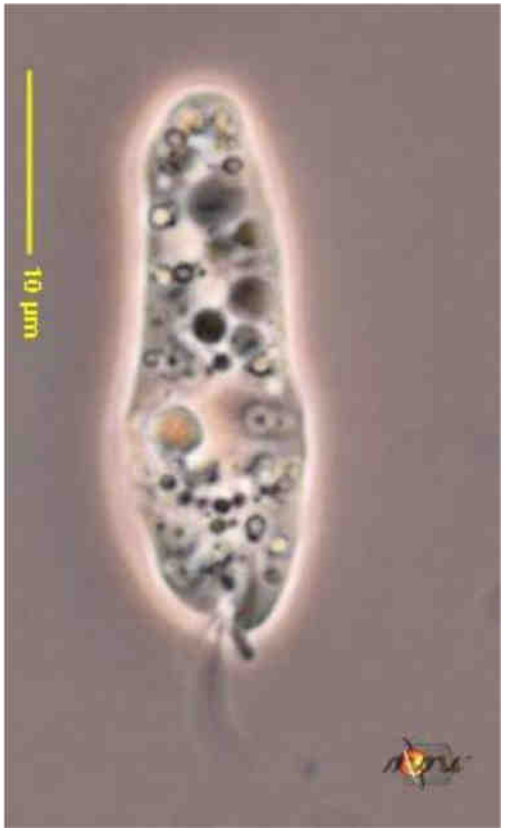
Phylum Euglenozoa



Subphylum Euglenoida



Class Kinetoplastea



Class Diplonemea

The TriTryp 2005

RESEARCH ARTICLE

The Genome of the African Trypanosome *Trypanosoma brucei*

Matthew Berriman,[1*] Elodie Ghedin,[2,3] Christiane Hertz-Fowler,[1] Gaëlle Blandin,[2] Hubert Renauld,[1] Daniella C. Bartholomeu,[2] Nicola J. Lennard,[1] Elisabet Caler,[2] Nancy E. Hamlin,[1] Brian Haas,[2] Ulrike Böhme,[1] Linda Hannick,[2] Martin A. Aslett,[1] Joshua Shallom,[2] Lucio Marcello,[4] Lihua Hou,[2] Bill Wickstead,[5] U. Cecilia M. Alsmark,[6] Claire Arrowsmith,[1] Rebecca J. Atkin,[1] Andrew J. Barron,[1] Frederic Bringaud,[7] Karen Brooks,[1] Mark Carrington,[8] Inna Cherevach,[1] Tracey-Jane Chillingworth,[1] Carol Churcher,[1] Louise N. Clark,[1] Craig H. Corton,[1] Ann Cronin,[1] Rob M. Davies,[1] Jonathon Doggett,[1] Appolinaire Djikeng,[2] Tamara Feldblyum,[2] Mark C. Field,[9] Audrey Fraser,[1] Ian Goodhead,[1] Zahra Hance,[1] David Harper,[1] Barbara R. Harris,[1] Heidi Hauser,[1] Jessica Hostetler,[2] Al Ivens,[1] Kay Jagels,[1] David Johnson,[1] Justin Johnson,[2] Kristine Jones,[2] Arnaud X. Kerhornou,[1] Hean Koo,[2] Natasha Larke,[1] Scott Landfear,[10] Christopher Larkin,[2] Vanessa Leech,[9] Alexandra Line,[1] Angela Lord,[1] Annette MacLeod,[4] Paul J. Mooney,[1] Sharon Moule,[1] David M. A. Martin,[11] Gareth W. Morgan,[12] Karen Mungall,[1] Halina Norbertczak,[1] Doug Ormond,[1] Grace Pai,[2] Chris S. Peacock,[1] Jeremy Peterson,[2] Michael A. Quail,[1] Ester Rabbinowitsch,[1] Marie-Adele Rajandream,[1] Chris Reitter,[9] Steven L. Salzberg,[2] Mandy Sanders,[1] Seth Schobel,[2] Sarah Sharp,[1] Mark Simmonds,[1] Anjana J. Simpson,[2] Luke Tallon,[2] C. Michael R. Turner,[13] Andrew Tait,[4] Adrian R. Tivey,[1] Susan Van Aken,[2] Danielle Walker,[1] David Wanless,[2] Shiliang Wang,[2] Brian White,[1] Owen White,[2] Sally Whitehead,[1] John Woodward,[1] Jennifer Wortman,[2] Mark D. Adams,[14] T. Martin Embley,[6] Keith Gull,[5] Elisabetta Ullu,[15] J. David Barry,[4] Alan H. Fairlamb,[11] Fred Opperdoes,[16] Barclay G. Barrell,[1] John E. Donelson,[17] Neil Hall,[1†] Claire M. Fraser,[2] Sara E. Melville,[9] Najib M. El-Sayed[2,3*]

African trypanosomes cause human sleeping sickness and livestock trypanosomiasis in sub-Saharan Africa. We present the sequence and analysis of the 11 megabase-sized chromosomes of *Trypanosoma brucei*. The 26-megabase genome contains current treatments are inadequate: Drugs for late-stage disease are highly toxic; there is no prophylactic chemotherapy and little or no

RESEARCH ARTICLE

The Genome of the Kinetoplastid Parasite, *Leishmania major*

Alasdair C. Ivens,[1*] Christopher S. Peacock,[1] Elizabeth A. Worthey,[2] Lee Murphy,[1] Gautam Aggarwal,[2] Matthew Berriman,[1] Ellen Sisk,[2] Marie-Adele Rajandream,[1] Ellen Adlem,[1] Rita Aert,[3] Atashi Anupama,[2] Zina Apostolou,[4] Philip Attipoe,[2] Nathalie Bason,[1] Christopher Bauser,[5] Alfred Beck,[6] Stephen M. Beverley,[7] Gabriella Bianchettin,[8] Katja Borzym,[6] Gordana Bothe,[5] Carlo V. Bruschi,[8,9] Matt Collins,[1] Eithon Cadag,[2] Laura Ciarloni,[8] Christine Clayton,[10] Richard M. R. Coulson,[11] Ann Cronin,[1] Angela K. Cruz,[12] Robert M. Davies,[1] Javier De Gaudenzi,[13] Deborah E. Dobson,[7] Andreas Duesterhoeft,[14] Gholam Fazelina,[2] Nigel Fosker,[1] Alberto Carlos Frasch,[13] Audrey Fraser,[1] Monika Fuchs,[4] Claudia Gabel,[4] Arlette Goble,[1] André Goffeau,[15] David Harris,[1] Christiane Hertz-Fowler,[1] Helmut Hilbert,[14] David Horn,[16] Yiting Huang,[2] Sven Klages,[6] Andrew Knights,[1] Michael Kube,[6] Natasha Larke,[1] Lyudmila Litvin,[2] Angela Lord,[1] Tin Louie,[2] Marco Marra,[17] David Masuy,[15] Keith Matthews,[18] Shulamit Michaeli,[19] Jeremy C. Mottram,[20] Silke Müller-Auer,[4] Heather Munden,[2] Siri Nelson,[2] Halina Norbertczak,[1] Karen Oliver,[1] Susan O'Neil,[1] Martin Pentony,[2] Thomas M. Pohl,[5] Claire Price,[1] Bénédicte Purnelle,[15] Michael A. Quail,[1] Ester Rabbinowitsch,[1] Richard Reinhardt,[6] Michael Rieger,[4] Joel Rinta,[2] Johan Robben,[3] Laura Robertson,[2] Jeronimo C. Ruiz,[12] Simon Rutter,[1] David Saunders,[1] Melanie Schäfer,[4] Jacquie Schein,[17] David C. Schwartz,[21] Kathy Seeger,[1] Amber Seyler,[2] Sarah Sharp,[1] Heesun Shin,[17] Dhileep Sivam,[2] Rob Squares,[1] Steve Squares,[1] Valentina Tosato,[8] Christy Vogt,[2] Guido Volckaert,[3] Rolf Wambutt,[22] Tim Warren,[1] Holger Wedler,[14] John Woodward,[1] Shiguo Zhou,[21] Wolfgang Zimmermann,[22] Deborah F. Smith,[23] Jenefer M. Blackwell,[24] Kenneth D. Stuart,[2,25] Bart Barrell,[1] Peter J. Myler[2,25,26*]

Leishmania species cause a spectrum of human diseases in tropical and subtropical chromosomes (Table 1, Plate 4, and table S1).

