

Supplementary Material To:
“Prokaryote Phylogeny Meets Taxonomy:
An Exhaustive Comparison of Composition Vector Trees
With Systematic Bacteriology”

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1 List of Genomes Used in this Study

A total of 440 complete genomes were used in this study that include 31 Archaea, 401 Bacteria and 8 Eukaryotes as of 31 December 2006 at the NCBI ftp-site^[1]. List of these complete genomes, the abbreviations of organism names, and their Bergey’s code are given in Table 1 (*Archaea*), Table 2 (*Bacteria*), and Table 3 (*Eukaryote*).

Abbreviations:

P=Phylum, C=Class, O=Order, F=Family, G=Genus, S=Species, str=strain; A=Archaea, B=Bacteria, E=Eukaryote.

The abbreviations of organism names follow that of the SWISS-PROT database. If absent in SWISS-PROT we concatenate the first three letters of the genus name and two or three letters from the rest. Thus *Thermococcus kodakaraensis* *KOD1* should be assigned an abbreviation as Theko according to our convention. However, as it was named Pyrko in SWISS-PROT we keep the latter (this was caused by the fact that this Archaea was considered a *Pyrococcus* before).

Bergey’s code:

A lineage in the *Bergey’s Manual of Systematic Bacteriology* or its online *Outline*^[2] is abbreviated as B13.3.2.6.2 or $B_{13}C_3O_2F_6G_2$ = Phylum BXIII (*Firmicutes*), Class III (*Bacilli*), Order II (*Lactobacillales*), Family VI (*Streptococcaceae*), Genus II (*Lactococcus*). The Bergey’s code was introduced in 2004 by Qi *et al.*^[3]. It must be noted that the Bergey’s code is a convenient shorthand that may change with each new edition of the Bergey’s Manual. The current code corresponds to Rel. 5.0 of the online *Outline*^[2].

Table 1: List of 31 Archaea genomes.

Organism	Abbr	Accession	Bergey Code
<i>Pyrobaculum aerophilum</i>	Pyrae	NC_003364	A1.1.1.1.3
<i>Pyrobaculum islandicum</i> DSM 4184	Pyris	NC_008701	A1.1.1.1.3
<i>Thermofilum pendens</i> Hrk 5	Thepe	NC_008698	A1.1.1.2.1
<i>Aeropyrum pernix</i> K1	Aerpe	NC_000854	A1.1.3.1.3
<i>Sulfolobus acidocaldarius</i> DSM 639	Sulac	NC_007181	A1.1.4.1.1
<i>Sulfolobus solfataricus</i>	Sulso	NC_002754	A1.1.4.1.1
<i>Sulfolobus tokodaii</i>	Sulto	NC_003106	A1.1.4.1.1
<i>Methanobacterium thermoautotrophicum</i>	Metth	NC_000916	A2.1.1.1.1
<i>Methanosphaera stadtmanae</i> DSM 3091	Metst	NC_007681	A2.1.1.1.3
<i>Methanococcus maripaludis</i> S2	Metmp	NC_005791	A2.2.1.1.1
<i>Methanocaldococcus jannaschii</i>	Metja	NC_000909 NC_001732.33	A2.2.1.2.1
<i>Methanospirillum hungatei</i> JF-1	Methj	NC_007796	A2.3.1.3.1
<i>Methanosarcina acetivorans</i> str. C2A	Metac	NC_003552	A2.3.2.1.1
<i>Methanosarcina barkeri</i> fusaro	Metbf	NC_007355	A2.3.2.1.1
<i>Methanosarcina mazei</i>	Metma	NC_003901	A2.3.2.1.1
<i>Methanococcoides burtonii</i> DSM 6242	Metbu	NC_007955	A2.3.2.1.2
<i>Methanosaeta thermophila</i> PT	MetthP	NC_008553	A2.3.2.2.1
<i>Haloquadratum walsbyi</i>	Halwd	NC_008212	A2.4.1.1.?
<i>Halobacterium</i> sp. NRC-1	Halsa	NC_002607	A2.4.1.1.1
<i>Haloarcula marismortui</i> ATCC 43049	Halma	NC_006396-97	A2.4.1.1.2
<i>Natronomonas pharaonis</i> DSM 2160	Natpd	NC_007426	A2.4.1.1.17
<i>Thermoplasma acidophilum</i>	Theac	NC_002578	A2.5.1.1.1
<i>Thermoplasma volcanium</i>	Thevo	NC_002689	A2.5.1.1.1
<i>Picrophilus torridus</i> DSM 9790	Picto	NC_005877	A2.5.1.2.1
<i>Thermococcus kodakaraensis</i> KOD1	Pyrko	NC_006624	A2.6.1.1.1
<i>Pyrococcus abyssi</i>	Pyrab	NC_000868	A2.6.1.1.3
<i>Pyrococcus furiosus</i>	Pyrfu	NC_003413	A2.6.1.1.3
<i>Pyrococcus horikoshii</i>	Pyrho	NC_000961	A2.6.1.1.3
<i>Archaeoglobus fulgidus</i>	Arcfu	NC_000917	A2.7.1.1.1
<i>Methanopyrus kandleri</i> AV19	Metka	NC_003551	A2.8.1.1.1
<i>Nanoarchaeum equitans</i> Kin4-M	Naneq	NC_005213	A3?

We note that there are 17 organisms which have not been listed in the Bergey's *Outline*, see Table 4. We assign them a tentative Bergey's code according to the NCBI taxonomy and, in some cases, taking into account the placement on CVTrees. Comparison of these assignments with future taxonomy may test the predictive power of the CVTrees.

Table 2: List of 401 Bacterial genomes.

Organism	Abbr	Accession	Bergey Code
<i>Aquifex aeolicus</i>	Aquae	NC_000918	B1.1.1.1.1
<i>Thermotoga maritima</i>	Thema	NC_000853	B2.1.1.1.1
<i>Deinococcus geothermalis</i> DSM 11300	Deigd	NC_008025	B4.1.1.1.1
<i>Deinococcus radiodurans</i> R1	Deira	NC_001263-64	B4.1.1.1.1
<i>Thermus thermophilus</i> HB27	Thet2	NC_005835	B4.1.2.1.1
<i>Thermus thermophilus</i> HB8	Thet8	NC_006461	B4.1.2.1.1
<i>Dehalococcoides</i> CBDB1	Dehsc	NC_007356	B6.2.1.1.?
<i>Dehalococcoides ethenogenes</i> 195	Dehe1	NC_002936	B6.2.1.1.?
<i>Thermosynechococcus elongatus</i> BP-1	Synel	NC_004113	B10.1.1.1.?
<i>Gloeobacter violaceus</i>	Glovi	NC_005125	B10.1.1.1.7
<i>Prochlorococcus marinus</i> MED4	Promp	NC_005072	B10.1.1.1.11
<i>Prochlorococcus marinus</i> NATL2A	Prompt	NC_007335	B10.1.1.1.11
<i>Prochlorococcus marinus</i> str. MIT 9312	Prom9	NC_007577	B10.1.1.1.11
<i>Prochlorococcus marinus</i> str. MIT 9313	Promm	NC_005071	B10.1.1.1.11
<i>Prochlorococcus marinus</i> subsp. <i>marinus</i> str. CCMP1375	Proma	NC_005042	B10.1.1.1.11
<i>Synechococcus elongatus</i> PCC 6301	Synp6	NC_006576	B10.1.1.1.13
<i>Synechococcus elongatus</i> PCC 7942	Synp7	NC_007604	B10.1.1.1.13
<i>Synechococcus</i> CC9311	Syns3	NC_008319	B10.1.1.1.13
<i>Synechococcus</i> sp. CC9605	Synsc	NC_007516	B10.1.1.1.13
<i>Synechococcus</i> sp. CC9902	Syns9	NC_007513	B10.1.1.1.13
<i>Synechococcus</i> sp. WH 8102	Synpx	NC_005070	B10.1.1.1.13
<i>Cyanobacteria bacterium</i> Yellowstone A-Prime	Synja	NC_007775	B10.1.1.1.13
<i>Cyanobacteria bacterium</i> Yellowstone B-Prime	Synjb	NC_007776	B10.1.1.1.13
<i>Synechocystis</i> sp. PCC 6803	Syny3	NC_000911	B10.1.1.1.14
<i>Trichodesmium erythraeum</i> IMS101	Triei	NC_008312	B10.1.3.1.17
<i>Anabaena variabilis</i> ATCC 29413	Anava	NC_007413	B10.1.4.1.1
<i>Nostoc</i> sp. PCC 7120	Anasp	NC_003272	B10.1.4.1.8
<i>Chlorobium chlorochromatii</i> CaD3	Chlch	NC_007514	B11.1.1.1.1
<i>Chlorobium phaeobacteroides</i> DSM 266	Chlph	NC_008639	B11.1.1.1.1
<i>Chlorobium tepidum</i> TLS	Chlte	NC_002932	B11.1.1.1.1
<i>Pelodictyon luteolum</i> DSM 273	Pelld	NC_007512	B11.1.1.1.5
<i>Magnetococcus</i> MC-1	Magmc	NC_008576	B12.1.?
<i>Rhodospirillum rubrum</i> ATCC 11170	Rhoru	NC_007643	B12.1.1.1.1
<i>Magnetospirillum magneticum</i> AMB-1	Magsa	NC_007626	B12.1.1.1.4
<i>Granulobacter bethesdensis</i> CGDNIH1	Grabc	NC_008343	B12.1.1.2.?
<i>Gluconobacter oxydans</i> 621H	Gluox	NC_006677	B12.1.1.2.9
<i>Candidatus Pelagibacter</i> ubique HTCC1062	Pelub	NC_007205	B12.1.2.?
<i>Rickettsia bellii</i> RML369-C	Ricbr	NC_007940	B12.1.2.1.1
<i>Rickettsia conorii</i>	Riccn	NC_003103	B12.1.2.1.1
<i>Rickettsia felis</i> URRWXCal2	Ricfe	NC_007109	B12.1.2.1.1
<i>Rickettsia prowazekii</i>	Ricpr	NC_000963	B12.1.2.1.1
<i>Rickettsia typhi</i> str. Wilmington	Ricty	NC_006142	B12.1.2.1.1
<i>Anaplasma marginale</i> str. <i>St. Maries</i>	Anamm	NC_004842	B12.1.2.2.1
<i>Anaplasma phagocytophilum</i> HZ	Anapz	NC_007797	B12.1.2.2.1
<i>Ehrlichia canis</i> Jake	Ehrcj	NC_007354	B12.1.2.2.4
<i>Ehrlichia chaffeensis</i> Arkansas	Ehrch	NC_007799	B12.1.2.2.4
<i>Ehrlichia ruminantium</i> Gardel	Ehrrg	NC_006831	B12.1.2.2.4
<i>Ehrlichia ruminantium</i> str. <i>Welgevonden</i>	Ehrru	NC_006832	B12.1.2.2.4
<i>Ehrlichia ruminantium</i> <i>Welgevonden</i>	Ehrrw	NC_005295	B12.1.2.2.4
<i>Neorickettsia sennetsu</i> str. <i>Miyayama</i>	Neosm	NC_007798	B12.1.2.2.5
<i>Wolbachia endosymbiont</i> of <i>Brugia malayi</i> TRS	Woltr	NC_006833	B12.1.2.2.6
<i>Wolbachia endosymbiont</i> of <i>Drosophila melanogaster</i>	Wolpm	NC_002978	B12.1.2.2.6

Table 2: List of 401 Bacterial genomes (continued).