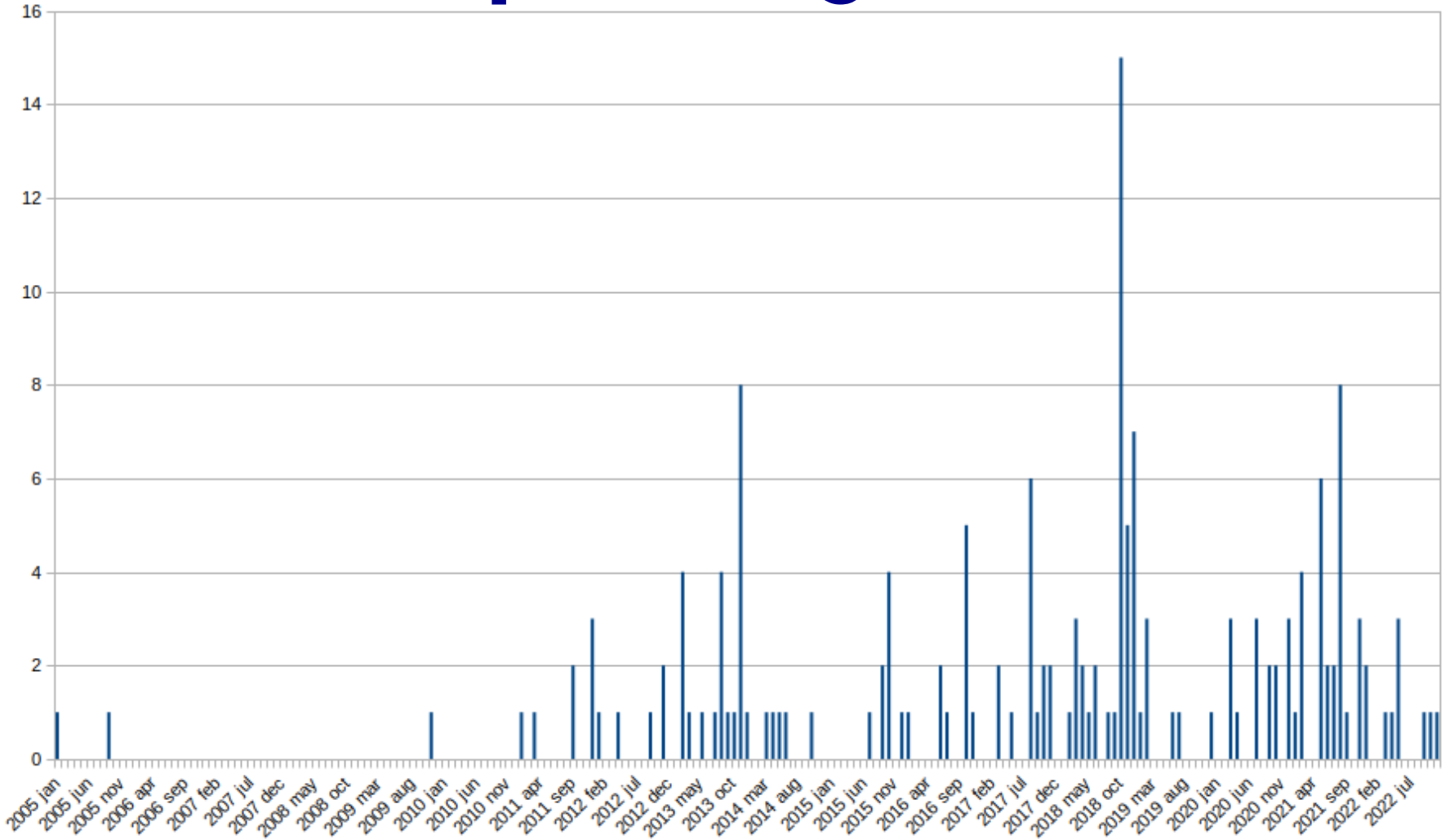
RESEARCH ARTICLE

The Genome Sequence of *Trypanosoma cruzi*, Etiologic Agent of Chagas Disease

Najib M. El-Sayed,[1,2*†] Peter J. Myler,[3,4,5*†] Daniella C. Bartholomeu,[1] Daniel Nilsson,[6] Gautam Aggarwal,[3] Anh-Nhi Tran,[6] Elodie Ghedin,[1,2] Elizabeth A. Worthey,[3] Arthur L. Delcher,[1] Gaëlle Blandin,[1] Scott J. Westenberger,[1,7] Elisabet Caler,[1] Gustavo C. Cerqueira,[1,8] Carole Branche,[6] Brian Haas,[1] Atashi Anupama,[3] Erik Arner,[6] Lena Åslund,[9] Philip Attipoe,[3] Esteban Bontempi,[6,10] Frédéric Bringaud,[11] Peter Burton,[12] Eithon Cadag,[3] David A. Campbell,[7] Mark Carrington,[13] Jonathan Crabtree,[1] Hamid Darban,[6] Jose Franco da Silveira,[14] Pieter de Jong,[15] Kimberly Edwards,[6] Paul T. Englund,[16] Gholam Fazelina,[3] Tamara Feldblyum,[1] Marcela Ferella,[6] Alberto Carlos Frasch,[17] Keith Gull,[18] David Horn,[19] Lihua Hou,[1] Yiting Huang,[3] Ellen Kindlund,[6] Michele Klingbeil,[20] Sindy Kluge,[6] Hean Koo,[1] Daniela Lacerda,[1,21] Mariano J. Levin,[22] Hernan Lorenzi,[22] Tin Louie,[3] Carlos Renato Machado,[8] Richard McCulloch,[12] Alan McKenna,[6] Yumi Mizuno,[6] Jeremy C. Mottram,[12] Siri Nelson,[3] Stephen Ochaya,[6] Kazutoyo Osoegawa,[15] Grace Pai,[1] Marilyn Parsons,[3,4] Martin Pentony,[3] Ulf Pettersson,[9] Mihai Pop,[1] Jose Luis Ramirez,[23] Joel Rinta,[3] Laura Robertson,[3] Steven L. Salzberg,[1] Daniel O. Sanchez,[17] Amber Seyler,[3] Reuben Sharma,[13] Jyoti Shetty,[1] Anjana J. Simpson,[1] Ellen Sisk,[3] Martti T. Tammi,[6,24] Rick Tarleton,[25] Santuza Teixeira,[8] Susan Van Aken,[1] Christy Vogt,[3] Pauline N. Ward,[12] Bill Wickstead,[18] Jennifer Wortman,[1] Owen White,[1] Claire M. Fraser,[1] Kenneth D. Stuart,[3,4] Björn Andersson[6†]

Whole-genome sequencing of the protozoan pathogen *Trypanosoma cruzi* revealed that the diploid genome contains a predicted 22,570 proteins encoded by genes, of which 12,570 represent allelic pairs. Over 50% of the genome marily in Central and South America, with 21,000 deaths reported each year (*1*). *T. cruzi* is normally transmitted by reduviid bugs via

Kinetoplastea genomes



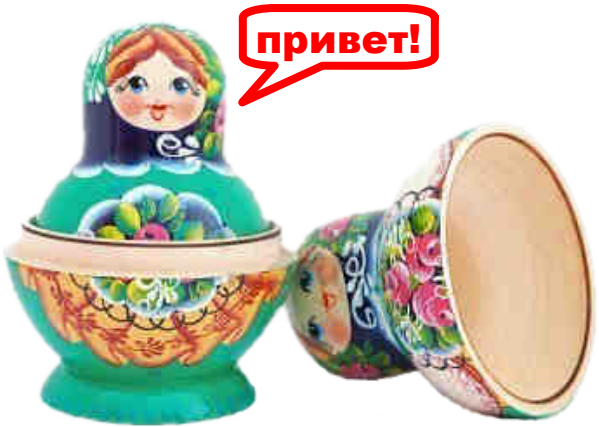

Perkinsela
Porcisia
Trypanosoma
Herpetomonas
Phytomonas
Crithidia
Angomonas
Novymonas
Lotmaria
Blechomonas
Leishmania
Strigomonas
Bodo
Leptomonas
Trypanosomatidae spp.
Endotrypanum
Vickermania
Paratrypanosoma