Organism	Abbr	Accession	Bergey Code
<i>Rhodobacter sphaeroides</i> 2.4.1	Rhos4	NC_007493-94	B12.1.3.1.1
<i>Hyphomonas neptunium</i> ATCC 15444	Hypna	NC_008358	B12.1.3.1.8
<i>Jannaschia</i> sp. CCS1	Jansc	NC_007802	B12.1.3.1.9
<i>Maricaulis maris</i> Mcs10	Marmm	NC_008347	B12.1.3.1.12
<i>Paracoccus denitrificans</i> PD1222	Parde	NC_008686-87	B12.1.3.1.17
<i>Roseobacter denitrificans</i> OCh 114	Rosdo	NC_008209	B12.1.3.1.25
<i>Silicibacter pomeroyi</i> DSS-3	Silpo	NC_003911	B12.1.3.1.30
<i>Silicibacter</i> Tm1040	Silst	NC_008044	B12.1.3.1.30
<i>Erythrobacter litoralis</i> HTCC2594	Eryli	NC_007722	B12.1.4.1.3
<i>Novosphingobium aromaticivorans</i> DSM 12444	Novad	NC_007794	B12.1.4.1.6
<i>Sphingopyxis alaskensis</i> RB2256	Sphal	NC_008048	B12.1.4.1.11
<i>Zymomonas mobilis</i> ZM4	Zymm	NC_006526	B12.1.4.1.12
<i>Caulobacter crescentus</i>	Caucr	NC_002696	B12.1.5.1.1
<i>Rhizobium etli</i> CFN 42	Rhiet	NC_007761	B12.1.6.1.1
<i>Rhizobium leguminosarum</i> bv <i>viciae</i> 3841	Rhil3	NC_008380	B12.1.6.1.1
<i>Agrobacterium tumefaciens</i> C58 Cereon	Agrt5	NC_003062-63	B12.1.6.1.2
<i>Agrobacterium tumefaciens</i> C58 Uwash	Agrt5W	NC_003304-05	B12.1.6.1.2
<i>Sinorhizobium meliloti</i> 1021	Rhime	NC_003047	B12.1.6.1.7
<i>Bartonella henselae</i> str. Houston-1	Barhe	NC_005956	B12.1.6.3.1
<i>Bartonella Quintana</i> str. Toulouse	Barqu	NC_005955	B12.1.6.3.1
<i>Brucella abortus</i> 9-941	Bruab	NC_006932.33	B12.1.6.4.1
<i>Brucella melitensis</i>	Brume	NC_003317-18	B12.1.6.4.1
<i>Brucella melitensis</i> biovar <i>Abortus</i> 2308	Brua2	NC_007618.24	B12.1.6.4.1
<i>Brucella suis</i> 1330	Brusu	NC_004310.11	B12.1.6.4.1
<i>Mesorhizobium loti</i> MAFF303099	Rhilo	NC_002678	B12.1.6.5.6
<i>Mesorhizobium</i> BNC1	Messb	NC_008254	B12.1.6.5.6
<i>Bradyrhizobium japonicum</i>	Braja	NC_004463	B12.1.6.8.1
<i>Nitrobacter hamburgensis</i> X14	Nithx	NC_007964	B12.1.6.8.6
<i>Nitrobacter winogradskyi</i> Nb-255	Nitwn	NC_007406	B12.1.6.8.6
<i>Rhodopseudomonas palustris</i> BisA53	Rhopa3	NC_008435	B12.1.6.8.9
<i>Rhodopseudomonas palustris</i> BisB18	Rhopb	NC_007925	B12.1.6.8.9
<i>Rhodopseudomonas palustris</i> BisB5	Rhops	NC_007958	B12.1.6.8.9
<i>Rhodopseudomonas palustris</i> CGA009	Rhopa	NC_005296	B12.1.6.8.9
<i>Rhodopseudomonas palustris</i> HaA2	Rhop2	NC_007778	B12.1.6.8.9
<i>Burkholderia cenocepacia</i> AU 1054	Burca	NC_008060-62	B12.2.1.1.1
<i>Burkholderia cenocepacia</i> HI2424	Burch	NC_008542-44	B12.2.1.1.1
<i>Burkholderia cepacia</i> AMMD	Burce	NC_008390-92	B12.2.1.1.1
<i>Burkholderia mallei</i> ATCC 23344	Burma	NC_006348.49	B12.2.1.1.1
<i>Burkholderia pseudomallei</i> 1710b	Burp1	NC_007434.35	B12.2.1.1.1
<i>Burkholderia pseudomallei</i> K96243	Burps	NC_006350.51	B12.2.1.1.1
<i>Burkholderia</i> sp. 383	Burs3	NC_007509-11	B12.2.1.1.1
<i>Burkholderia thailandensis</i> E264	Burth	NC_007650.51	B12.2.1.1.1
<i>Burkholderia xenovorans</i> LB400	Burxl	NC_007951-53	B12.2.1.1.1
<i>Ralstonia solanacearum</i>	Ralso	NC_003295	B12.2.1.1.8
<i>Wautersia (Ralstonia) eutropha</i> JMP134	Ralej	NC_007347-48	B12.2.1.1.10
<i>Wautersia (Ralstonia) eutropha</i> H16	Raleu	NC_008313-14	B12.2.1.1.10
<i>Wautersia (Ralstonia) metallidurans</i> CH34	Ralme	NC_007973-74	B12.2.1.1.10
<i>Bordetella bronchiseptica</i>	Borbr	NC_002927	B12.2.1.3.3
<i>Bordetella parapertussis</i>	Borpa	NC_002928	B12.2.1.3.3
<i>Bordetella pertussis</i>	Borpe	NC_002929	B12.2.1.3.3
<i>Polaromonas</i> JS666	Polsj	NC_007948	B12.2.1.4.13
<i>Rhodoferrax ferrireducens</i> DSM 15236	Rhofd	NC_007908	B12.2.1.4.15
<i>Thiobacillus denitrificans</i> ATCC 25259	Thida	NC_007404	B12.2.2.1.2
<i>Methylobacillus flagellatus</i> KT	Metfl	NC_007947	B12.2.3.1.2
<i>Neisseria gonorrhoeae</i> FA 1090	Neig1	NC_002946	B12.2.4.1.1
<i>Neisseria meningitidis</i> MC58	Neimb	NC_003112	B12.2.4.1.1
<i>Neisseria meningitidis</i> Z2491	Neima	NC_003116	B12.2.4.1.1
<i>Chromobacterium violaceum</i> ATCC 12472	Chrvo	NC_005085	B12.2.4.1.4

Table 2: List of 401 Bacterial genomes (continued).

Organism	Abbr	Accession	Bergey Code
<i>Nitrosomonas europaea</i> ATCC 19718	Niteu	NC_004757	B12.2.5.1.1
<i>Nitrosomonas europaea</i> C71	NiteuC	NC_008344	B12.2.5.1.1
<i>Nitrosospira multififormis</i> ATCC 25196	Nitmu	NC_007614	B12.2.5.1.3
<i>Azoarcus</i> sp. EbN1	Azose	NC_006513	B12.2.6.1.2
<i>Azoarcus</i> BH72	Azobh	NC_008702	B12.2.6.1.2
<i>Dechloromonas aromatica</i> RCB	Decar	NC_007298	B12.2.6.1.6
<i>Candidatus Carsonella ruddii</i> PV	Carru	NC_008512	B12.3.?
<i>Candidatus Ruthia magnifica</i> Cm (<i>Calyptogenia magnifica</i>)	Rutma	NC_008610	B12.3.?
<i>Nitrosococcus oceani</i> ATCC 19707	Nitoc	NC_007484	B12.3.1.1.9
<i>Alkalilimnicola ehrlichei</i> MLHE-1	Alheh	NC_008340	B12.3.1.2.2
<i>Xanthomonas axonopodis</i> citri 306	Xanac	NC_003919	B12.3.3.1.1
<i>Xanthomonas campestris</i>	Xancp	NC_003902	B12.3.3.1.1
<i>Xanthomonas campestris</i> 8004	Xanc8	NC_007086	B12.3.3.1.1
<i>Xanthomonas campestris</i> pv. vesicatoria str. 85-10	Xanc5	NC_007508	B12.3.3.1.1
<i>Xanthomonas oryzae</i> KACC10331	Xanor	NC_006834	B12.3.3.1.1
<i>Xanthomonas oryzae</i> MAFF311018	Xanom	NC_007705	B12.3.3.1.1
<i>Xylella fastidiosa</i>	Xylfa	NC_002488	B12.3.3.1.12
<i>Xylella fastidiosa</i> Temecula 1	Xylft	NC_004556	B12.3.3.1.12
<i>Francisella tularensis holarctica</i>	Frath	NC_007880	B12.3.5.2.1
<i>Francisella tularensis</i> subsp. <i>tularensis</i>	Fratt	NC_006570	B12.3.5.2.1
<i>Francisella tularensis</i> FSC 198	Frat1	NC_008245	B12.3.5.2.1
<i>Francisella tularensis holarctica</i> OSU18	Frato	NC_008369	B12.3.5.2.1
<i>Francisella tularensis novicida</i> U112	Fratn	NC_008601	B12.3.5.2.1
<i>Thiomicrospira crunogena</i> XCL-2	Thicr	NC_007520	B12.3.5.3.6
<i>Thiomicrospira denitrificans</i> ATCC 33889	Thidn	NC_007575	B12.3.5.3.6
<i>Legionella pneumophila</i> str. Lens	Legpl	NC_006369	B12.3.6.1.1
<i>Legionella pneumophila</i> str. Paris	Legpa	NC_006368	B12.3.6.1.1
<i>Legionella pneumophila</i> str. Philadelphia 1	Legph	NC_002942	B12.3.6.1.1
<i>Coxiella burnetii</i> RSA 493	Coxbu	NC_002971	B12.3.6.2.1
<i>Methylococcus capsulatus</i> str. Bath	Metca	NC_002977	B12.3.7.1.1
<i>Alcanivorax borkumensis</i> SK2	Alcbs	NC_008260	B12.3.8.2.1
<i>Hahella chejuensis</i> KCTC 2396	Hahch	NC_007645	B12.3.8.3.1
<i>Chromohalobacter salexigens</i> DSM 3043	Chrsd	NC_007963	B12.3.8.4.3
<i>Pseudomonas aeruginosa</i>	Pseae	NC_002516	B12.3.9.1.1
<i>Pseudomonas aeruginosa</i> UCBPP-PA14	PseaeU	NC_008463	B12.3.9.1.1
<i>Pseudomonas entomophila</i> L48	Pseen	NC_008027	B12.3.9.1.1
<i>Pseudomonas fluorescens</i> Pf-5	Psef5	NC_004129	B12.3.9.1.1
<i>Pseudomonas fluorescens</i> PfO-1	Psepf	NC_007492	B12.3.9.1.1
<i>Pseudomonas putida</i> KT2440	Psepk	NC_002947	B12.3.9.1.1
<i>Pseudomonas syringae phaseolicola</i> 1448A	Pse14	NC_005773	B12.3.9.1.1
<i>Pseudomonas syringae</i> pv B728a	Pseu2	NC_007005	B12.3.9.1.1
<i>Pseudomonas syringae</i> pv. tomato str. DC3000	Psesm	NC_004578	B12.3.9.1.1
<i>Acinetobacter</i> sp. ADP1	Aciaa	NC_005966	B12.3.9.2.2
<i>Psychrobacter arcticum</i> 273-4	Psyar	NC_007204	B12.3.9.2.3
<i>Psychrobacter cryohalolentis</i> K5	Psyck	NC_007969	B12.3.9.2.3
<i>Saccharophagus degradans</i> 2-40	Sacd2	NC_007912	B12.3.10.1.?
<i>Colwellia psychrerythraea</i> 34H	Colp3	NC_003910	B12.3.10.1.4
<i>Idiomarina loihiensis</i> L2TR	Idilo	NC_006512	B12.3.10.1.7
<i>Pseudoalteromonas haloplanktis</i> TAC125	Pseht	NC_007481-82	B12.3.10.1.12
<i>Pseudoalteromonas atlantica</i> T6c	Pseha6	NC_008228	B12.3.10.1.12
<i>Psychromonas ingrahamii</i> 37	Psyin	NC_008709	B12.3.10.1.13
<i>Shewanella amazonensis</i> SB2B	Sheam	NC_008700	B12.3.10.1.14
<i>Shewanella</i> ANA-3	Shean	NC_008577	B12.3.10.1.14
<i>Shewanella denitrificans</i> OS217	Shedo	NC_007954	B12.3.10.1.14
<i>Shewanella frigidimarina</i> NCIMB 400	Shefn	NC_008345	B12.3.10.1.14
<i>Shewanella</i> MR-4	Shesm	NC_008321	B12.3.10.1.14
<i>Shewanella</i> MR-7	Shesr	NC_008322	B12.3.10.1.14
<i>Shewanella oneidensis</i> MR-1	Sheon	NC_004347	B12.3.10.1.14

Table 2: List of 401 Bacterial genomes (continued).

Organism	Abbr	Accession	Bergey Code
<i>Vibrio cholerae</i>	Vibch	NC_002505.06	B12.3.11.1.1
<i>Vibrio fischeri</i> ES114	Vibf1	NC_006840.41	B12.3.11.1.1
<i>Vibrio parahaemolyticus</i> RIMD 2210633	Vibpa	NC_004603.05	B12.3.11.1.1
<i>Vibrio vulnificus</i> CMCP6	Vibvu	NC_004459.60	B12.3.11.1.1
<i>Vibrio vulnificus</i> YJ016	Vibvy	NC_005139.40	B12.3.11.1.1
<i>Photobacterium profundum</i> SS9	Phopr	NC_006370-71	B12.3.11.1.7
<i>Aeromonas hydrophila</i> ATCC 7966	Aerhy	NC_008570	B12.3.12.1.1
<i>Baumannia cicadellinica</i> <i>Homalodisca coagulate</i>	Bauch	NC_007984	B12.3.13.1.?
<i>Candidatus Blochmannia floridanus</i>	Blofl	NC_005061	B12.3.13.1.?
<i>Candidatus Blochmannia pennsylvanicus</i> BPEN	Blopb	NC_007292	B12.3.13.1.?
<i>Escherichia coli</i> 536	Ecoli5	NC_008253	B12.3.13.1.1
<i>Escherichia coli</i> APEC O1	EcoliA	NC_008563	B12.3.13.1.1
<i>Escherichia coli</i> CFT073	EcoliC	NC_004431	B12.3.13.1.1
<i>Escherichia coli</i> K12	EcoliK	NC_000913	B12.3.13.1.1
<i>Escherichia coli</i> O157:H7	EcoliO	NC_002695	B12.3.13.1.1
<i>Escherichia coli</i> O157:H7 EDL933	EcoliE	NC_002655	B12.3.13.1.1
<i>Escherichia coli</i> UTI89	EcoliU	NC_007946	B12.3.13.1.1
<i>Escherichia coli</i> W3110	EcoliW	AC_000091	B12.3.13.1.1
<i>Buchnera aphidicola</i> (Baizongia pistaciae)	Bucbp	NC_004545	B12.3.13.1.5
<i>Buchnera aphidicola</i> Sg	Bucap	NC_004061	B12.3.13.1.5
<i>Buchnera aphidicola</i> Cc <i>Cinara cedri</i>	Bucac	NC_008513	B12.3.13.1.5
<i>Buchnera</i> sp. APS	Bucal	NC_002528	B12.3.13.1.5
<i>Erwinia carotovora</i> subsp. <i>atroseptica</i> SCRI1043	Erwct	NC_004547	B12.3.13.1.13
<i>Photobacterium luminescens</i> subsp. <i>laumondii</i> TTO1	Pholl	NC_005126	B12.3.13.1.26
<i>Salmonella enterica</i> <i>Choleraesuis</i>	Salch	NC_006905	B12.3.13.1.34
<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar <i>Paratyphi</i> A str. ATCC 9150	Salpa	NC_006511	B12.3.13.1.34
<i>Salmonella typhi</i>	Salti	NC_003198	B12.3.13.1.34
<i>Salmonella Typhi</i> Ty2	SaltyT	NC_004631	B12.3.13.1.34
<i>Salmonella typhimurium</i> LT2	Salty	NC_003197	B12.3.13.1.34
<i>Shigella boydii</i> Sb227	Shibs	NC_007613	B12.3.13.1.37
<i>Shigella dysenteriae</i> Sd197	Shids	NC_007606	B12.3.13.1.37
<i>Shigella flexneri</i> 2a str. 2457T	ShifT	NC_004741	B12.3.13.1.37
<i>Shigella flexneri</i> 2a str. 301	Shif1	NC_004337	B12.3.13.1.37
<i>Shigella flexneri</i> 5 8401	Shif5	NC_008258	B12.3.13.1.37
<i>Shigella sonnei</i> Ss046	Shiss	NC_007384	B12.3.13.1.37
<i>Sodalis glossinidius</i> str. 'morsitans'	Sodgl	NC_007712	B12.3.13.1.38
<i>Wigglesworthia brevipalpis</i>	Wigbr	NC_004344	B12.3.13.1.41
<i>Yersinia pestis</i> <i>Antiqua</i>	Yerpa	NC_008150	B12.3.13.1.43
<i>Yersinia pestis</i> <i>Nepal516</i>	Yerpn	NC_008149	B12.3.13.1.43
<i>Yersinia pestis</i> biovar <i>Mediaevails</i> str. 91001	YerpeM	NC_005810	B12.3.13.1.43
<i>Yersinia pestis</i> KIM	YerpeK	NC_004088	B12.3.13.1.43
<i>Yersinia pestis</i> strain CO92	YerpeC	NC_003143	B12.3.13.1.43
<i>Yersinia pseudotuberculosis</i> IP 32953	Yerps	NC_006155	B12.3.13.1.43
<i>Pasteurella multocida</i> PM70	Pasmu	NC_002663	B12.3.14.1.1
<i>Haemophilus ducreyi</i> 35000HP	Haedu	NC_002940	B12.3.14.1.4
<i>Haemophilus influenzae</i> 86 028NP	Haei8	NC_007146	B12.3.14.1.4
<i>Haemophilus influenzae</i> Rd	Haein	NC_000907	B12.3.14.1.4
<i>Haemophilus somnus</i> 129PT	Haes1	NC_008309	B12.3.14.1.4
<i>Mannheimia succiniciproducens</i> MBEL55E	Mansm	NC_006300	B12.3.14.1.6
<i>Desulfovibrio desulfuricans</i> G20	Desdg	NC_007519	B12.4.2.1.1
<i>Desulfovibrio vulgaris</i> str. Hildenborough	Desvh	NC_002937	B12.4.2.1.1
<i>Lawsonia intracellularis</i> PHE MN1-00	Lawip	NC_008011	B12.4.2.1.3
<i>Desulfotalea psychrophila</i> LSv54	Desps	NC_006138	B12.4.3.2.5
<i>Pelobacter carbinolicus</i>	Pelcd	NC_007498	B12.4.5.1.4
<i>Pelobacter propionicus</i> DSM 2379	Pelpr	NC_008609	B12.4.5.1.4

Table 2: List of 401 Bacterial genomes (continued).

Organism	Abbr	Accession	Bergey Code
<i>Geobacter metallireducens</i> GS-15	Geomg	NC_007517	B12.4.5.2.1
<i>Geobacter sulfurreducens</i> PCA	Geosl	NC_002939	B12.4.5.2.1
<i>Syntrophobacter fumaroxidans</i> MPOB	Synfu	NC_008554	B12.4.6.1.1
<i>Syntrophus aciditrophicus</i> SB	Synas	NC_007759	B12.4.6.2.1
<i>Bdellovibrio bacteriovorus</i> HD100	Bdeba	NC_005363	B12.4.7.1.1
<i>Anaeromyxobacter dehalogenans</i> 2CP-C	Anade	NC_007760	B12.4.(8.1).1.2
<i>Myxococcus xanthus</i> DK 1622	Myxxd	NC_008095	B12.4.(8.1).2.1
<i>Campylobacter jejuni</i>	Camje	NC_002163	B12.5.1.1.1
<i>Campylobacter jejuni</i> RM1221	Camjr	NC_003912	B12.5.1.1.1
<i>Campylobacter fetus</i> 82-40	Camfe	NC_008599	B12.5.1.1.1
<i>Helicobacter acinonychis</i> Sheeba	Helac	NC_008229	B12.5.1.2.1
<i>Helicobacter hepaticus</i> ATCC 51449	Helhp	NC_004917	B12.5.1.2.1
<i>Helicobacter pylori</i> 26695	Helpy	NC_000915	B12.5.1.2.1
<i>Helicobacter pylori</i> J99	Helpj	NC_000921	B12.5.1.2.1
<i>Helicobacter pylori</i> HPAG1	Helph	NC_008086	B12.5.1.2.1
<i>Wolinella succinogenes</i>	Wolsu	NC_005090	B12.5.1.2.4
<i>Clostridium acetobutylicum</i> ATCC824	Cloab	NC_003030	B13.1.1.1.1
<i>Clostridium novyi</i> NT	Clono	NC_008593	B13.1.1.1.1
<i>Clostridium perfringens</i> ATCC 13124	Clop1	NC_008261	B13.1.1.1.1
<i>Clostridium perfringens</i> SM101	Clops	NC_008262	B13.1.1.1.1
<i>Clostridium perfringens</i>	Clope	NC_003366	B13.1.1.1.1
<i>Clostridium tetani</i> E88	Clote	NC_004557	B13.1.1.1.1
<i>Carboxydothermus hydrogenoformans</i> Z-2901	Carhz	NC_007503	B13.1.1.5.2
<i>Desulfotobacterium hafniense</i> Y51	Deshy	NC_007907	B13.1.1.5.4
<i>Syntrophomonas wolfei</i> Goettingen	Synww	NC_008346	B13.1.1.8.1
<i>Moorella thermoacetica</i> ATCC 39073	Mooth	NC_007644	B13.1.2.1.7
<i>Thermoanaerobacter tengcongensis</i>	Thetn	NC_003869	B13.1.2.1.11
<i>Mycoplasma capricolum</i> subsp. <i>capricolum</i> ATCC 27343	Mycca	NC_007633	B13.2.1.1.1
<i>Mycoplasma gallisepticum</i> R	Mycga	NC_004829	B13.2.1.1.1
<i>Mycoplasma genitalium</i>	Mycge	NC_000908	B13.2.1.1.1
<i>Mycoplasma hyopneumoniae</i> 232	Mych2	NC_006360	B13.2.1.1.1
<i>Mycoplasma hyopneumoniae</i> 7448	Mych7	NC_007332	B13.2.1.1.1
<i>Mycoplasma hyopneumoniae</i> J	Mychj	NC_007295	B13.2.1.1.1
<i>Mycoplasma mobile</i> 163K	Mycmo	NC_006908	B13.2.1.1.1
<i>Mycoplasma mycoides</i> subsp. <i>mycoides</i> SC	Mycms	NC_005364	B13.2.1.1.1
<i>Mycoplasma penetrans</i>	Mycpe	NC_004432	B13.2.1.1.1
<i>Mycoplasma pneumoniae</i>	Mycpn	NC_000912	B13.2.1.1.1
<i>Mycoplasma pulmonis</i> UAB CTIP	Mycpu	NC_002771	B13.2.1.1.1
<i>Mycoplasma synoviae</i> 53	Myes5	NC_007294	B13.2.1.1.1
<i>Ureaplasma urealyticum</i>	Urepa	NC_002162	B13.2.1.1.4
<i>Mesoplasma florum</i> L1	Mesfl	NC_006055	B13.2.2.1.2
<i>Aster yellows witches'-broom phytoplasma</i> AYWB	Aywbp	NC_007716	B13.2.3.1.2
<i>Onion yellows phytoplasma</i>	Onype	NC_005303	B13.2.3.1.2

Table 2: List of 401 Bacterial genomes (continued).

Organism	Abbr	Accession	Bergey Code
<i>Bacillus anthracis</i> str. Ames	BacanM	NC_003997	B13.3.1.1.1
<i>Bacillus anthracis</i> str. Ames 0581	BacanE	NC_007530	B13.3.1.1.1
<i>Bacillus anthracis</i> str. Sterne	BacanS	NC_005945	B13.3.1.1.1
<i>Bacillus cereus</i> ATCC 10987	Bacc1	NC_003909	B13.3.1.1.1
<i>Bacillus cereus</i> ATCC 14579	Baccr	NC_004722	B13.3.1.1.1
<i>Bacillus cereus</i> ZK	Baccz	NC_006274	B13.3.1.1.1
<i>Bacillus clausii</i> KSM-K16	Bacsk	NC_006582	B13.3.1.1.1
<i>Bacillus halodurans</i>	Bachd	NC_002570	B13.3.1.1.1
<i>Bacillus licheniformis</i> ATCC 14580	Bac1A	NC_006270	B13.3.1.1.1
<i>Bacillus licheniformis</i> DSM 13	Bac1D	NC_006322	B13.3.1.1.1
<i>Bacillus subtilis</i>	Bacsu	NC_000964	B13.3.1.1.1
<i>Bacillus thuringiensis</i> serovar konkukian str. 97-27	Bachk	NC_005957	B13.3.1.1.1
<i>Bacillus thuringiensis</i> Al Hakam	BacthA	NC_008600	B13.3.1.1.1
<i>Geobacillus kaustophilus</i> HTA426	Geoka	NC_006510	B13.3.1.1.6
<i>Oceanobacillus iheyensis</i>	Oceih	NC_004193	B13.3.1.1.12
<i>Listeria innocua</i> Clip11262	Lisin	NC_003212	B13.3.1.4.1
<i>Listeria monocytogenes</i> EGD-e	Lismo	NC_003210	B13.3.1.4.1
<i>Listeria monocytogenes</i> str. 4b F2365	Lismf	NC_002973	B13.3.1.4.1
<i>Listeria welshimeri</i> serovar 6b SLCC5334	Liswe	NC_008555	B13.3.1.4.1
<i>Staphylococcus aureus</i> Mu50	Staam	NC_002758	B13.3.1.8.1
<i>Staphylococcus aureus</i> MW2	Staaw	NC_003923	B13.3.1.8.1
<i>Staphylococcus aureus</i> N315	Staan	NC_002745	B13.3.1.8.1
<i>Staphylococcus aureus</i> RF122	Staab	NC_007622	B13.3.1.8.1
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> COL	Staac	NC_002951	B13.3.1.8.1
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MRSA252	Staar	NC_002952	B13.3.1.8.1
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> MSSA476	Staas	NC_002953	B13.3.1.8.1
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> NCTC 8325	StaaU	NC_007795	B13.3.1.8.1
<i>Staphylococcus aureus</i> subsp. <i>aureus</i> USA300	Staa3	NC_007793	B13.3.1.8.1
<i>Staphylococcus epidermidis</i> ATCC 12228	Staes	NC_004461	B13.3.1.8.1
<i>Staphylococcus epidermidis</i> RP62A	Staeq	NC_002976	B13.3.1.8.1
<i>Staphylococcus haemolyticus</i>	Stahj	NC_007168	B13.3.1.8.1
<i>Staphylococcus saprophyticus</i>	Stas1	NC_007350	B13.3.1.8.1
<i>Lactobacillus acidophilus</i> NCFM	Lacac	NC_006814	B13.3.2.1.1
<i>Lactobacillus brevis</i> ATCC 367	Lacbr	NC_008497	B13.3.2.1.1
<i>Lactobacillus casei</i> ATCC 334	Lacca	NC_008526	B13.3.2.1.1
<i>Lactobacillus delbrueckii bulgaricus</i>	Lacda	NC_008054	B13.3.2.1.1
<i>Lactobacillus delbrueckii bulgaricus</i> ATCC BAA-365	Lacde	NC_008529	B13.3.2.1.1
<i>Lactobacillus gasseri</i> ATCC 33323	Lacga	NC_008530	B13.3.2.1.1
<i>Lactobacillus johnsonii</i> NCC 533	Lacjo	NC_005362	B13.3.2.1.1
<i>Lactobacillus plantarum</i> WCFS1	Lacpl	NC_004567	B13.3.2.1.1
<i>Lactobacillus sakei</i> subsp. <i>sakei</i> 23K	Lacss	NC_007576	B13.3.2.1.1
<i>Lactobacillus salivarius</i> UCC118	Lacs1	NC_007929	B13.3.2.1.1
<i>Pediococcus pentosaceus</i> ATCC 25745	Pedpe	NC_008525	B13.3.2.1.3
<i>Enterococcus faecalis</i> V583	Entfa	NC_004668	B13.3.2.4.1
<i>Leuconostoc mesenteroides</i> ATCC 8293	Leume	NC_008531	B13.3.2.5.1
<i>Oenococcus oeni</i> PSU-1	Oenoe	NC_008528	B13.3.2.5.2

Table 2: List of 401 Bacterial genomes (continued).