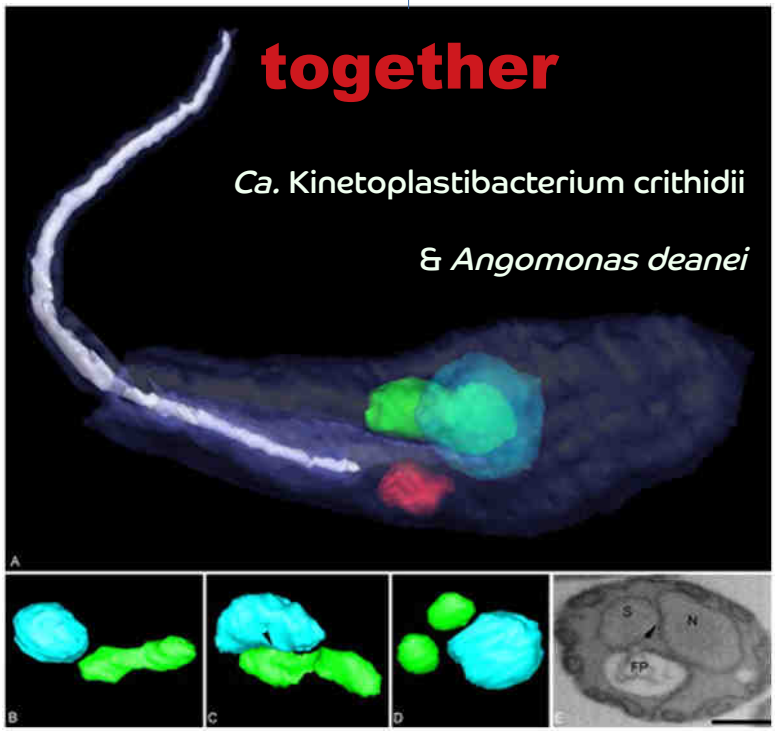
life

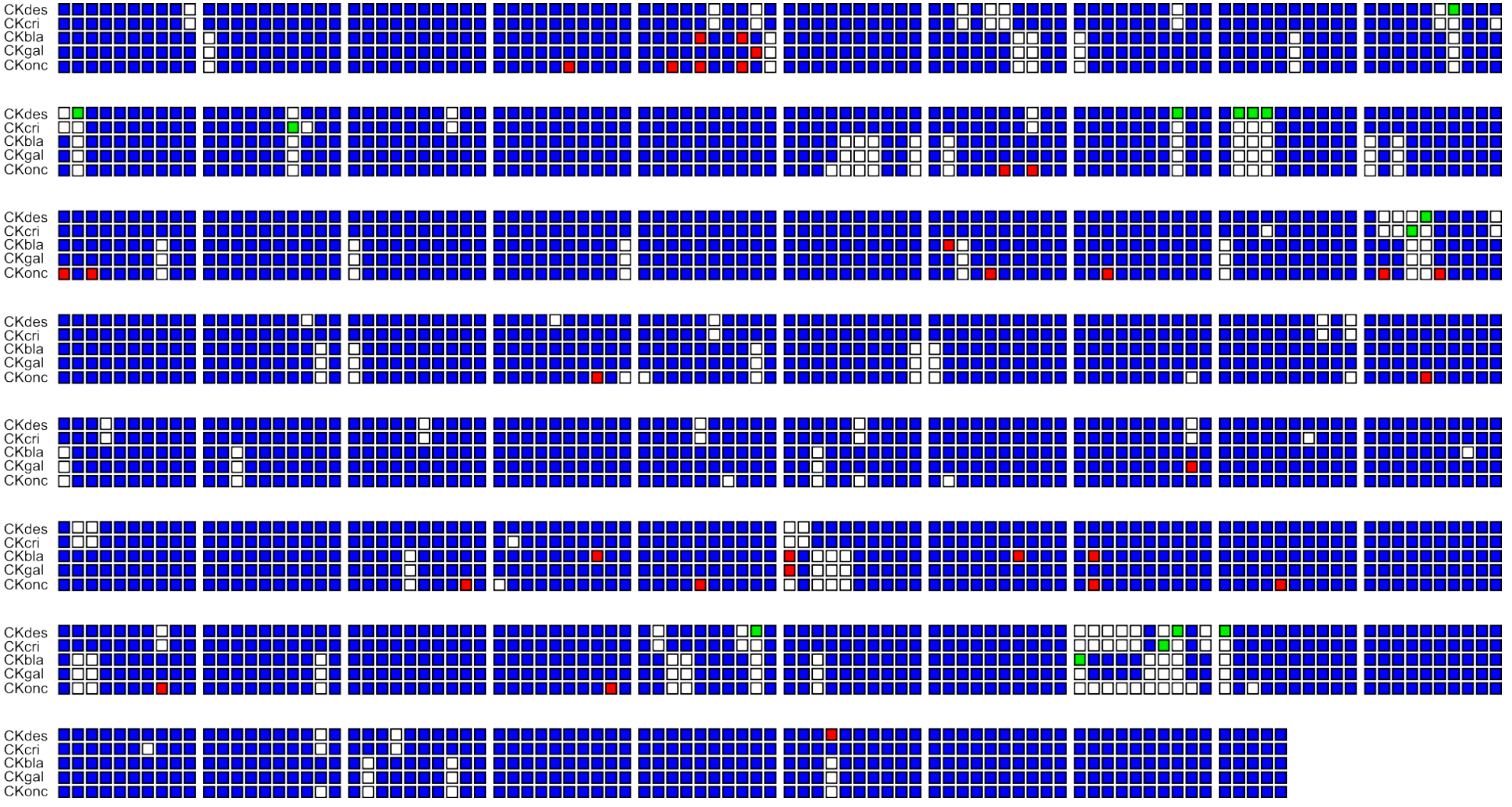
ENDOSYMBIOSIS

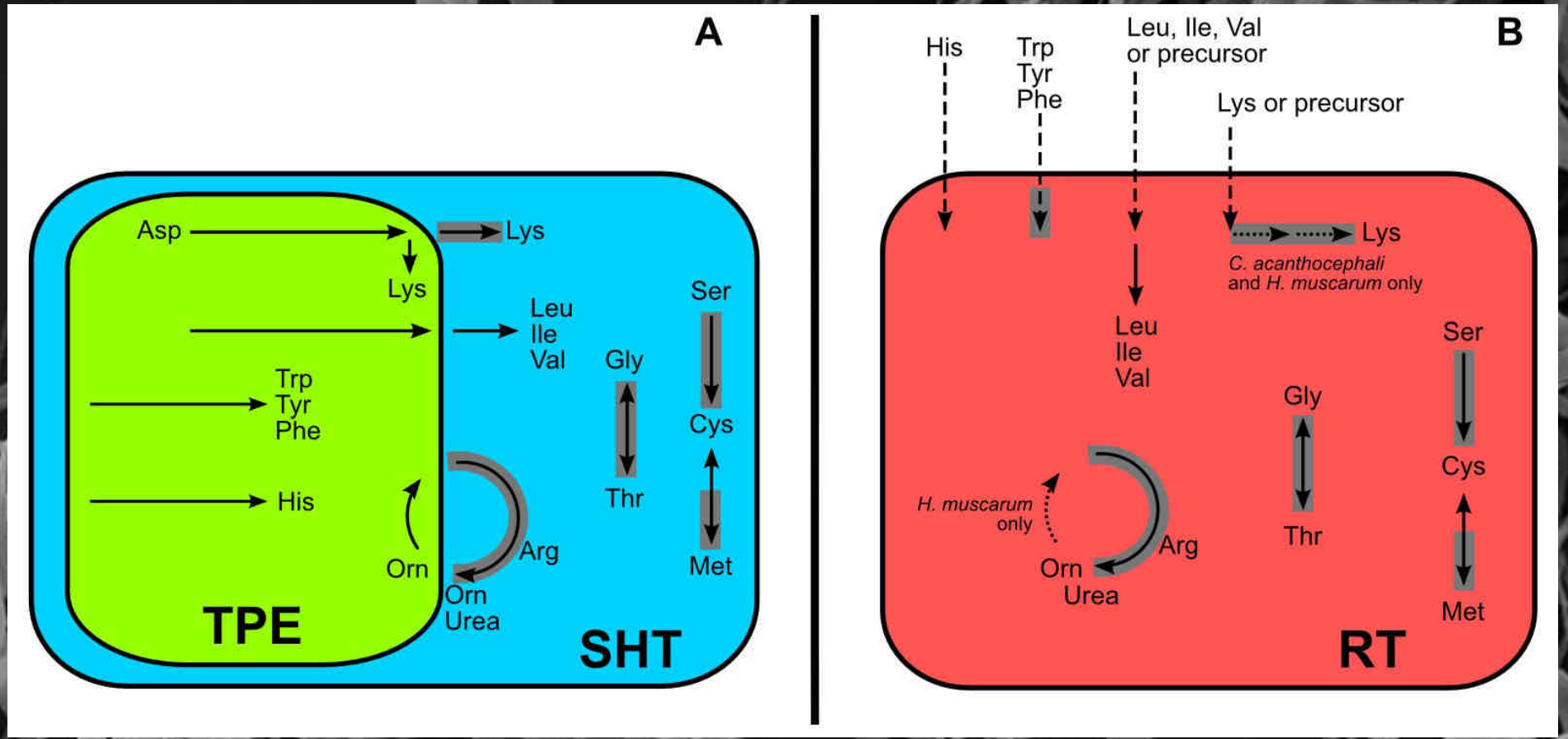
within

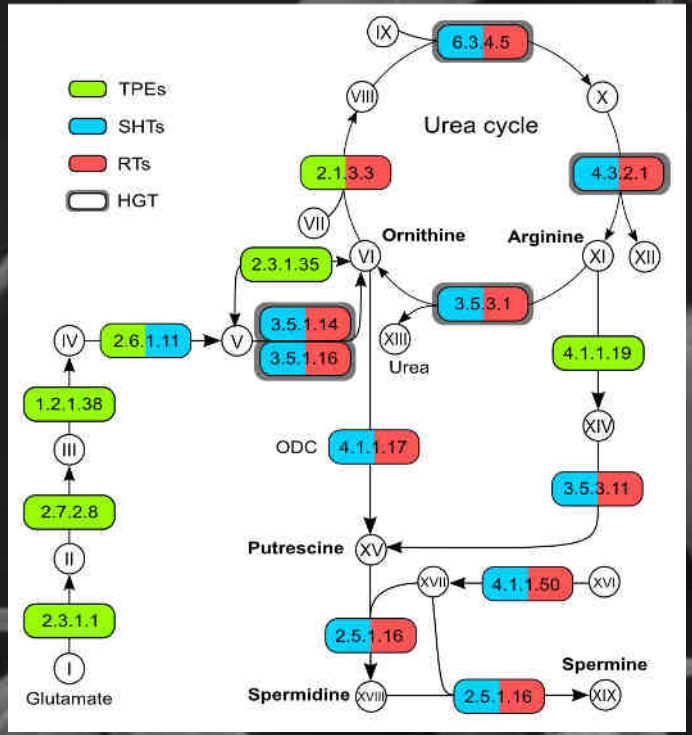
together

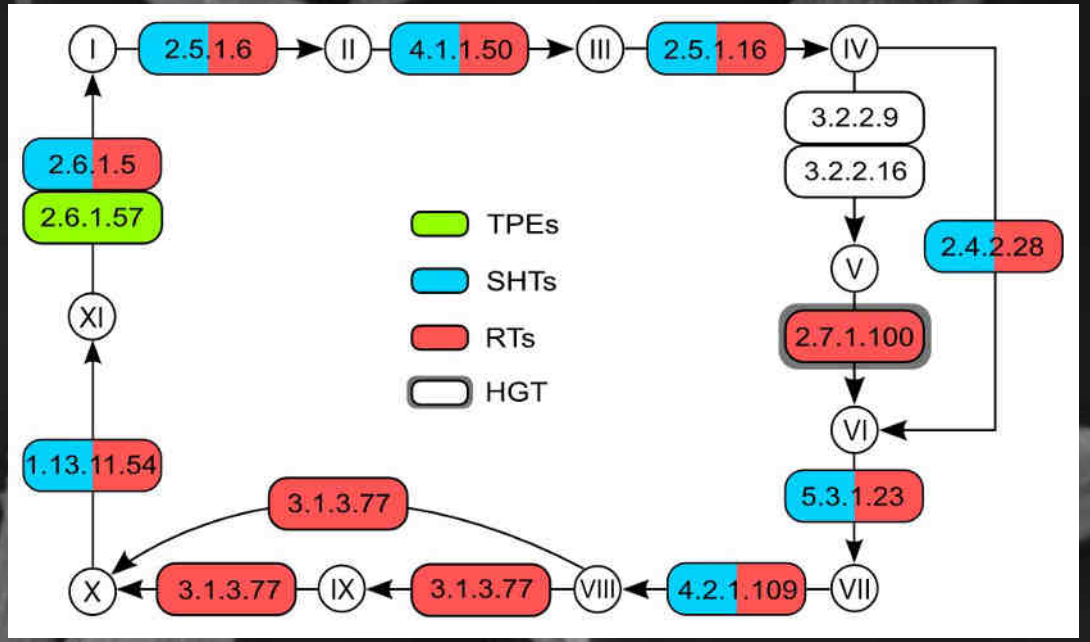


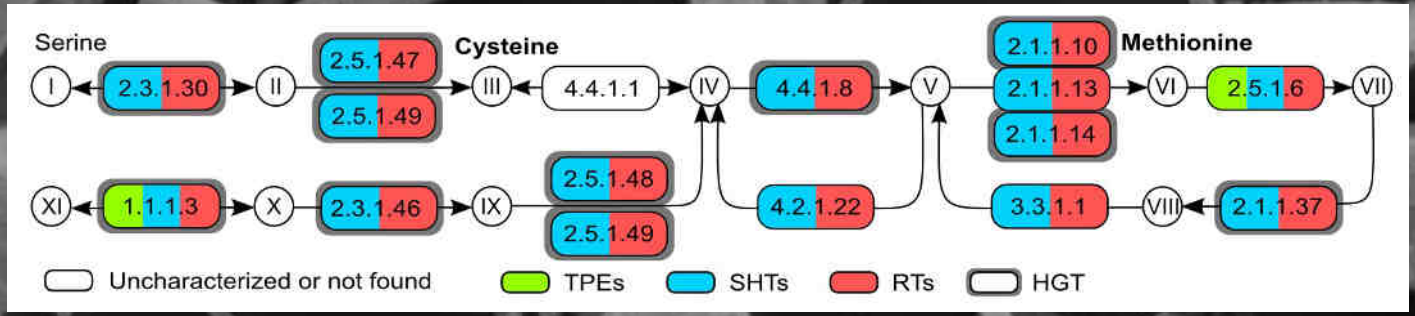


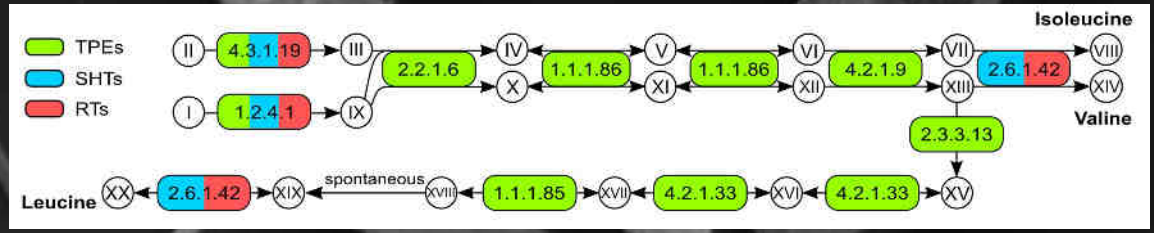

CKdes
CKcri
CKbla
CKgal
CKonc

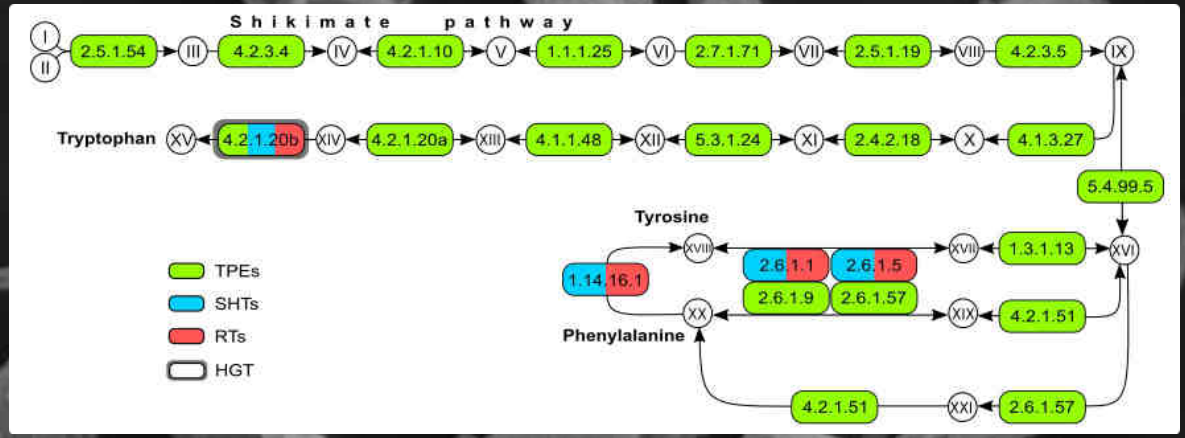

A
Asp
Lys
Lys
Leu
Ile
Val
Ser
Gly
Trp
Tyr
Phe
Cys
His
Thr
Orn
Arg
Orn
Urea
Met
TPE
SHT
B
His
Trp
Tyr
Phe
Leu, Ile, Val
or precursor
Lys or precursor