Organism	Abbr	Accession	Bergey Code
<i>Streptococcus agalactiae</i> 2603V/R	Stra5	NC_004116	B13.3.2.6.1
<i>Streptococcus agalactiae</i> A909	Stra1	NC_007432	B13.3.2.6.1
<i>Streptococcus agalactiae</i> NEM316	Stra3	NC_004368	B13.3.2.6.1
<i>Streptococcus mutans</i> UA159	Strmu	NC_004350	B13.3.2.6.1
<i>Streptococcus pneumoniae</i> D39	StrpnD	NC_008533	B13.3.2.6.1
<i>Streptococcus pneumoniae</i> R6	Strr6	NC_003098	B13.3.2.6.1
<i>Streptococcus pneumoniae</i> TIGR4	Strpn	NC_003028	B13.3.2.6.1
<i>Streptococcus pyogenes</i> M1 GAS	Strp1G	NC_002737	B13.3.2.6.1
<i>Streptococcus pyogenes</i> MGAS10394	Strp6	NC_006086	B13.3.2.6.1
<i>Streptococcus pyogenes</i> MGAS315	Strp3	NC_004070	B13.3.2.6.1
<i>Streptococcus pyogenes</i> MGAS5005	Strp1	NC_007297	B13.3.2.6.1
<i>Streptococcus pyogenes</i> MGAS6180	Strpm	NC_007296	B13.3.2.6.1
<i>Streptococcus pyogenes</i> MGAS8232	Strp8	NC_003485	B13.3.2.6.1
<i>Streptococcus pyogenes</i> MGAS10270	Strpd	NC_008022	B13.3.2.6.1
<i>Streptococcus pyogenes</i> MGAS10750	Strpf	NC_008024	B13.3.2.6.1
<i>Streptococcus pyogenes</i> MGAS2096	Strpb	NC_008023	B13.3.2.6.1
<i>Streptococcus pyogenes</i> MGAS9429	Strpc	NC_008021	B13.3.2.6.1
<i>Streptococcus pyogenes</i> SSI-1	Strp3S	NC_004606	B13.3.2.6.1
<i>Streptococcus thermophilus</i> CNRZ1066	Strt1	NC_006449	B13.3.2.6.1
<i>Streptococcus thermophilus</i> LMG 18311	Strt2	NC_006448	B13.3.2.6.1
<i>Streptococcus thermophilus</i> LMD-9	Strtr	NC_008532	B13.3.2.6.1
<i>Lactococcus lactis cremoris</i> SK11	Lacl	NC_008527	B13.3.2.6.2
<i>Lactococcus lactis</i> sp. IL1403	Lacla	NC_002662	B13.3.2.6.2
<i>Rubrobacter xylanophilus</i> DSM 9941	Rubxd	NC_008148	B14.(1.2)(1.5)1.1
<i>Arthrobacter aurescens</i> TC1	Artau	NC_008711	B14.(1.5).(1.9).1.2
<i>Arthrobacter</i> FB24	Artfb	NC_008541	B14.(1.5).(1.9).1.2
<i>Tropheryma whipplei</i> str. Twist	Trowt	NC_004572	B14.(1.5).(1.9).6.3
<i>Tropheryma whipplei</i> TW08/27	Trow8	NC_004551	B14.(1.5).(1.9).6.3
<i>Leifsonia xyli</i> subsp. <i>xyli</i> str. CTCB07	Leixx	NC_006087	B14.(1.5).(1.9).12.10
<i>Corynebacterium diphtheriae</i>	Cordi	NC_002935	B14.(1.5).(1.10).1.1
<i>Corynebacterium efficiens</i> YS-314	Coref	NC_004369	B14.(1.5).(1.10).1.1
<i>Corynebacterium glutamicum</i> ATCC 13032 Bielefeld	CorglB	NC_006958	B14.(1.5).(1.10).1.1
<i>Corynebacterium glutamicum</i> ATCC 13032 Kitasato	Corgl	NC_003450	B14.(1.5).(1.10).1.1
<i>Corynebacterium jeikeium</i> K411	Corjk	NC_007164	B14.(1.5).(1.10).1.1
<i>Mycobacterium avium</i> 104	Mycav	NC_008595	B14.(1.5).(1.10).4.1
<i>Mycobacterium avium</i> subsp. <i>paratuberculosis</i> str. k10	Mycpa	NC_002944	B14.(1.5).(1.10).4.1
<i>Mycobacterium bovis</i> subsp. <i>bovis</i> AF2122/97	Mycbo	NC_002945	B14.(1.5).(1.10).4.1
<i>Mycobacterium</i> KMS	Myckm	NC_008705	B14.(1.5).(1.10).4.1
<i>Mycobacterium leprae</i> TN	Mycle	NC_002677	B14.(1.5).(1.10).4.1
<i>Mycobacterium</i> MCS	Mycss	NC_008146	B14.(1.5).(1.10).4.1
<i>Mycobacterium smegmatis</i> MC2 155	Mydsm	NC_008596	B14.(1.5).(1.10).4.1
<i>Mycobacterium tuberculosis</i> CDC1551	MyctuC	NC_002755	B14.(1.5).(1.10).4.1
<i>Mycobacterium tuberculosis</i> H37Rv	MyctuH	NC_000962	B14.(1.5).(1.10).4.1
<i>Mycobacterium ulcerans</i> AgY99	Mycul	NC_008611	B14.(1.5).(1.10).4.1
<i>Mycobacterium vanbaalenii</i> PYR-1	Mycvn	NC_008726	B14.(1.5).(1.10).4.1
<i>Nocardia farcinica</i> IFM10152	Nocfa	NC_006361	B14.(1.5).(1.10).5.1
<i>Rhodococcus</i> RHA1	Rhosr	NC_008268	B14.(1.5).(1.10).5.2
<i>Propionibacterium acnes</i> KPA171202	Proac	NC_006085	B14.(1.5).(1.12).1.1
<i>Nocardioides</i> JS614	Nocjs	NC_008699	B14.(1.5).(1.12).2.1
<i>Streptomyces avermitilis</i> MA-4680	Straw	NC_003155	B14.(1.5).(1.14).1.1
<i>Streptomyces coelicolor</i> A3(2)	Strco	NC_003888	B14.(1.5).(1.14).1.1
<i>Thermobifida fusca</i> YX	Thefy	NC_007333	B14.(1.5).(1.15).2.3
<i>Frankia alni</i> ACN14a	Fraal	NC_008278	B14.(1.5).(1.16).1.1
<i>Frankia</i> sp. CcI3	Frasc	NC_007777	B14.(1.5).(1.16).1.1
<i>Acidothermus cellulolyticus</i> 11B	Acice	NC_008578	B14.(1.5).(1.16).5.1
<i>Bifidobacterium adolescentis</i> ATCC 15703	Bifad	NC_008618	B14.(1.5).2.1.1
<i>Bifidobacterium longum</i> NCC2705	Biflo	NC_004307	B14.(1.5).2.1.1
<i>Symbiobacterium thermophilum</i> IAM 14863	Symth	NC_006177	B14.1.?

Table 2: List of 401 Bacterial genomes (continued).

Organism	Abbr	Accession	Bergey Code
<i>Pirellula</i> sp.	Rhoba	NC_005027	B15.1.1.1.4
<i>Chlamydia muridarum</i>	Chlmu	NC_002620	B16.1.1.1.1
<i>Chlamydia trachomatis</i>	Chltr	NC_000117	B16.1.1.1.1
<i>Chlamydia trachomatis</i> A/HAR-13	Chlta	NC_007429	B16.1.1.1.1
<i>Chlamydophila abortus</i> S26 3	Chlab	NC_004552	B16.1.1.1.2
<i>Chlamydophila caviae</i> GPIC	Chlcv	NC_003361	B16.1.1.1.2
<i>Chlamydophila felis</i> Fe/C-56	Chlff	NC_007899	B16.1.1.1.2
<i>Chlamydophila pneumoniae</i> AR39	ChlpnA	NC_002179	B16.1.1.1.2
<i>Chlamydophila pneumoniae</i> CWL029	ChlpnC	NC_000922	B16.1.1.1.2
<i>Chlamydophila pneumoniae</i> J138	ChlpnJ	NC_002491	B16.1.1.1.2
<i>Chlamydophila pneumoniae</i> TW-183	ChlpnT	NC_005043	B16.1.1.1.2
<i>Parachlamydia</i> sp. UWE25	Paruw	NC_005861	B16.1.1.2.1
<i>Borrelia afzelii</i> PKo	Borap	NC_008277	B17.1.1.1.2
<i>Borrelia burgdorferi</i>	Borbu	NC_001318	B17.1.1.1.2
<i>Borrelia garinii</i> PBI	Borga	NC_006156	B17.1.1.1.2
<i>Treponema denticola</i> ATCC 35405	Trede	NC_002967	B17.1.1.1.9
<i>Treponema pallidum</i>	Trepa	NC_000919	B17.1.1.1.9
<i>Leptospira borgpetersenii</i> serovar <i>Hardjo-bovis</i> JB197	Lepbo	NC_008510-11	B17.1.1.3.1
<i>Leptospira borgpetersenii</i> serovar <i>Hardjo-bovis</i> L550	Lepbl	NC_008508-09	B17.1.1.3.1
<i>Leptospira interrogans</i> serovar Copenhageni str. <i>Fiocruz</i> L1-130	Lepic	NC_005823-24	B17.1.1.3.1
<i>Leptospira interrogans</i> serovar <i>lai</i> str. 56601	Lepin	NC_004342-43	B17.1.1.3.1
<i>Solibacter usitatus</i> Ellin6076	Solus	NC_008536	B19.?
<i>Acidobacteria bacterium</i> Ellin345	Acibl	NC_008009	B19.1.1.1.1
<i>Bacteroides fragilis</i> NCTC 9434	Bacfn	NC_003228	B20.1.1.1.1
<i>Bacteroides fragilis</i> YCH46	Bacfr	NC_006347	B20.1.1.1.1
<i>Bacteroides thetaiotaomicron</i> VPI-5482	Bactn	NC_004663	B20.1.1.1.1
<i>Porphyromonas gingivalis</i> W83	Porgi	NC_002950	B20.1.1.3.1
<i>Gramella forsetii</i> KT0803	Grafo	NC_008571	B20.2.1.1.?
<i>Cytophage hutchinsonii</i> ATCC 33406	Cyth3	NC_008255	B20.3.1.3.4
<i>Salinibacter ruber</i> DSM 13855	Salrd	NC_007677	B20.3.1.5.4
<i>Fusobacterium nucleatum</i> ATCC 25586	Fusnn	NC_003454	B21.1.1.1.1

Table 3: List of 8 Eukaryotic genomes.

Species	Abbreviation	Accession Numbers
<i>Saccharomyces cerevisiae</i>	Yeast	NC_001133~48
<i>Schizosaccharomyces pombe</i>	Schpo	NC_003421.23.24
<i>Caenorhabditis elegans</i>	Worm	NC_003279~84
<i>Arabidopsis thaliana</i>	Arath	NC_003070.71.74.75.76
<i>Plasmodium falciparum</i>	Plafa	NC_000521,000910,004314~18,25~31
<i>Encephalitozoon cuniculi</i>	Enccu	NC_003242.29~38
<i>Eremothecium gossypii</i> (<i>Ashbya gossypii</i>)	Ashgo	NC_005782~88
<i>Drosophila melanogaster</i>	Drome	NC_004353.54, NT_033777.79.7436

Table 4: The 17 organisms not listed in Bergey’s *Outline*.

Abbr.	NCBI Taxonomy	Tentative Bergey’s Code
Halwd	Euryarchaeota, Halobacteria, Halobacterales	A2.4.1.1.?
	Halobacteraceae, Haloquadra	
Naneq	Nanoarchaeota, Nanoarchaeum	A3.?
Dehsc	Chloroflexi, Dehalococcoidetes, Dehalococcoides	B6.2.1.1.?
Dehe1	Chloroflexi, Dehalococcoidetes, Dehalococcoides	B6.2.1.1.?
Synel	Cyanobacteria, Chroococcales	B10.1.1.1.?
Magmc	Proteobacteria, Magnetococcus MC-1	B12.?
Grabc	Rhodospirillales, Acetobacteraceae, Granulobacter	B12.1.1.2.?
Pelub	Alphaproteobacteria, Rickettsiales, SAR11 Cluster	B12.1.2.?
Carru	Gammaproteobacteria, Candidatus Carsonella	B12.3.?
Rutma	Gammaproteobacteria, sulfur-oxidizing symbionts	B12.3.?
Sacd2	Alteromonadales, Alteromonadaceae	B12.3.10.1.?
Bauch	Gammaproteobacteria, Baumannia	B12.3.13.1.?
Blofl	Enterobacteriales, Enterobacteriaceae	B12.3.13.1.?
Blopb	Enterobacteriales, Enterobacteriaceae	B12.3.13.1.?
Symth	Actinobacteria (class), unclassified Actinobacteria	B14.1.?
Solus	Acidobacteria, Solibacterales, Solibacteraceae	B19.?
Grafo	Flavobacteria, Flavobacteriales, Flavobacteriaceae	B20.2.1.1.?

2 Taxon Statistics

We base our analysis on the collection of 432 complete prokaryote genomes as of 31 December 2006. The taxon statistics shown in Table 5 was obtained according to the Bergey’s code of the 432 prokaryotes including 17 tentative ones explained above.

The “Total” lines in Table 6 to Table 11 should satisfy the following check sums leading to the taxon numbers given in the “Total” line of Table 5:

$$\begin{aligned}
&273 + 31 + 14 + 3 + 3 + 1 + 1 + 1 = 327 \\
&273 + 31 \times 2 + 14 \times 3 + 3 \times 4 + 3 \times 5 + 1 \times 8 + 1 \times 9 + 1 \times 11 = 432 \\
&128 + 32 + 12 + 8 + 5 + 2 + 2 + 1 = 190 \\
&128 + 32 \times 2 + 12 \times 3 + 8 \times 4 + 5 \times 5 + 2 \times 7 + 2 \times 9 + 1 \times 10 = 327 \\
&82 + 26 + 5 + 3 + 1 + 1 + 1 + 1 = 120 \\
&82 + 26 \times 2 + 5 \times 3 + 3 \times 4 + 1 \times 5 + 1 \times 6 + 1 \times 7 + 1 \times 11 = 190 \\
&50 + 20 + 7 + 1 + 1 = 79 \\
&50 + 20 \times 2 + 7 \times 3 + 1 \times 4 + 1 \times 5 = 120 \\
&23 + 4 + 3 + 2 + 2 + 1 = 35 \\
&23 + 4 \times 2 + 3 \times 3 + 2 \times 6 + 2 \times 7 + 1 \times 13 = 79 \\
&13 + 3 + 1 + 1 = 18 \\
&13 + 3 \times 3 + 1 \times 5 + 1 \times 8 = 35
\end{aligned}$$

We perform an exhaustive analysis of the CVTrees from $K = 3$ to $K = 6$ and a comprehensive comparison with the latest prokaryote taxonomy as reflected in the May 2004 online *Outline of Prokaryotes*^[2]. This is an *exhaustive* analysis because we study all cases from strains to phyla as ensured by the above check sums, not restricting to a few successful examples and ignoring “minor” exceptions.

The analysis is carried out in several steps:

1. We take all the available prokaryote complete genomes without making any selection. For a fixed K the CVTree algorithm^[3, 4] generates a distance matrix. Then the Neighbor-Joining

Table 5: Taxon statistics of the 432 prokaryotic complete genomes.

Phylum	C	O	F	G	S	str
A1	1	3	4	4	7	7
A2	8	9	12	18	23	23
A3	1	1	1	1	1	1
Subtotal 3	10	13	17	23	31	31
B1	1	1	1	1	1	1
B2	1	1	1	1	1	1
B4	1	2	2	2	3	4
B6	1	1	1	1	2	2
B10	1	3	3	8	15	19
B11	1	1	1	2	4	4
B12	5	33	53	99	157	208
B13	3	7	14	22	58	96
B14	3	9	15	16	31	35
B15	1	1	1	1	1	1
B16	1	1	2	3	7	11
B17	1	1	2	3	7	9
B19	1	1	1	2	2	2
B20	3	3	5	5	6	7
B21	1	1	1	1	1	1
Subtotal 15	25	66	103	167	296	401
Total 18	35	79	120	190	327	432

Table 6: Number of strains in a species.

$i =$	1	2	3	4	5	8	9	11	$\sum_{i>1}$
A1	7								
A2	23								
A3	1								
Subtotal	31								0
B1	1								
B2	1								
B4	2	1							1
B6	2								
B10	13	1		1					2
B11	4								
B12	130	15	7	1	3	1			27
B13	43	6	7				1	1	15
B14	27	4							4
B15	1								
B16	5	1		1					2
B17	5	2							2
B19	2								
B20	5	1							1
B21	1								
Subtotal	242	31	14	3	3	1	1	1	54
Total	273	31	14	3	3	1	1	1	54

Table 7: Number of species in a genus.

$i =$	1	2	3	4	5	7	9	10	$\sum_{i>1}$
A1	2	1	1						2
A2	15	1	2						3
A3	1								
Subtotal	18	2	3						5
B1	1								
B2	1								
B4	1	1							1
B6		1							1
B10	6			1	1				2
B11	1		1						1
B12	67	19	6	3	3	1			32
B13	14	1	1	2	1	1	1	1	8
B14	10	4		1			1		6
B15	1								
B16	1	1		1					2
B17		2	1						3
B19	2								
B20	4	1							1
B21	1								
Subtotal	110	30	9	8	5	2	2	1	57
Total	128	32	12	8	5	2	2	1	62

Table 8: Number of genera in a family.

$i =$	1	2	3	4	5	6	7	11	$\sum_{i>1}$
A1	4								
A2	8	3		1					4
A3	1								
Subtotal	13	3		1					4
B1	1								
B2	1								
B4	2								
B6	1								
B10	1	1			1				2
B11		1							1
B12	33	11	4	2		1	1	1	20
B13	7	6	1						7
B14	14	1							1
B15	1								
B16	1	1							1
B17	1	1							1
B19		1							1
B20	5								
B21	1								
Subtotal	69	23	5	2	1	1	1	1	34
Total	82	26	5	3	1	1	1	1	38

Table 9: Number of families in an order.

$i =$	1	2	3	4	5	$\sum_{i>1}$
A1	2	1				1
A2	6	3				2
A3	1					
Subtotal	9	4				3
B1	1					
B2	1					
B4	2					
B6	1					
B10	3					
B11	1					
B12	19	10	3		1	14
B13	4		2	1		3
B14	5	2	2			4
B15	1					
B16		1				1
B17		1				1
B19	1					
B20	1	2				2
B21	1					
Subtotal	41	16	7	1	1	25
Total	50	20	7	1	1	28

Table 10: Number of orders in a class.

$i =$	1	2	3	6	7	13	$\sum_{i>1}$
A1			1				1
A2	7	1					1
A1	1						
Subtotal	8	1	1				2
B1	1						
B2	1						
B4		1					1
B6	1						
B10			1				1
B11	1						
B12	1			2	1	1	4
B13		2	1				3
B14	2				1		1
B15	1						
B16	1						
B17	1						
B19	1						
B20	3						
B21	1						
Subtotal	15	3	2	2	2	1	10
Total	23	4	3	2	2	1	12

Table 11: Number of classes in a phylum.

$i =$	1	3	5	8	$\sum_{i>1}$
A1	1				
A2				1	1
A3	1				
Subtotal	2			1	1
B1	1				
B2	1				
B4	1				
B6	1				
B10	1				
B11	1				
B12			1		1
B13		1			1
B14		1			1
B15	1				
B16	1				
B17	1				
B19	1				
B20		1			1
B21	1				
Subtotal	11	3	1		4
Total	13	3	1	1	5

program in the Phylip package^[5] is used to produce a tree. The original outputs are organism trees. The $K = 3$ to 6 trees are given in the last section of this *Supplementary Material*.

2. Compare different strains of the same species if there are more than one strain in that species. If all strains stay together we keep one representative for the species. Note that this representative is kept after the analysis, not in the input data as usually done in some phylogenetic studies. This produces a species tree.
3. Compare different species in one and the same genus. If all species within a genus stay together we keep one species as representative of the genus. Again, this representative is kept after the analysis, not before. This produces a genus tree.
4. Study the relation among taxa higher than genus. If all genera in a family form a monophyletic group, these genera are represented by the family only. If all families in an order form a monophyletic group they are represented by the order, etc. In general, we look for the largest monophyletic group at fixed K .

Although the phylogeny of Eukaryotes is not the subject of this study, we note that the 8E branch of the trees are the same for $K = 4, 5, 6$, namely, (Encucu, (Plafa, ((Schpo, (Yeast, Ashgo)), (Arath, (Drome, Worm))))).

3 Comparison of CVTrees with Bergey's Taxonomy

It is not easy to comprehend trees with as many as 440 leaves. Only a detailed, bottom to top and taxon by taxon, comparison of the trees with the biologist's taxonomy is capable to show how good the CVTrees are. Such a detailed analysis is given in this *Supplementary Material*. A summary of the key points of this analysis appears in the main paper. To the best of our knowledge this is the first comparison of this kind in prokaryotic phylogeny.

3.1 Analysis of the Domain Archaea

Since at present only one genome per each Archaea species has been sequenced we start the analysis by looking at the convergence of species in those genera where more than one species have been sequenced. There are six such genera and all species converge within the genus for $K = 3 \sim 6$ as shown in Table 12 and 13.

3.1.1 Phylum A1 (*Crenarchaeota*)

The taxonomic lineage of the 7 species in Phylum A1 are listed in Table 12. The grouping of species in the CVTrees for genera with more than two species is also given.

Table 12: The 7 species in Phylum A1.

Bergey's Taxonomy				CVTrees		
Class	Order	Family	Genus	Species	Grouping	K
C_1	O_1	F_1	G_3	2	Pyrae(II)	3,4,5,6
		F_2	G_1	1	Thepe	
	O_3	F_1	G_3	1	Aerpe	3,5,6
		F_1	G_1	3	Sulso(III)	

3.1.2 Phylum A2: *Euryarchaeota*

Table 13: The 23 species in Phylum A2.

Bergey's Taxonomy				CVTrees		
Class	Order	Family	Genus	Species	Grouping	K
C_1	O_1	F_1	G_1	1	Metth	
			G_3	1	Metst	
C_2	O_1	F_1	G_1	2	Metja(II)	3,4,5,6
C_3	O_1	F_3	G_1	1	Methj	
	O_2	F_1	G_1	3	Metac(III)	4,5,6
C_4	O_1	F_1	G_2	1	Metbu	
			F_2	G_1	1	MetthP
			G_7	1	Halwd	
			G_1	1	Halsa	
			G_2	1	Halma	
C_5	O_1	F_1	G_{17}	1	Natpd	
			G_1	2	Theac(II)	3,4,5,6
			F_2	G_1	1	
			C_6	O_1	F_1	G_1
G_3	3	Pyrab(III)				3,4,5,6
C_7	O_1	F_1	G_1	1	Arcfu	
C_8	O_1	F_1	G_1	1	Metka	

Genus Convergence:

1. The two genera G_1 (Metch) and G_3 (Metst) in the family $A_2C_1O_1F_1$ form a monophyletic group for $K = 3 \sim 6$.
2. The two genera G_1 (Metac(III)) and G_2 (Metbu) in the family $A_2C_3O_2F_1$ form a monophyletic group for $K = 3 \sim 6$.

3. The two genera G_1 (pyrko) and G_3 (Pyrab(III)) in the family $A_2C_6O_1F_1$ form a monophyletic group for $K = 3 \sim 6$.
4. The three genera, G_1 (Halsa), G_2 (Halma) and G_{17} (Natpd) in the family $A_2C_4O_1F_1$ (*Halobacteriaceae*) always form a monophyletic group for $K = 3 \sim 6$, no matter whether it gets into the domain Bacteria ($K = 3, 4$) or remains within the domain Archaea ($K = 5, 6$).

Family Convergence:

The two Families F_1 (Theac(II)) and F_2 (Picto) in the order A_2C_5 form a monophyletic group for $K = 3 \sim 6$. However, this group joins the phylum A_1 in CVTrees. This agrees with the classification in *Five Kingdoms*^[6], but not with Bergey's Manual.

Order Convergence:

The two Orders O_1 (Methj) and O_2 (Metac(III)+Metbu) in Class C_3 form a monophyletic group for $K = 3 \sim 6$.

Class Convergence:

The 7 out of 8 classes in Phylum A_2 form a monophyletic cluster for $K = 5, 6$. Only class O_5 (Theac(II), Picto) joins A_1 at $K = 5, 6$.

3.1.3 Phylum A3 (*Nanoarchaeota*)

This is a new phylum not included in the Bergey's Manual yet. It contains only one genus and one species *Nanoarchaeum equitans*.

Convergence of the Archaea Domain:

Now we are in a position to summarize the CVTree convergence for all the 31 organisms in the Archaea domain, see Fig. 1.

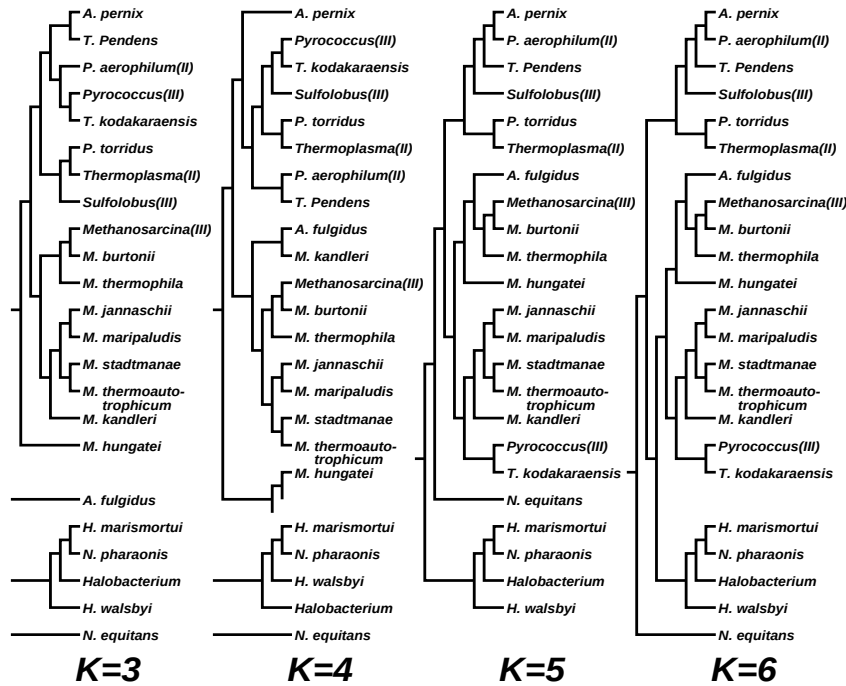


Figure 1: Archaea form a monophyletic clad in CVTree at $K = 5$ and 6 .

We make the following remark. Since in taxonomy all classes are juxtaposed under a phylum the trees at $K = 5$ and 6 shown in Fig. 1 are perfect in the sense of agreement of phylogeny with taxonomy except for the grouping of A_2C_5 with A_1 . However, this discrepancy appears only if we compare it with the Bergey’s Manual. There exist other opinions on the placement of A_2C_5 among biologists. For example, in the systematics of *Five Kingdoms*^[6] the genus *Thermoplasma* (under A_2C_5 in Bergey’s Manual) is put in the Phylum *Crenarchaeota*, i.e., A_1 of Bergey’s Manual, together with *Sulfolobus* (A_1C_1 according to Bergey’s). The CVTree results suggest that A_2C_5 should be assigned to Phylum A_1 .

3.2 Analysis of the Domain Bacteria

Only when a taxon contains two or more lower taxa it corresponds to one or more branching points in a tree. If a taxon contains more than three lower taxa these lower ones are simply juxtaposed in a taxonomy. However, in any phylogenetic tree, faithful or not, there appears a branching order among lower taxa. This adds a new dimension to the comparison of taxonomy with trees and may bring about new evolutionary knowledge. This is why we have started with a collection of the number of taxa contained in an higher taxon at all taxonomic ranks in Table 6 to 11. A summary of these tables for the domain *Bacteria* is given in Table 14.