Lys
C. acanthocephali
and H. muscarum only
Leu
Ile
Val
Ser
Gly
Cys
H. muscarum
only
Arg
Orn
Urea
Thr
Met
RT

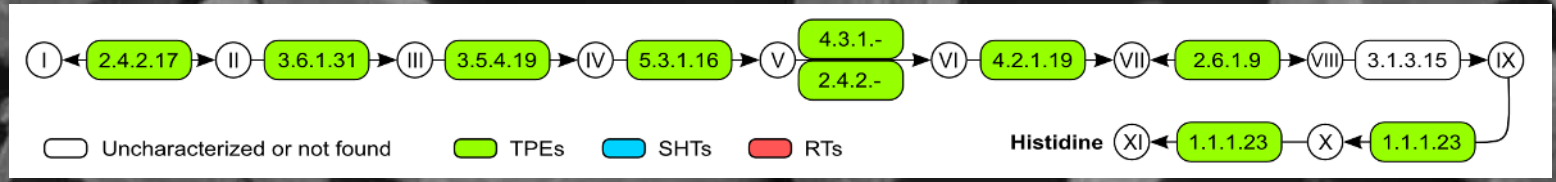

TPEs
SHTs
RTs
HGT
Urea cycle
Ornithine
Arginine
Urea
ODC
Putrescine
Spermidine
Spermine
Glutamate
6.3.4.5
2.1.3.3
4.3.2.1
2.3.1.35
3.5.3.1
3.5.1.14
3.5.1.16
2.6.1.11
4.1.1.19
1.2.1.38
4.1.1.17
2.7.2.8
3.5.3.11
2.3.1.1
4.1.1.50
2.5.1.16
2.5.1.16


TPEs
SHTs
RTs
HGT
2.5.1.6
4.1.1.50
2.5.1.16
3.2.2.9
3.2.2.16
2.4.2.28
2.6.1.5
2.6.1.57
2.7.1.100
1.13.11.54
5.3.1.23
3.1.3.77
3.1.3.77
3.1.3.77
4.2.1.109

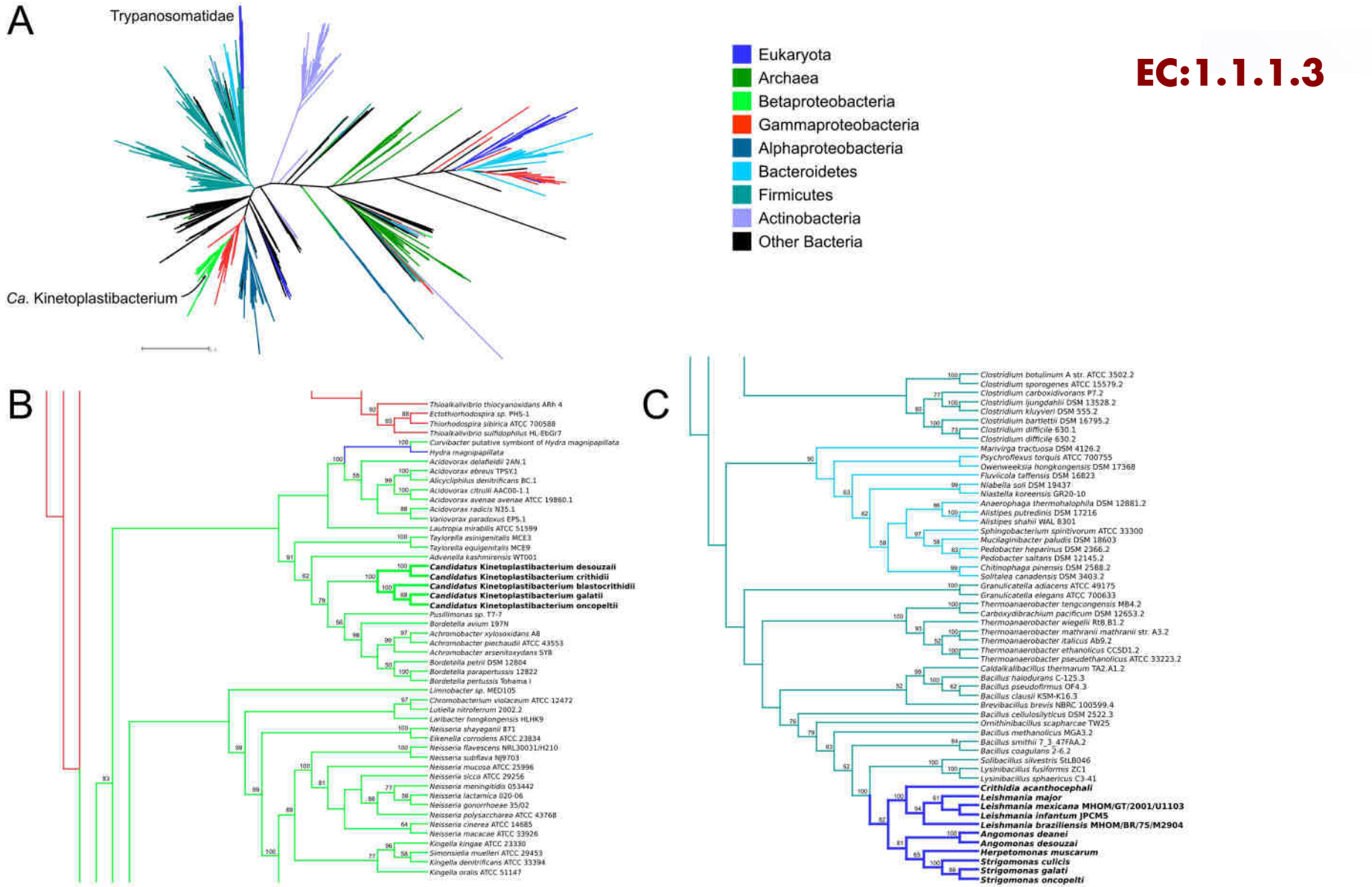

Serine
Cysteine
Methionine
2.3.1.30
2.5.1.47
2.5.1.49
4.4.1.1
4.4.1.8
2.1.1.10
2.1.1.13
2.1.1.14
2.5.1.6
1.1.1.3
2.3.1.46
2.5.1.48
2.5.1.49
4.2.1.22
3.3.1.1
2.1.1.37
Uncharacterized or not found
TPEs
SHTs
RTs
HGT


TPEs
SHTs
RTs
Isoleucine
II
4.3.1.19
III
2.2.1.6
IV
1.1.1.86
V
1.1.1.86
VI
4.2.1.9
VII
2.6.1.42
VIII
I
1.2.4.1
IX
X
XI
XII
XIII
XIV
Valine
2.3.3.13
Leucine
XX
2.6.1.42
XIX
spontaneous
XVIII
1.1.1.85
XVII
4.2.1.33
XVI
4.2.1.33
XV

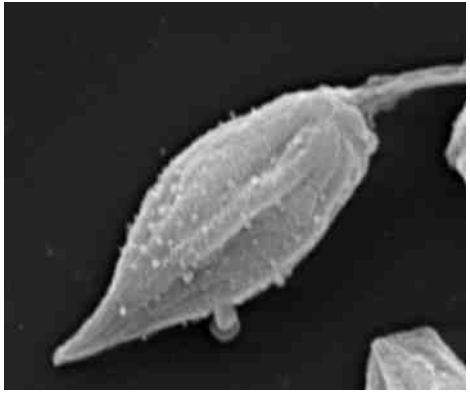

Shikimate pathway
I
II
2.5.1.54
III
4.2.3.4
IV
4.2.1.10
V
1.1.1.25
VI
2.7.1.71
VII
2.5.1.19
VIII
4.2.3.5
IX
Tryptophan
XV
4.2.1.20b
XIV
4.2.1.20a
XIII
4.1.1.48
XII
5.3.1.24
XI
2.4.2.18
X
4.1.3.27
5.4.99.5
Tyrosine
XVIII
2.6.1.1
2.6.1.5
XVII
1.3.1.13
XVI
1.14.16.1
2.6.1.9
2.6.1.57
XIX
4.2.1.51
XX
Phenylalanine
4.2.1.51
XXI
2.6.1.57
TPEs
SHTs
RTs
HGT


I
2.4.2.17
II
3.6.1.31
III
3.5.4.19
IV
5.3.1.16
V
4.3.1.-
2.4.2.-
VI
4.2.1.19
VII
2.6.1.9
VIII
3.1.3.15
IX
Uncharacterized or not found
TPEs
SHTs
RTs
Histidine
XI
1.1.1.23
X
1.1.1.23

Origins

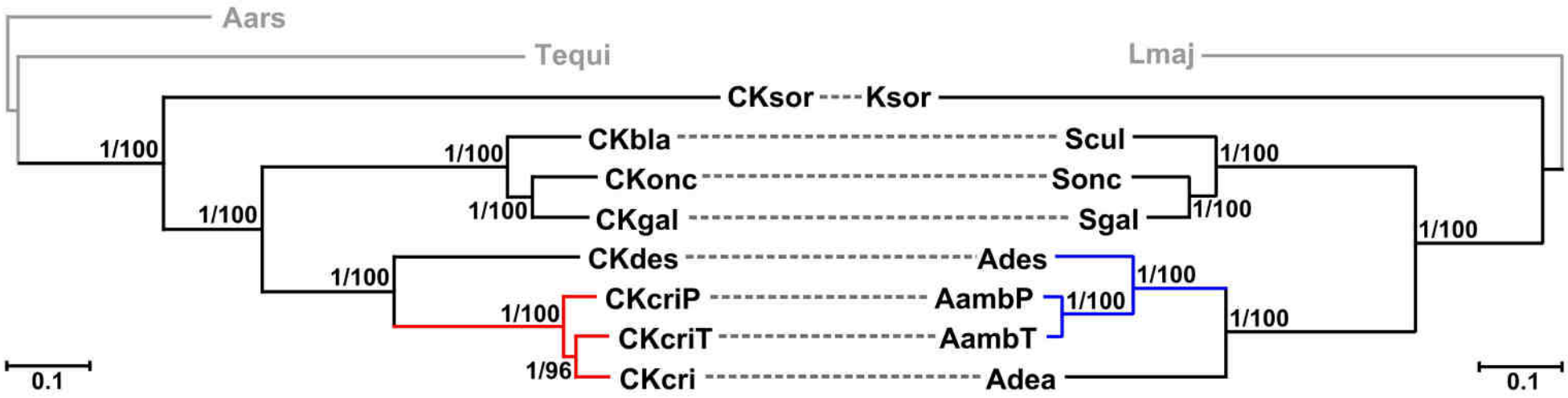

A
Trypanosomatidae
Ca. Kinetoplastibacterium
Eukaryota
Archaea
Betaproteobacteria
Gammaproteobacteria
Alphaproteobacteria
Bacteroidetes
Firmicutes
Actinobacteria
Other Bacteria
EC:1.1.1.3
B
Thioalkalivibrio thiocyanoxidans ARh 4
Ectothiorhodospira sp. PHS-1
Thiorhodospira sibirica ATCC 700588
Thioalkalivibrio sulfidophilus HL-EbGr7
Curvibacter putative symbiont of Hydra magnipapillata
Hydra magnipapillata
Acidovorax delafieldii 2AN.1
Acidovorax ebreus TPSY.1
Alicycliphilus denitrificans BC.1
Acidovorax citrulli AAC00-1.1
Acidovorax avenae avenae ATCC 19860.1
Acidovorax radicis N35.1
Variovorax paradoxus EPS.1
Lautropia mirabilis ATCC 51599
Taylorella asinigenitalis MCE3
Taylorella equigenitalis MCE9
Advenella kashmirensis WT001
Candidatus Kinetoplastibacterium desouzaii
Candidatus Kinetoplastibacterium crithidii
Candidatus Kinetoplastibacterium blastocrithidii
Candidatus Kinetoplastibacterium galatii
Candidatus Kinetoplastibacterium oncopeltii
Pusillimonas sp. T7-7
Bordetella avium 197N
Achromobacter xylosoxidans A8
Achromobacter piechaudii ATCC 43553
Achromobacter arsenitoxydans SY8
Bordetella petrii DSM 12804
Bordetella parapertussis 12822
Bordetella pertussis Tohama I
Limnobacter sp. MED105
Chromobacterium violaceum ATCC 12472
Lutiella nitroferrum 2002.2
Laribacter hongkongensis HLHK9
Neisseria shayeganii 871
Eikenella corrodens ATCC 23834
Neisseria flavescens NRL30031/H210
Neisseria subflava NJ9703
Neisseria mucosa ATCC 25996
Neisseria sicca ATCC 29256
Neisseria meningitidis 053442
Neisseria lactamica 020-06
Neisseria gonorrhoeae 35/02
Neisseria polysaccharea ATCC 43768
Neisseria cinerea ATCC 14685
Neisseria macacae ATCC 33926
Kingella kingae ATCC 23330
Simonsiella muelleri ATCC 29453
Kingella denitrificans ATCC 33394
Kingella oralis ATCC 51147
C
Clostridium botulinum A str. ATCC 3502.2
Clostridium sporogenes ATCC 15579.2
Clostridium carboxidivorans P7.2
Clostridium ljungdahlii DSM 13528.2
Clostridium kluyveri DSM 555.2
Clostridium bartlettii DSM 16795.2
Clostridium difficile 630.1
Clostridium difficile 630.2
Mariniga tractuosa DSM 4126.2
Psychroflexus torquis ATCC 700755
Owenweeksia hongkongensis DSM 17368
Fluviicola taffensis DSM 16823
Niabella soli DSM 19437
Niastella koreensis GR20-10
Anaerophaga thermohalophila DSM 12881.2
Alistipes putredinis DSM 17216
Alistipes shahii WAL 8301
Sphingobacterium spiritivorum ATCC 33300
Mucilaginibacter paludis DSM 18603
Pedobacter heparinus DSM 2366.2
Pedobacter saltans DSM 12145.2
Chitinophaga pinensis DSM 2588.2
Solitalea canadensis DSM 3403.2
Granulicatella adiacens ATCC 49175
Granulicatella elegans ATCC 700633
Thermoanaerobacter tengcongensis MB4.2
Carboxydibrachium pacificum DSM 12653.2
Thermoanaerobacter wiegelii Rt8.B1.2
Thermoanaerobacter mathranii mathranii str. A3.2
Thermoanaerobacter italicus Ab9.2
Thermoanaerobacter ethanolicus CCSD1.2
Thermoanaerobacter pseudethanolicus ATCC 33223.2
Caldalkalibacillus thermarum TA2.A1.2
Bacillus halodurans C-125.3
Bacillus pseudofirmus OF4.3
Bacillus clausii KSM-K16.3
Brevibacillus brevis NBRC 100599.4
Bacillus cellulosilyticus DSM 2522.3
Ornithinibacillus scapharcae TW25
Bacillus methanolicus MGA3.2
Bacillus smithii 7_3_47FAA.2
Bacillus coagulans 2-6.2
Solibacillus silvestris StLB046
Lysinibacillus fusiformis ZC1
Lysinibacillus sphaericus C3-41
Crithidia acanthocephali
Leishmania major
Leishmania mexicana MHOM/GT/2001/U1103
Leishmania infantum JPCM5
Leishmania braziliensis MHOM/BR/75/M2904
Angomonas deanei
Angomonas desouzai
Herpetomonas muscarum
Strigomonas culicis
Strigomonas galati
Strigomonas oncopelti