Table 14: Number of taxa contained in an higher taxon (domain *Bacteria*).

$i =$	1	2	3	4	5	6	7	8	9	10	11	13	$\sum_{i>1}$
Strains/Species	242	31	14	3	3			1	1		1		54
Species/Genus	110	30	9	8	5		2	1	1	1			57
Genera/Family	69	23	5	2	1	1	1				1		34
Families/Order	41	16	7	1	1								25
Orders/Class	15	3	2			2	2					1	10
Classes/Phylum	11	1	2		1								4
Total	488												184

So far we have dealt with taxonomy only. The cases listed in the last column of Table 14 are to be checked in CVTrees. Among the 184 cases 139 are consistent. It is remarkable that the remaining 45 “different” cases are either known to biologists to some extent or may imply taxonomic revisions. The number of consistent and different cases at each taxonomic rank are listed in Table 15. The description of all these consistent and different cases are given in the subsequent sections.

Table 15: Number of consistent and different cases between CVTrees and the Bergey’s taxonomy (domain *Bacteria*).

	Total	Consistent	Different
Strains/Species	54	47	7
Species/Genus	57	46	11
Genera/Family	34	26	8
Families/Order	25	14	11
Orders/Class	10	5	5
Classes/Phylum	4	1	3
Total	184	139	45

In order to make the narration more readable and the related cases conveniently connected we use a double numbering scheme. First, the text is organized according to the Bergey’s code, i.e.,

from B1 to B21. Second, the different cases between CVTrees and Bergey’s taxonomy are labeled from [S–1] to [S–7] for Strains in Species, from [G–1] to [G–11] for Species in Genus, from [F–1] to [F–8] for Genera in Family, from [O–1] to [O–11] for Families in Order, from [C–1] to [C–5] for Orders in Class, from [P–1] to [P–4] for Classes in Phylum, so the corresponding instances out of various different cases may be cross-referred.

In what follows we proceed with the case study phylum by phylum. The convergent cases at strain and species levels are listed in tables together with their taxonomic distribution. Notations: Synpx(4) means 4 strains stay together, Promt(II) means 2 species stay together, Burma(V+2+2) means there are 5 single species and 2 species each containing 2 strains, all converging with K . The convergence range in K is also given, e.g., as $K = 3, 4, 5, 6$ or $K = 5, 6$ in the tables. A prime on the Arabic or Roman numeral such as Xancp(3’) indicates that there are some variations in the convergence pattern and an explanation follows.

3.2.1 Phylum B1 (*Aquificae*)

The Phylum B1 is represented by a single genome in the dataset. Therefore, no discussion until the phylum level.

3.2.2 Phylum B2 (*Thermotogae*)

The Phylum B2 is represented by a single genome in the dataset. Therefore, no discussion until the phylum level.

3.2.3 Phylum B4 (*Deinococcus – Thermus*)

The 4 organisms in Phylum B4 and the convergence at the strain and species level are given in Table 16

Table 16: The 4 organisms in Phylum B4.

Bergey’s Taxonomy				CVTrees			
Class	Order	Family	Genus	Species	Strain	Grouping	K
C_1	O_1	F_1	G_1	2	2	Deira(II)	3,4,5,6
	O_2	F_1	G_1	1	2	Thet8(2)	3,4,5,6

Intra-Phylum Convergence:

The Phylum B4 converges as (Deira, Thet8(2)) for $K = 3 \sim 6$.

3.2.4 Phylum B6 (*Chloroflexi*)

The 2 species in Phylum B6 and their convergence are given in Table 17

Table 17: The 2 species in Phylum B6.

Bergey’s Taxonomy				CVTrees			
Class	Order	Family	Genus	Species	Strain	Grouping	K
C_2	O_1	F_1	$G_?$	2	2	Dehsc(II)	3,4,5,6

Table 18: The 19 organisms in Phylum B10.

Bergey's Taxonomy				CVTrees			
Class	Subsection	Family	Genus	Species	Strain	Grouping	K
C_1	1	F_1	G_7	1	1	Glovi	
			G_{11}	5	5	Prom9(II)	3,4,5,6
						Promt(II)	4,5,6
						Promm	
			G_{13}	3	8	Synja(II)	3,4,5,6
	3	F_1				Synp6(2)	3,4,5,6
						Synpx(4)	3,4,5,6
			G_{14}	1	1	Syny3	
			$G_?$	1	1	Synel	
			G_{17}	1	1	Triei	
	4	F_1	G_1	1	1	Anava	
			G_8	1	1	Anasp	

3.2.5 Phylum B10 (*Cyanobacteria*)

The Phylum *Cyanobacteria* is represented by 19 genomes in the dataset. Their taxonomic distribution and convergence at the strain and species levels in the CVTrees are shown in Table 18.

The CVTrees for $K = 3 \sim 6$ are given in the main text of the paper. We note that at $K = 4, 5$ and 6 these 19 organisms do form a monophyletic cluster.

Species Convergence:

The *Prochlorococcus* species are the smallest known photosynthetic bacteria, discovered in the late 1980s. Although these 5 ecotypes are listed as strains in the NCBI and EBI taxonomy, they behave much like different species in the CVTrees.

Genus Convergence:

The 2 genera G_1 (Anava) and G_8 (Anasp) in the Family O_4 stay together for $K = 3 \sim 6$.

Bacteriologists have different opinion in classifying the *Cyanobacteria*. In Footnote 45 on page 32 of the Bergey's *Outline* we read:

"Ludwig recognizes the *Cyanobacteria* as a separate line of descent, along with the chloroplasts. PCA plots show a high level of variation in the chloroplasts."

"In Wilmotte and Herdman's chapter on the phylogeny of *Cyanobacteria* (Volume 1 of the 2nd Ed.), they state there is considerable variation in the branching order of the *Cyanobacteria*, especially at the base of the tree. Presumably, this arises from an explosive radiation shortly after the evolution of oxygenic photosynthesis. However, terminal nodes tend to cluster in a predictable manner.

"Wilmotte and Herdman also note that there is a multiplicity of confounding problems in linking available phenotype and genotype information. Part of the difficulty stems from misidentified reference material, including that which is held in collections. There also seems to be a problem with the quality of sequence data (especially short sequences). They urge any experimenter to confirm the identity of each strain using a polyphasic approach. Only then might it be possible to link the taxonomy and phylogeny in a meaningful way."

In the Bergey's taxonomy there is only one Class *Cyanobacteria* in this Phylum with 5 unnamed Subsections thereunder. All but 3 species (Triei, Abava, Anasp) in Table 18 are assigned to Subsection I. In the NCBI taxonomy there are one class *Gloeobacteria* containing only one order *Gloeobacterales* and 6 parallel orders among which *Chroococcales* corresponds to Subsection I, *Oscillatorales* (Triei) corresponds to Subsection III and *Nostocales* (Anava, Anasp) corresponds to Subsection IV.

According to the Bergey’s *Outline* *P. marinus* belongs to Class *Cyanobacteria* – Subsection I – Family 1.1 – Form Genus XI without special names at the intermediate ranks. In the NCBI taxonomy *P. marinus* belongs to Class *Cyanobacteria*, Order *Prochlorales*, Family *Prochlorococcaceae*, i.e., a whole new lineage has been introduced. Furthermore, Glovi from genus G_7 of Subsection I – Family 1.1 has been assigned to order *Gloeobacterales* under the class *Gloeobacteria*.

This situation makes the CVTree approach an important independent source to evaluate taxonomic designations.

Difference between CVTrees and Taxonomy:

- G–1 The *Synechococcus* strains Synpx(4) do not get into Genus G_{13} . Instead they join the *Prochlorococcus* species Promm at all K . In fact, Synpx strains live in the same habitat as Promm and are considered “potential competitor” of the latter^[7]. The grouping (Promm, Synpx(4)) persists from $K = 3$ to 6. The same grouping has been observed in trees built by other means^[9]. It might be reasonable to recognize Synpx(4) as a member of *Prochlorales*.
- G–2 Although *Thermosynechococcus* (Synel) has not been listed in the Bergey’s *Outline* its lineage may be determined up to genus as $B_{10}C_1O_1F_1G_7$ from the CVTrees. Apparently it is closer to Synp6(2).
- F–1 The designation of G_7 (Glovi) and G_{11} (*Prochlorococcus*) to the same family as *Synechococcus* is not justified in the CVTrees, see [C–1] below.
- C–1 The CVTrees suggest that the NCBI taxonomy of putting *Prochlorococcus* (and Synpx) in the order *Prochlorales* and Glovi in the order *Gloeobacterales* might be more natural than the Bergey’s.

3.2.6 Phylum B11 (*Chlorobi*)

The 4 species in Phylum B11 are listed in Table 19.

Table 19: The 4 organisms in Phylum B11.

Bergey’s Taxonomy				CVTrees			
Class	Order	Family	Genus	Species	Strain	Grouping	K
C_1	O_1	F_1	G_1	3	3	Chlch(III’)	5,6
			G_5	1	1	Pelld	

Genus Convergence:

The family F_1 (*Chlorobiaceae*) is well defined regardless of genus assignment of Pelld, see [G–3].

Difference between CVTrees and Taxonomy:

- G–3 The species Pelld prevents the 3 species in Genus G_1 *Chlorobium* to form a monophyletic cluster. We have to denote them by Chlch(III’). The problem may be resolved by assigning Pelld to the same genus G_1 instead of keeping another genus G_5 (*Pelodisctyon*) for it.

Intra-Phylum Convergence:

The Phylum B11 forms a monophyletic cluster for $K = 3 \sim 6$ as long as it is represented by the 4 species independent on the assignment of genera: (Chlch, (Chlph, (Chlte, Pelld))) at $K = 3$, ((Chlch, Chlte), (Chlph, Pelld)) at $K = 4$, and (Chlch, (Chlte, (Chlph, Pelld))) at $K = 5, 6$.

3.2.7 Phylum B12 (*Proteobacteria*)

Since the Phylum B12 are represented by 208 organisms, i.e., more than half of the available bacterial genomes, we do the analysis separately for the five groups/classes.

B12 Alpha Group

The 55 genomes and their convergence at the strain and species levels are listed in Table 20.

The agreement between CVTrees and the Bergey's taxonomy is perfect at strain and species levels. We make only one remark. There are some confusion about the species and strains of *Brucella* due to the common name *melitensis* that appears in many ways. According to Footnote 126 on P. 55 of the Bergey's *Outline* the four organisms in the genus *Brucella* should be treated as 4 species. However, we take *Brucella abortus* 9-941 (Bruab) and *Brucella melitensis* biovar *Abortus* 2308 (Brua2) as different strains of one and the same species according to the NCBI taxonomy. They converge for all $K = 3 \sim 6$. We denote them as Bruab(2) on a species tree and Burab(II+2) on a genus tree.

Genus Convergence:

1. The 2 genera G_1 (Rhoru) and G_4 (Magsa) in Family O_1F_1 (*Rhodospirillaceae*) form a monophyletic group for $K = 3 \sim 6$.
2. The 2 species in family O_1F_2 (*Acetobacteraceae*) represent 2 genera: G_7 (*Granulobacter*) and G_9 (*Gluconobacter*). They stay together at all $K = 3 \sim 6$.
3. The 4 genera in Family O_2F_2 (*Anaplasmataceae*): G_1 (*Anaplasma*), G_4 (*Ehrlichia*), G_5 (*Neorickettsia*) and G_6 (*Wollbachia*), form a monophyletic group (Neosm, (Wolpm(II), (Ehrru(II+3), Anamm(II)))) for $K = 3 \sim 6$.
4. The 4 species in the Family O_4F_1 (*Sphingomonadaceae*), representing 4 genera G_3 (*Erythrobacter*), G_6 (*Novosphingobium*), G_{11} (*Sphingopyxis*), and G_{12} (*Zymomonas*), form a monophyletic group (Zymmo, (Sphal, (Novad, Eryli))) at $K = 5$ and 6.
5. The 5 organismss in the Family O_6F_1 (*Rhizobiaceae*), representing 3 genera G_1 (*Rhizobium*), G_2 (*Agrobacterium*) and G_7 (*Sinorhizobium*), form a monophyletic group (Agrt5(2), (Rhiet(II), Rhime)) at $K = 3 \sim 6$.
6. The 8 organisms in the Family O_6F_8 (*Bradyrhizobiaceae*), representing 3 genera G_1 (*Bradyrhizobium*), G_6 (*Nitrobacter*), and G_9 (*Rhizopseudomonas*), form a monophyletic group (Nitwn(II), (Braja, Rhopa(5))) at $K = 3, 4$ and (Braja, (Nitwn(II), Rhopa(5))) at $K = 5, 6$. Therefore, the family is proper defined at all $K = 3 \sim 6$.

Family Convergence:

1. The 2 families F_1 (*Rhodospirillaceae*) and F_2 (*Acetobacteraceae*) in the order O_1 (*Rhodospirillales*) stay together for $K = 5$ and 6. At $K = 3, 4$ the two families are separated within the B12 Alpha group.
2. The 3 Families in the Order O_2 (*Rickettsiales*), F_1 (*Rickettsiaceae*) and F_2 (*Anaplasma*), plus a species Pelub in an unnamed Family, form a monophyletic group (Pelub, (F_1 , F_2)) for $K = 3 \sim 6$. This hints on the necessity to assign a new family to Pelub (there is no lineage of Pelub indicated in Bergey's Manual).
3. The 5 families in the order O_6 (*Rhizobiales*) form a monophyletic group (F_8 , (F_3 , (F_5 , (F_4 , F_1)))) for $K = 5$ to 6. At $K = 4$ one family F_3 escapes from the group, but remains in the *Alphaproteobacteria*. At $K = 3$ two families F_3 and F_8 escape but staying within B12 Alpha group. .

Table 20: The 55 organisms in Alpha group of Phylum B12 and their strain and species convergence in the CVTrees.

Bergey's Taxonomy			CVTrees			
Order	Family	Genus	Species	Strain	Grouping	K
O_1	F_1	G_1	1	1	Rhoru	
		G_4	1	1	Magsa	
	F_2	G_7	1	1	Grabc	
		G_9	1	1	Gluox	
O_2	F_1	G_1	5	5	Riccn(V)	3,4,5,6
		G_1	2	2	Anamm(II)	3,4,5,6
	F_2	G_4	3	5	Ehrru(II+3)	3,4,5,6
		G_5	1	1	Neosm	
		G_6	2	2	Wolpm(II)	3,4,5,6
		G_7	1	1	Pelub	
O_3	F_1	G_1	1	1	Rhos4	
		G_8	1	1	Hypna	
		G_9	1	1	Jansc	
		G_{12}	1	1	Marmmm	
		G_{17}	1	1	Parde	
		G_{25}	1	1	Rosdo	
		G_{30}	2	2	Silpo(II)	3,5,6
		G_3	1	1	Eryli	
O_4	F_1	G_6	1	1	Novad	
		G_{11}	1	1	Sphal	
		G_{12}	1	1	Zymmo	
		G_1	1	1	Caucr	
O_5	F_1	G_1	1	1	Caucr	
O_6	F_1	G_1	2	2	Rhiet(II)	3,4,5,6
		G_2	1	2	Agrr5(2)	3,4,5,6
		G_7	1	1	Rhime	
	F_3	G_1	2	2	Barhe(II)	3,4,5,6
	F_4	G_1	3	4	Bruab(II+2)	3,4,5,6
	F_5	G_6	2	2	Rhilo(II)	4,5,6
	F_8	G_1	1	1	Braja	
		G_6	2	2	Nitwn(II)	3,4,5,6
		G_9	1	5	Rhopa(5)	3,4,5,6
	F_7	G_7	1	1	Magmc	

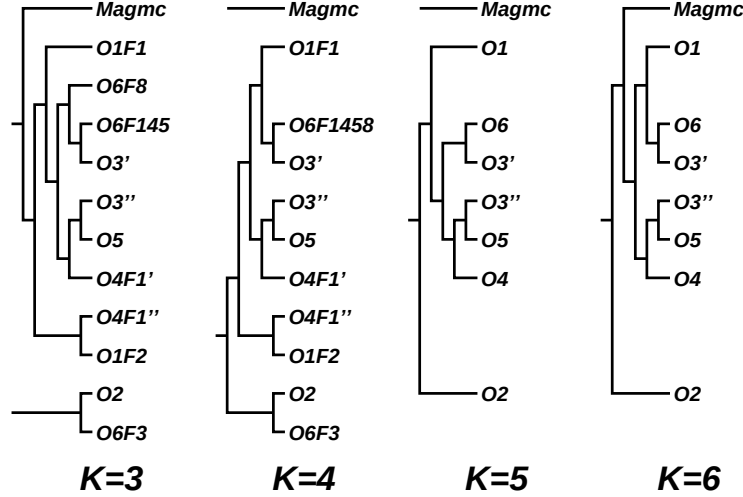


Figure 2: Convergence of orders in Alpha group with K . Note that at $K = 4$ to 6 the six orders defined in the Bergey's Manual form a monophyletic cluster.

Order Convergence:

As shown in Table. 20 there are 6 orders in the Alpha group plus a newly sequenced species *Magnetococcus MC-1* (Magmc) which has not been listed in the Bergey's *Outline*. The CVTrees in terms of orders are given in Fig. 2. This is yet another good example of convergence of the CVTrees. The 6 orders form a monophyletic cluster at $K = 4, 5$ and 6 . These trees also hint on the possibility of assigning a new order to Magmc within the Alpha group.

Difference between CVTrees and Taxonomy:

F-2 Among the 33 genera of family O_3F_1 (*Rhodobacteraceae*) 7 genera are represented by 8 species in the dataset. Apparently there is a stable separation into two clusters in CVTrees from $K = 3$ to 6 : $O_3F_1' = ((G_1(\text{Rhos4}), G_{17}(\text{Parde})), (G_9(\text{Jansc}), (G_{25}(\text{Rosdo}), G_{30}(\text{Silpo}(\text{II}))))$ and $O_3F_1'' = (G_8(\text{Hypna}), G_{12}(\text{Marmmm}))$. Since O_3 is represented by F_1 only for the time being, we can divide the order into two: $O_3' \equiv O_3F_1'$, $O_3'' \equiv O_3F_1''$.

C-2 There is only one revision needed to make the $K = 5, 6$ order trees self-consistent: assign O_3' to O_6 and O_3'' to O_5 , see Fig. 2.

B12 Beta Group

The 30 genomes in the Beta group and their convergence at strain and species levels are given in Table 21.

Species Convergence:

The 4 organisms in the genus *Ralstonia* converge for $K = 3 \sim 6$. They are denoted as Ralso(II+2) on a genus tree. The species *Ralstonia eutropha* JMP134 (Ralej) was called *Cupriavidus necator* JMP134 where the genus *Cupriavidus* corresponds to Bergey's code B12.2.1.1.2. Our result shows that it indeed belongs to *Ralstonia* (B12.2.1.1.8).

Genus Convergence:

1. The two genera G_1 (Burma(V+2+2)) and G_8 (Ralso(II+2)) in the Family O_1F_1 (*Burkholderiaceae*) form a monophyletic group for $K = 3 \sim 6$.
2. The two genera G_{13} (Polsj) and G_{15} (Rhofd) in the Family O_1F_4 (*Comamonadaceae*) form a monophyletic group for $K = 3 \sim 6$.

Table 21: The 30 organisms in Beta group of Phylum B12 and their strain and species convergence in CVTrees.

Bergey's Taxonomy			CVTrees			
Order	Family	Genus	Species	Strain	Grouping	K
O_1	F_1	G_1	7	9	Burca(2),Burps(2)	3,4,5,6
					Burma(V+2+2)	4.5.6
	F_3	G_8	3	4	Ralej(2)	3,4,5,6
					Ralso(II+2)	3.4.5.6
		G_3	3	3	Borpe(III)	3,4,5,6
		G_{13}	1	1	Polsj	
O_2	F_1	G_2	1	1	Rhofd	
		G_{15}	1	1	Thida	
O_3	F_1	G_2	1	1	Metfl	
O_4	F_1	G_1	2	3	Neima(2)	3,4,5,6
					Neima(I+2)	?
		G_4	1	1	Chrvo	
O_5	F_1	G_1	1	2	Niteu(2)	3,4,5,6
		G_3	1	1	Nitmu	
O_6	F_1	G_2	2	2	Azose(II)	3,4,5,6
		G_6	1	1	Decar	

3. The two genera G_1 (Neima(I+2)) and G_4 (Chrvo) in the Family O_4F_1 (*Neisseriaceae*) form a monophyletic group for $K = 4 \sim 6$, Chrvo being separated at $K = 3$.
4. The two genera G_1 (Niteu(2)) and G_3 (Nitmu) in the Family O_5F_1 (*Nitrosomonadaceae*) form a monophyletic group for $K = 3 \sim 6$.
5. The two genera G_2 (Azose(II)) and G_6 (Decar) in the Family O_6F_1 (*Rhodocyclaceae*) form a monophyletic group for $K = 3 \sim 6$.

Family Convergence:

The three families F_1 (*Burkholderiaceae*), F_3 (*Alcaligenaceae*) and F_4 (*Comamonadaceae*) in the Order O_1 (*Burkholderiales*) form a monophyletic group for $K = 3 \sim 6$ with some variation of inter-order placement, see Fig. 3. This is satisfactory agreement of CVTrees with the taxonomy at the rank of order.

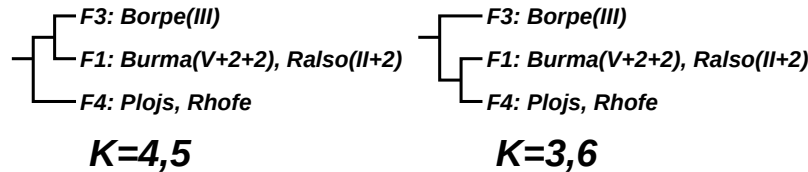


Figure 3: Convergence of the 3 families in the Order *Burkholderiales*.

Order Convergence:

The 6 Orders in the Beta group form a monophyletic cluster for $K = 5$ and 6, with O_5 standing out at $K = 4$ and a more scattered placement at $K = 3$. See Fig. 4 for the order convergence with K .

Woese and coworkers observed in their study of 16S rRNA trees, “The β subdivision is actually a highly divergent branch within γ , and these two together show a sister relationship to α ”^[10].

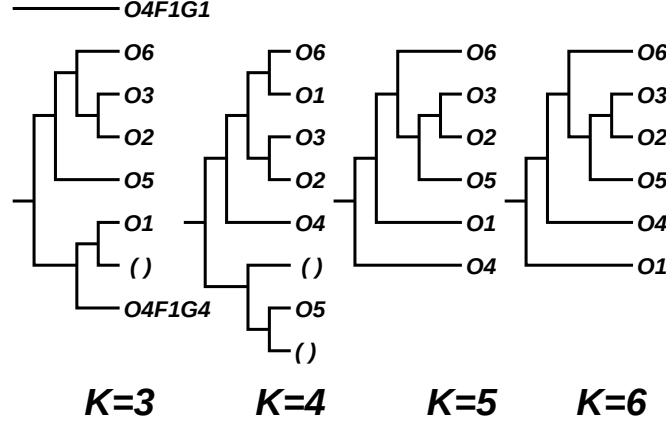


Figure 4: The convergence of the 6 orders in the Beta group. The monophyletic structure at $K = 5$ and 6 shows a satisfactory agreement of phylogeny with taxonomy. The blank parentheses at $K = 3, 4$ denote some organisms from the Gamma group.

This happens in all CVTrees as well. However, we now have more to say on this point, see [C-3] below. We note also that the appearance of some members of the Gamma group in the $K = 3$ and 4 trees in Fig. 4 may be viewed as a manifestation of the mixing-up at low resolution.

B12 Gamma Group

The 101 organisms in the Gamma group and their convergence in the CVTrees at the strain and species levels are listed in Table 22.

Species Convergence:

The convergence of species in *Pseudomonas* deserves special mentioning since it was a long-standing problem in bacterial taxonomy. “*Pseudomonas* may belong to any group” (in *Proteobacteria*)^[6]. In CVTrees the 5 species in the genus *Pseudomonas* including Pseae(2), Psepf(2) and Psesm(3) converge for $K = 3 \sim 6$, denoted as Pseae(II+2+2+3) in a genus tree, see Fig. 5.

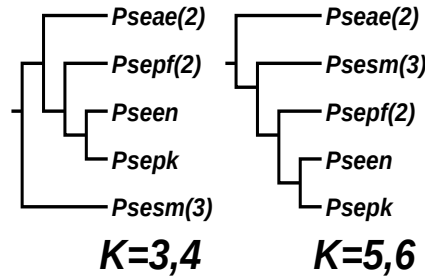


Figure 5: Convergence of the 9 organisms in the genus *Pseudomonas*.

Genus Convergence:

1. The 2 genera G_1 (*Xanthomonas*) and G_{12} (*Xylella*) in the Family O_3F_1 (*Xanthomonadaceae*) form a monophyletic group for $K = 3 \sim 6$.
2. The 2 genera G_2 (*Acinetobacter*) and G_3 (*Psychrobacter*) in O_9F_2 (*Pseudomonanadaceae*) stay together for $K = 3 \sim 6$.

Table 22: The 101 organisms in Gamma group of Phylum B12.

Bergey's Taxonomy			CVTrees			
Order	Family	Genus	Species	Strain	Grouping	<i>K</i>
O_1	F_1	G_9	1	1	Nitoc	
	F_2	G_2	1	1	Alheh	
O_3	F_1	G_1	3	6	Xanom(2),Xancp(3')	3,4,5,6
					Xancp(I+2+3')	3,4,5,6
		G_{12}	1	2	Xylfa(2)	3,4,5,6
	$F_?$	$G_?$	1	1	Rutma	
O_5	F_2	G_1	1	5	Fratt(5)	4,5,6
	F_3	G_6	2	2	Thicr,Thidn	?
O_6	F_1	G_1	1	3	Legpa(3)	4,5,6
	F_2	G_1	1	1	Coxbu	
O_7	F_1	G_1	1	1	Metca	
O_8	F_2	G_1	1	1	Alchs	
	F_3	G_1	1	1	Hahch	
	F_4	G_3	1	1	Chrsd	
O_9	F_1	G_1	5	9	Pseae(2),Psepf(2),Psesm(3)	3,4,5,6
					Pseae(II+2+2+3)	5,6
	F_2	G_2	1	1	Aciad	
		G_3	2	2	Psyar(II)	3,4,5,6
O_{10}	F_1	$G_?$	1	1	Sacd2	
		G_4	1	1	Colp3	
		G_7	1	1	Idilo	
		G_{12}	2	2	Psea6,Pseht	3,4,5,6
		G_{13}	1	1	Psyin	
		G_{14}	5	7	Shean(3)	3,4,5,6
					Shean(IV+3)	3,5,6
O_{11}	F_1	G_1	4	5	Vibvu(III+2)	3,4,5,6
		G_7	1	1	Phopr	
O_{12}	F_1	G_1	1	1	Aerhy	
O_{13}	F_1	$G_?$	2	2	Blopb(II)	3,4,5,6
		$G_?$	1	1	Bauch	
		G_1	1	8	Ecoli(8)	?
		G_5	4	4	Bucbp(4)	3,4,5,6
		G_{13}	1	1	Erwct	
		G_{26}	1	1	Pholl	
		G_{34}	4	5	Salti(2)	3,4,5,6
					Salti(III+2)	4,5,6
		G_{37}	4	6	Shifl(3)	4,5,6
					Shifl(III+3)	?
		G_{38}	1	1	Sodgl	
		G_{41}	1	1	Wigbr	
		G_{43}	2	6	Yerpe(I+5)	4,5,6
O_{14}	F_1	G_1	1	1	Pasmu	
		G_4	3	4	Haein(2)	3,4,5,6
					Haein(II+2)	?
		G_6	1	1	Mansm	
$O_?$	$F_?$	$G_?$	1	1	Carru	?