Strigomonas culicis	***Candidatus* Kinetoplastibacterium blastocrithidii**
Strigomonas galati	***Ca.* K. galatii**
Strigomonas oncopelti	***Ca.* K. oncopeltii**
Angomonas desouzai	***Ca.* K. desouzaii**
Angomonas ambiguus	***Ca.* K. crithidii**
Angomonas deanei	
Kentomonas sorsogonicus	***Ca.* K. sorsogonicusi**



TPE

SHT



pathogens

MDPI

Article

Endosymbiont Capture, a Repeated Process of Endosymbiont Transfer with Replacement in Trypanosomatids *Angomonas* spp.

Tomáš Skalický [1,†], João M. P. Alves [2,†], Anderson C. Morais [2], Jana Režnarová [3], Anzhelika Butenko [1,3], Julius Lukeš [1,4], Myrna G. Serrano [5], Gregory A. Buck [5], Marta M. G. Teixeira [2], Erney P. Camargo [2], Mandy Sanders [6], James A. Cotton [6], Vyacheslav Yurchenko [3,7] and Alexei Y. Kostygov [3,8,*]

Parasitology

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The reduced genome of *Candidatus* Kinetoplastibacterium sorsogonicusi, the endosymbiont of *Kentomonas sorsogonicus* (Trypanosomatidae): loss of the haem-synthesis pathway

Flávia M. Silva[1], Alexei Y. Kostygov[2,3], Viktoria V. Spodareva[2,3], Anzhelika Butenko[2,4], Regis Tossou[1], Julius Lukeš[4,5], Vyacheslav Yurchenko[2,4] and João M. P. Alves[1]

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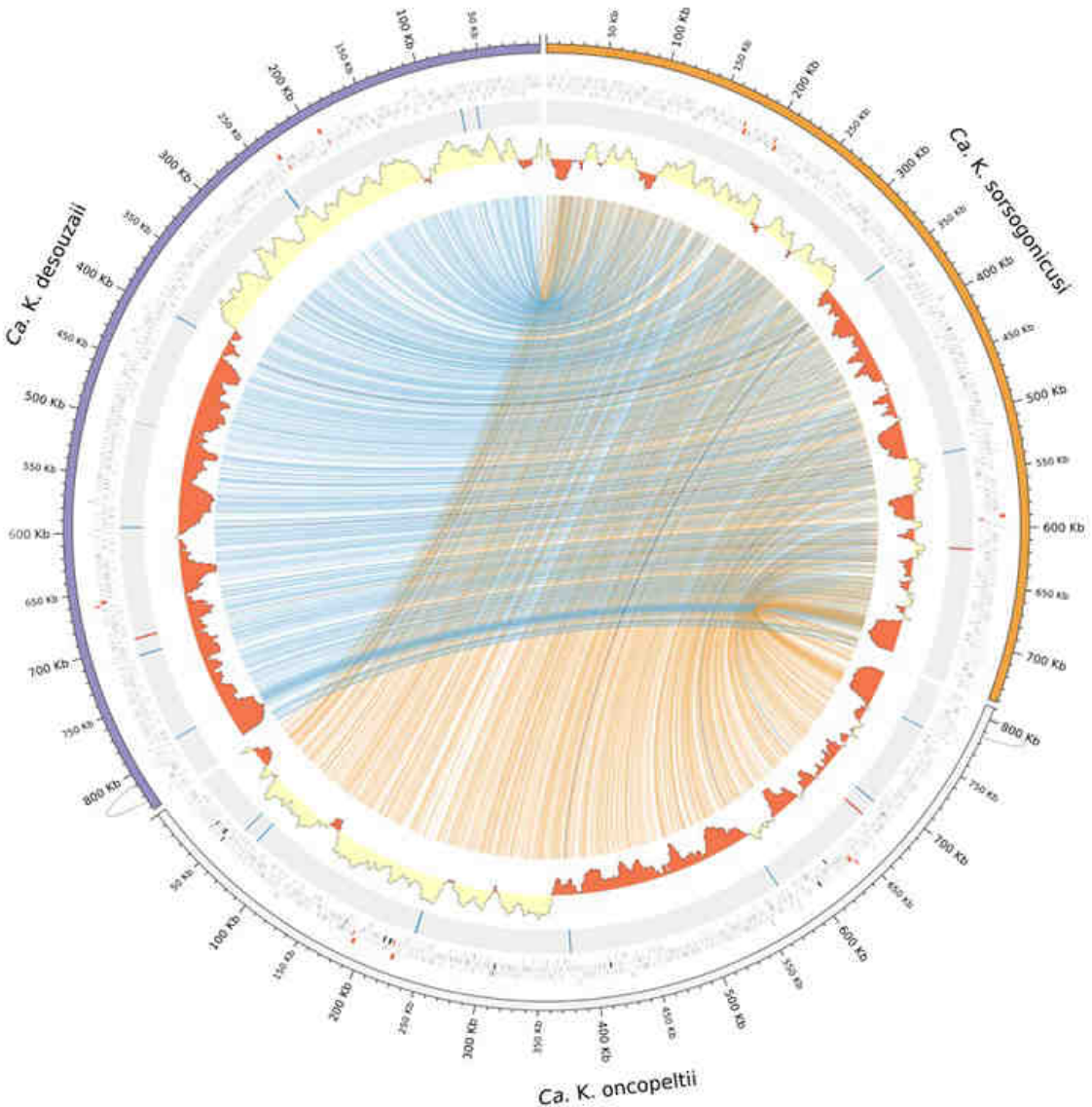
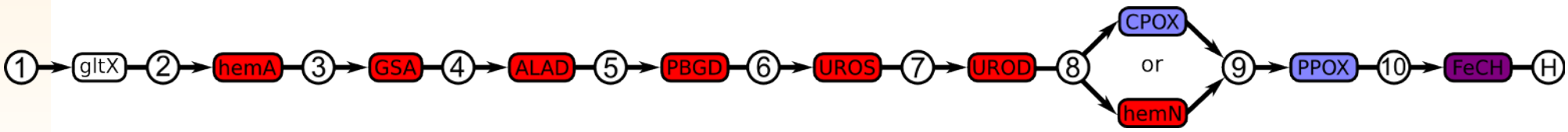
Abstract

Trypanosomatids of the genera *Angomonas* and *Strigomonas* (subfamily Strigomonadinae) have long been known to contain intracellular beta-proteobacteria, which provide them with many important nutrients such as haem, essential amino acids and vitamins. Recently, *Kentomonas sorsogonicus*, a divergent member of Strigomonadinae, has been described. Herein, we characterize the genome of its endosymbiont, *Candidatus*

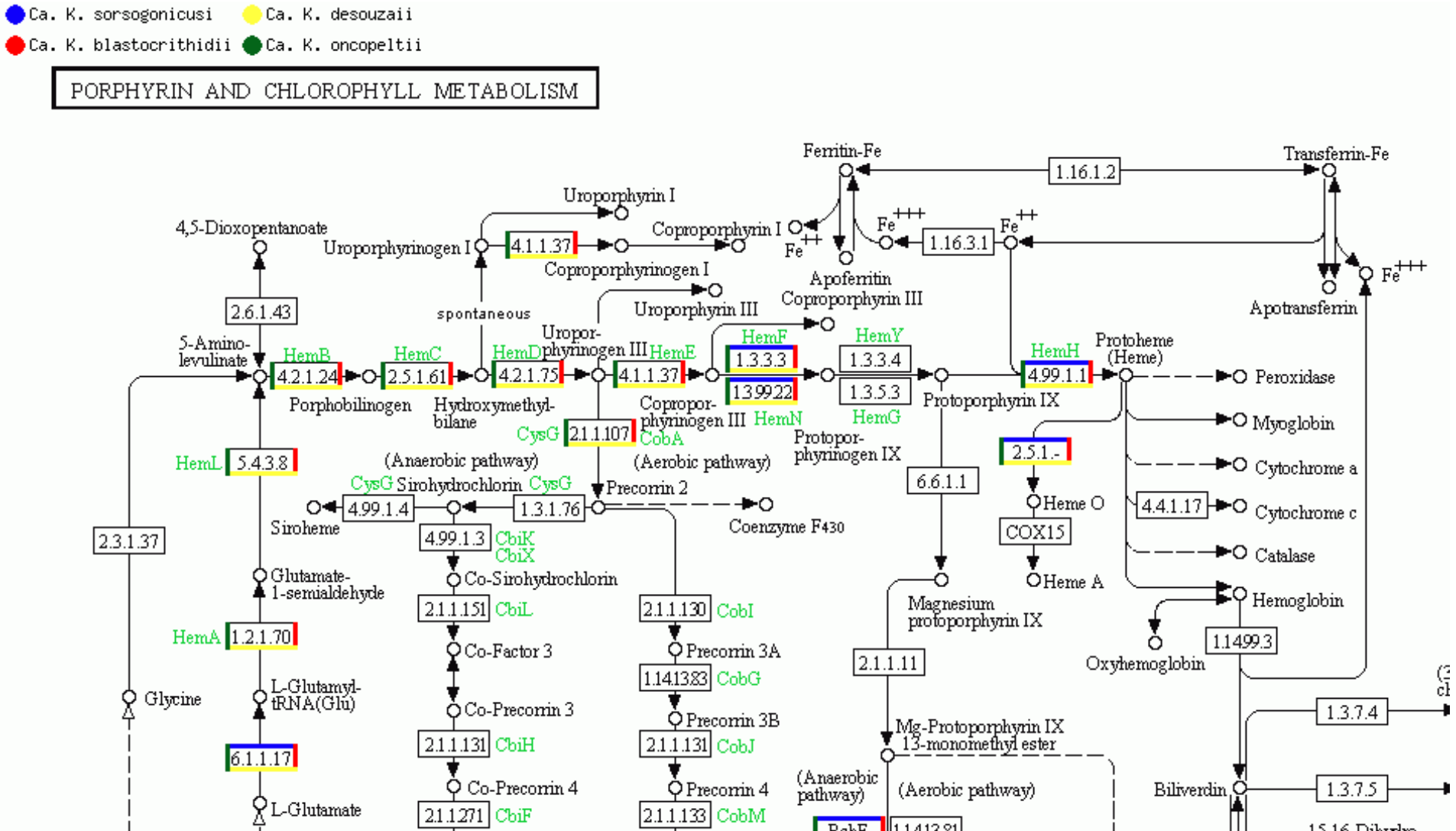


Heme synthesis

- For decades, the hemin test has been applied
  - Need hemin: no endosymbiont present
  - Don't need it: endosymbiont present
- Kill the TPE, then a source of heme becomes essential to the trypanosomatid



Ca. K. sorsogonicusi Ca. K. desouzaii
Ca. K. blastocrithidii Ca. K. oncopeltii



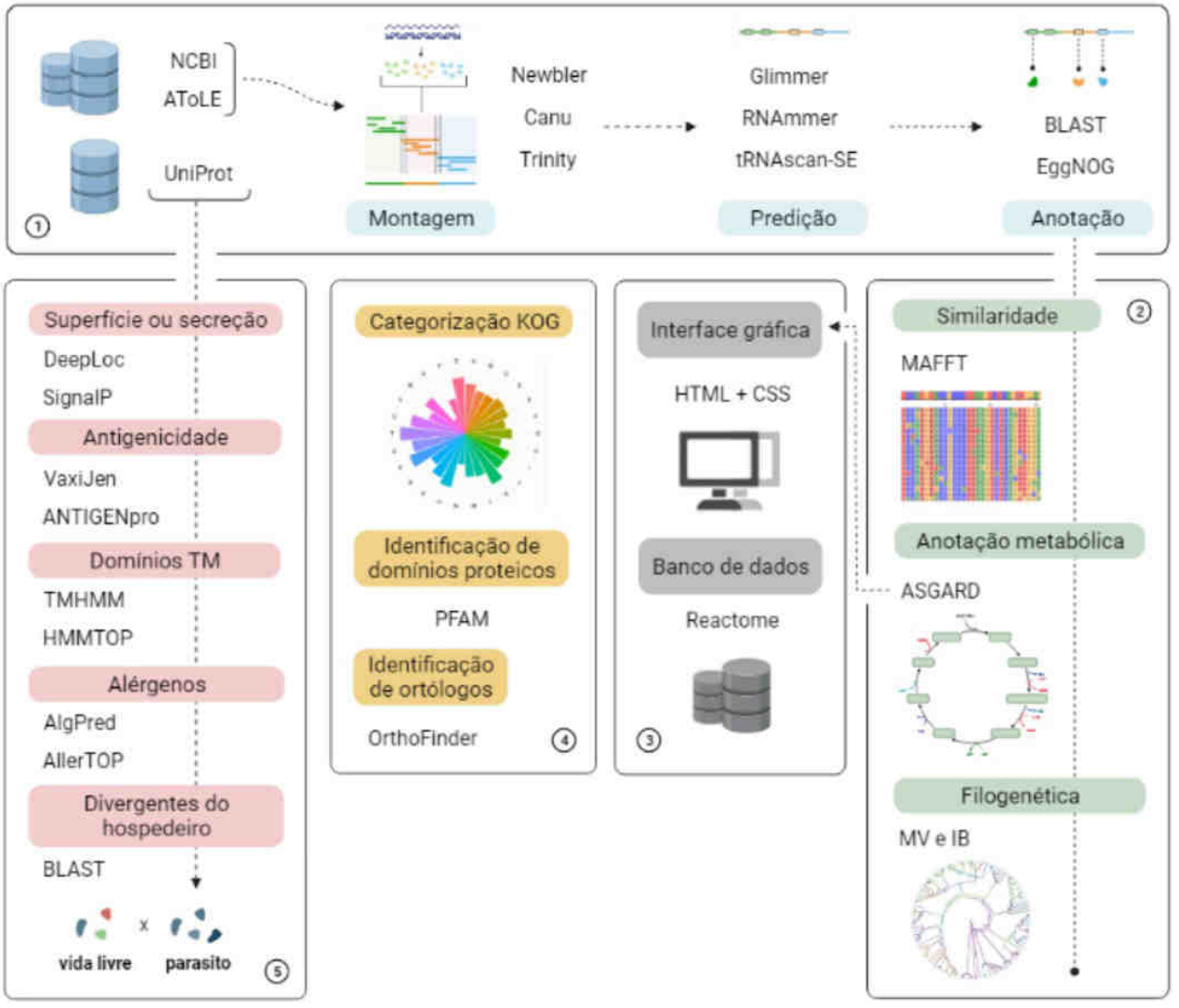
	LmjF	*Lpanam*	*Lbrazi*	*Emonte*	*Eschau*	Dominio
PF00004	115	116	120	123	126	Familia ATPase (AAA)
PF00005	118	110	117	127	116	Transportador tipo ABC
PF00012	25	15	27	23	15	Proteina HSP70
PF00069	206	195	197	202	209	Proteina quinase (PKs)
PF00076	85	84	84	80	80	Reconhecimento ao RNA
PF00153	42	33	36	35	34	Transportador mitocondrial
PF00173	25	23	26	25	23	União ao esteroide e heme
PF00400	121	122	120	115	123	Dominio WD40, Repetição β G
PF00515	88	90	93	93	95	Repetições (TPR)
PF00612	25	26	24	27	30	União a calmodulina
PF00642	38	43	45	37	38	Dedo de Zinco (c-x8-c-x5-x3-h)
PF00648	68	25	24	27	24	Cisteina protease (Calpaina)
PF00806	11	10	11	12	12	Familia pumilio união ao RNA
PF01187	2	1	1	2	1	Inibição da migração do macrófago
PF01457	6	5	38	177	161	Leishmanolisina (GP63)
PF01490	27	23	27	26	23	Transportador de aminoácidos trans.
PF02493	21	21	21	21	21	Repetições MORN
PF03133	9	9	10	10	10	Familia ligase tirosina-tubulina
PF07344	68	38	62	22	21	Glicoproteina de superficie Amastina
PF12796	34	31	30	31	34	Repetições de Anquirina
PF13855	114	90	94	160	195	Repetições ricas em leucine (LRR)
PF13920	69	65	63	48	62	Dedos de Zinco tipo (c3hc4)

Anotação PFAM

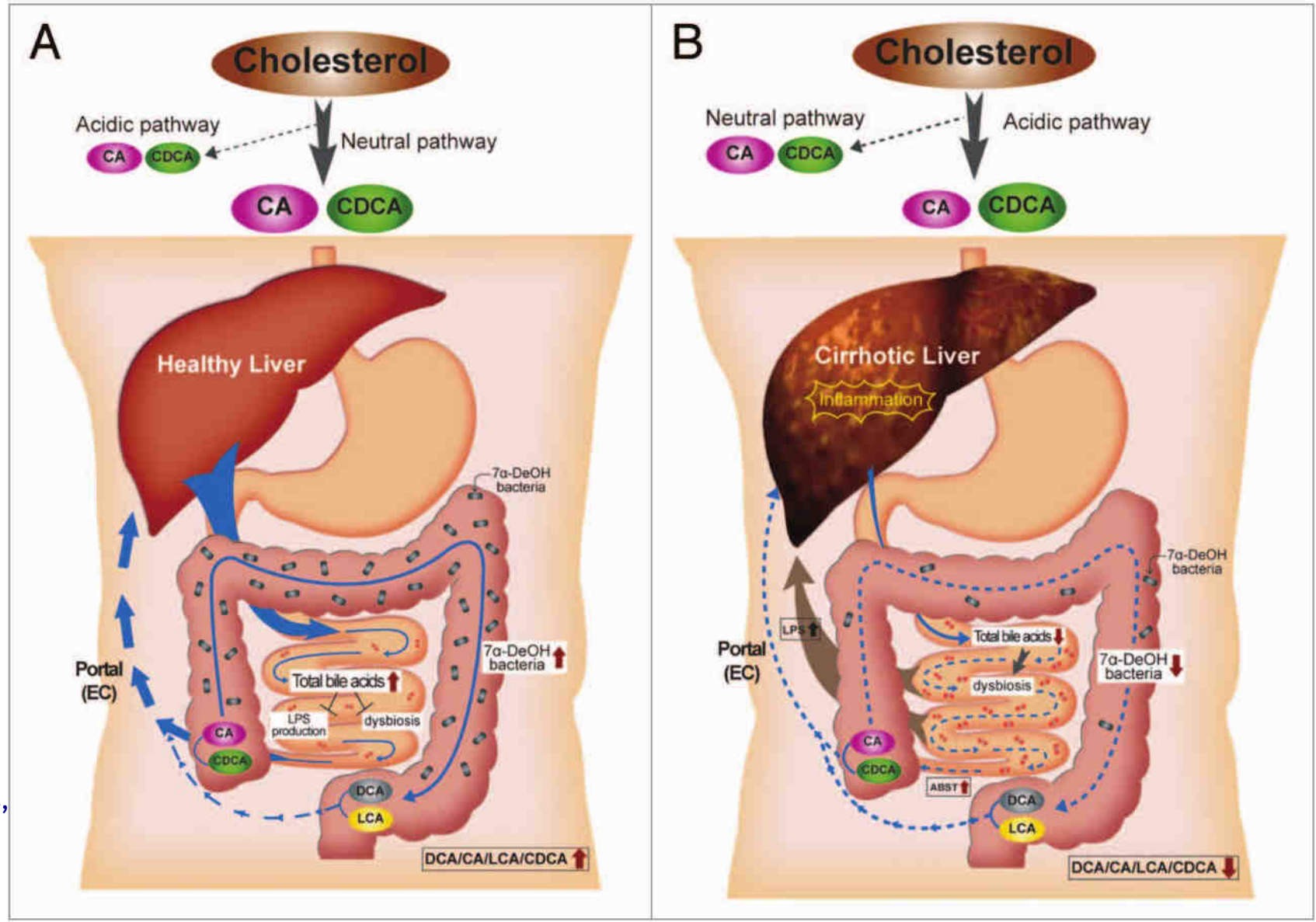
< 35
70
105
140
209

Percy O.T. Vergara

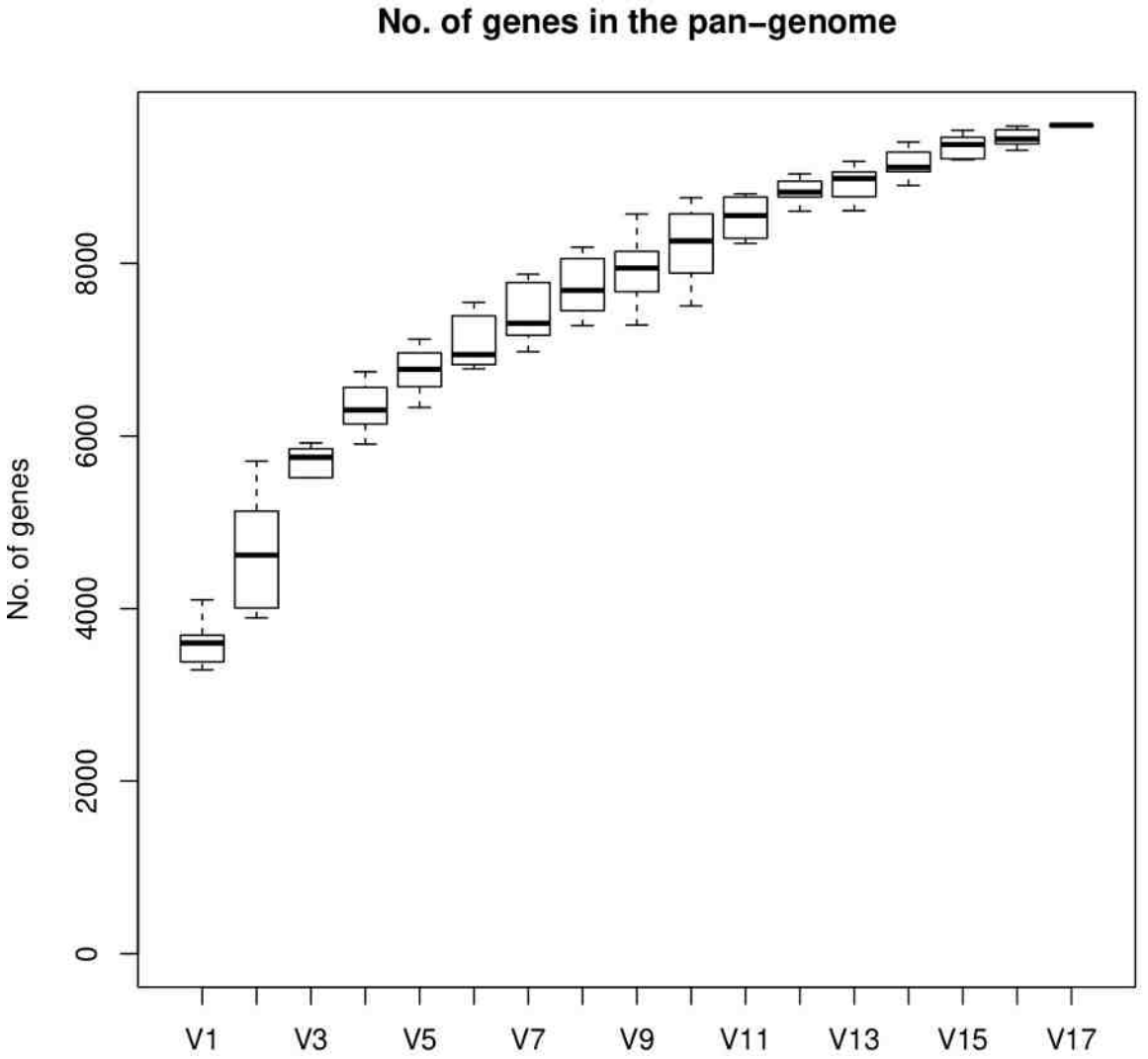
Immunoinformatics

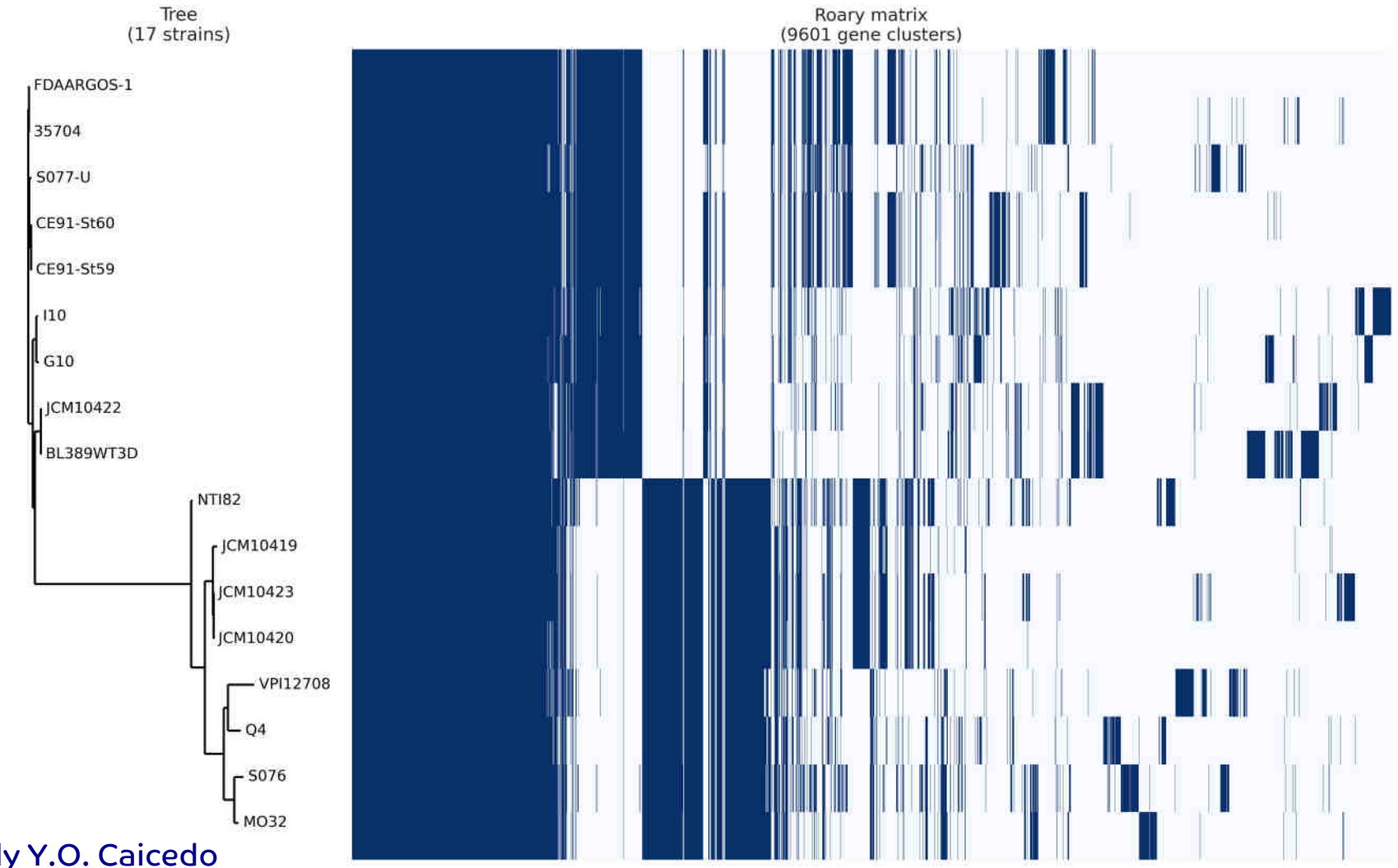


Davi S. Xavier



From: Ridlon, J.M., Alves, J.M.P., Hylemon, P.B. & Bajaj, J.S. *Gut. Microbes* 4(5):382, 2013


No. of genes in the pan−genome
No. of genes
0
2000
4000
6000
8000
V1
V3
V5
V7
V9
V11
V13
V15
V17



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TO BE
CONTINUED...

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