3. The 2 genera G_1 (*Vibrio*) and G_7 (*Photobacterium*) in the Family $O_{11}F_1$ (*Vibrionaceae*) form a monophyletic group for $K = 4 \sim 6$.
4. The family $O_{14}F_1$ (*Pateurellaceae*) is properly defined for all $K = 3 \sim 6$, although there is problem in the assignment of of the 3 underlying genera, see [G-6] and Fig. 7.

Family Convergence:

The 2 families F_1 (*Legionellaceae*) and F_2 (*Coriellaceae*) in the Order O_6 (*Legionellales*) form a monophyletic group for $K = 5 \sim 6$.

Difference between CVTrees and Taxonomy:

- S-1 The three strains in the species *Xanthomonas campestris* stay as ((Xanac, Xanc5), (Xanc8, Xancp)) for $K = 3 \sim 6$ with another species *X. axonopodis* (Xanac) mixed in, forming a paraphyletic cluster for the three *campestris* strains. We denote them conditionally as Xancp(3').
- S-2 There are 8 strains of the species *Escherichia coli*. They form a monophyletic cluster at $K = 3, 4, 6$ but get mixed with some *Shigella* strains at $K = 5$. This situation will be discussed later in [G-5] together with the *Shigella* species. For brevity we introduce the notations: Ecoli(4) = (EcoliC, (Ecoli5, (EcoliA, EcoliU))); Ecoli(4') = ((EcoliK, EcoliW), (EcoliE, EcoliO)); Ecoli(8) = (Ecoli(4), Ecoli(4')); Ecoli(8') = ((Ecoli, EcoliO), ((EcoliK, EcoliW), Ecoli(4))).
- G-4 The two species in the genus *Thiomicrospira* does not come together in CVTrees at all K . While *T. crunogena* (Thicr) remains within the Gamma group, *T. denitrificans* (Thidn) joins the Epsilon group in all CVTrees, see Fig. 14. This fact agrees with Footnote 229 on page 87 of Bergey's *Outline*: "The identity of *Thiomicrospira denitrificans* is questionable as it belongs within Epsilonproteobacteria."¹
- In all the CVTrees from $K = 3$ to 6 Thicr gets paired with Rutma which has not been listed in the Bergey's *Outline*, see Table 4. The placement of *T. crunogena* may cause further problem at higher taxonomic ranks. For example, we do not know whether it is suitable to assign both Thicr and Rutma to the order O_5 , see [O-2].
- G-5 The 4 species in the genus *Shigella* including Shifl(3) form a monophyletic cluster for $K = 3$ and 4, but they get mixed at $K = 5$ and 6. This makes the establishment of the genus *Shigella* questionable. Using the notations introduced in [S-2], we show their mixing up in Fig 6.

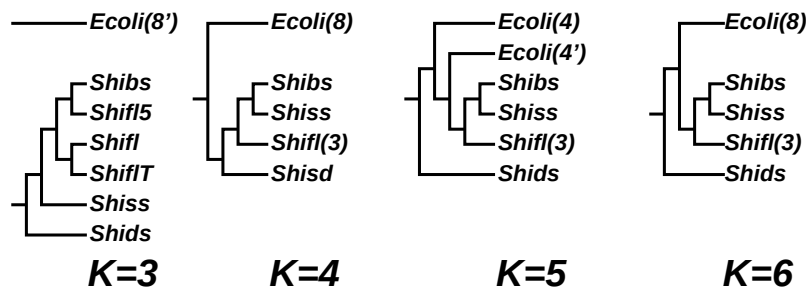


Figure 6: The mixing-up of the *Escherichia* and *Shigella* strains.

In fact, the mixing up and distinction of these two “genera” has been a long-debated problem^[11]. Some authors even called them *Shigella* clone of *Escherichia*^[12]. From a

¹ *T. denitrificans* has been moved to the Epsilon group as *Sulfurimonas denitrificans* in George M. Garrity *et al.*, *Taxonomic Outline of Bacteria and Archaea* (TOBA) Rel. 7.7, 6 March 2007. Note added on 30 May 2007.

genomic point of view it may be reasonable to combine *Shigella* and *Escherichia* into one genus. However, mainly due to clinic distinction of the disease caused by *Shigella* there is good reason to keep the genus name.

- G-6 The assignment of the 6 organisms from the family $O_{14}F_1$ (*Pasteurellaceae*) into 3 different genera G_1 (*Pasteurella*), G_4 (*Haemophilus*), and G_6 (*Mannheimia*) is questionable. However, this does not prevent them to form a monophyletic cluster as a well-defined family in the CVTrees, see Fig. 7.

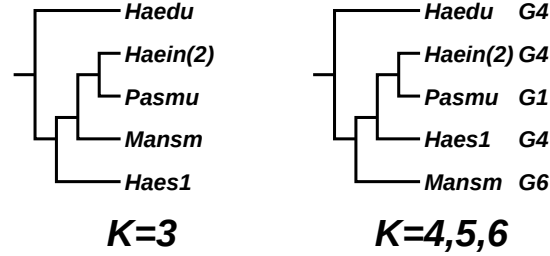


Figure 7: The family *Pasteurellaceae* is properly defined in the CVTrees despite possible problems in genus assignment.

- F-3 The 5 genera in family $O_{10}F_1$ do not form a monophyletic cluster in all CVTrees from $K = 3$ to 6, but they do form a monophyletic group with O_{11} and O_{12} , see Fig. 8. We denote this greater cluster as $O_{10}/O_{11}/O_{12}$ in some subsequent figures.

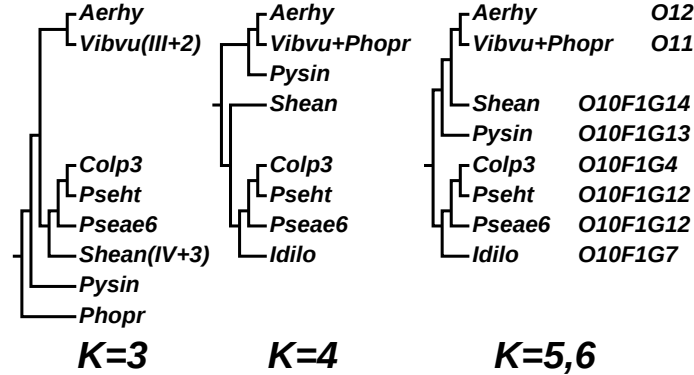


Figure 8: The order O_{10} enters a monophyletic cluster together with O_{11} and O_{12} .

We note also that *Saccharophagus degradans* (Sacd2) was assigned a tentative Bergey's code B12.3.10.1.? up to an unlisted genus according to the NCBI taxonomy, see Table 4. However, the CVTrees suggest that it is more appropriate to put it into O_8 , see [O-4] and Fig. 11.

- F-4 The order O_{13} (*Enterobacteriales*) is represented by only one family F_1 (*Enterobacteriaceae*) in the dataset. It is one of the most studied bacterial family. In Bergey's Manual this family is subdivided into 44 genera. As of 31 December 2006, genomes of 36 organisms have been sequenced. They come from 11 genera, including a genus not listed in Bergey's Manual (*Candidatus Blochmannia*).

Interestingly, in all CVTrees for $K = 3 \sim 6$ this family (hence the order O_{13} for the time being) is disunited into two subgroups with sharp contrast in their genome size. We call them the upper and lower group of O_{13} , see Table 23 and Table 24.

The upper subgroup consists of 28 species/strains from 7 genera. They always form a monophyletic cluster with minor variations of internal relations as shown in Fig. 9. If we take into account what has been said before on the mixing up of *E. coli* and *Shigella* and name the monophyletic branch formed by these organisms as one unit, then the clusters in Fig. 9 happen to be identical for $K = 4 \sim 6$.

The lower subgroup consists of 8 organisms from 4 genera. They always form a monophyletic cluster for $K = 3 \sim 6$ with slight variation of internal relation as shown in Fig. 9.

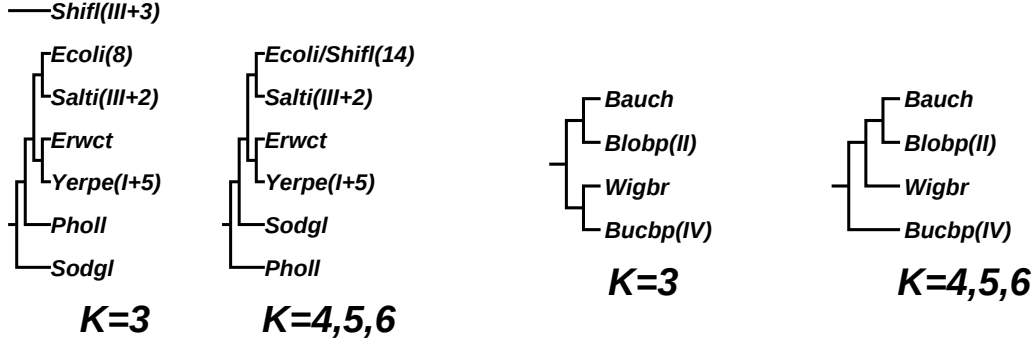


Figure 9: Left: The upper group of O_{13} consists of 28 organisms. Right: The lower group consists of 8 organisms.

Taking into account [F-3] and [F-4], it is appropriate to recollect Note 258 on p. 104 of Bergey's *Outline*: "Ludwig indicates that the *Aeromonadales* (O_{12}), *Alteromonadales* (O_{10}), *Enterobacteriales* (O_{13}), *Pasteurellales* (O_{14}), and *Vibrionales* (O_{11}) cluster together in both the ARB and RDP trees." However, the split of O_{13} into two groups has not been reflected in the Bergey's Manual. In fact, the upper group of O_{13} is clustered with order O_{14} represented by the family *Pasteurellaceae* in CVTrees at $K = 4, 5, 6$, while the lower group of O_{13} escapes from the aforementioned cluster of the 5 orders.

O-1 The 2 families O_1F_1 (*Chromatiaceae*, represented by Nitoc) and O_1F_2 (*Ectothiorhodospiraceae*, represented by Alheh) come closer with K increasing, but the only member from O_7 (Metca) gets firmly inserted, see Fig. 10. We have to wait for more sequenced genomes to see whether O_1 and O_7 actually form a monophyletic cluster.

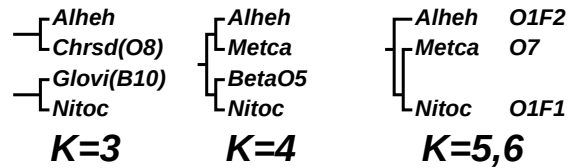


Figure 10: The order O_1 and O_7 form a monophyletic cluster.

O-2 In the order O_5 the 2 families F_2 (*Franciselaceae*) and F_3 (*Piscirickettsiaceae*) (*Thiotrichales*, represented by the only remaining member of *Thiomicrospira* — Thicr) never gets together for $K = 3 \sim 6$. This might be a problem with the placement of the genus *Thiomicrospira*, see [G-4] above.

O-3 The 2 families F_1 (*Pseudomonadaceae*) and F_2 (*Moraxellaceae*) in order O_9 (*Pseudomonadales*) stay close but do not form a monophyletic branch for $K = 3 \sim 6$,

Table 23: The 28 organisms in the upper group of order O_{13} .

Name	Abbr.	Genome Size	Gene Number
<i>Escherichia coli</i> 536	Ecoli5	4 938 920	4 629
<i>Escherichia coli</i> APEC O1	EcoliA	5 082 025	4 467
<i>Escherichia coli</i> CFT073	EcoliC	5 231 428	5 379
<i>Escherichia coli</i> K12	EcoliK	4 639 675	4 237
<i>Escherichia coli</i> O157:H7	EcoliO	5 498 450	5 253
<i>Escherichia coli</i> O157:H7 EDL933	EcoliE	5 528 445	5 324
<i>Escherichia coli</i> UT189	EcoliU	5 065 741	5 066
<i>Escherichia coli</i> W3110	EcoliW	4 646 332	4 227
<i>Erwinia carotovora</i> ssp. <i>atroseptica</i> SCRI043	Erwct	5 064 019	4 472
<i>Photorhabdus luminescens</i> ssp. <i>laumondii</i>	Pholl	5 688 987	4 683
<i>Salmonella enterica</i> ssp. <i>Paratyphi</i> A str. ATCC 9150	Salpa	4 585 229	4 093
<i>Salmonella enterica</i> <i>Choleraesuis</i>	Salch	4 755 700	4 441
<i>Salmonella typhimurium</i>	Salty	4 857 432	4 425
<i>Salmonella Typhi</i> Ty2	SaltyT	4 791 961	4 318
<i>Salmonella typhi</i>	Salti	4 809 037	4 395
<i>Shigella boydii</i> Sb227	Shibs	4 519 823	4 136
<i>Shigella dysenteriae</i> Sd197	Shids	4 369 232	4 274
<i>Shigella sonnei</i> Ss046	Shiss	4 825 265	4 223
<i>Shigella flexneri</i> 2a str. 301	Shifl	4 607 203	4 182
<i>Shigella flexneri</i> 2a str. 2457T	ShiffT	4 599 354	4 068
<i>Shigella flexneri</i> 58401	Shiff5	4 574 284	4 116
<i>Sodalis glossinidius</i> str. ‘ <i>morsitans</i> ’	Sodgl	4 171 146	2 432
<i>Yersinia pseudotuberculosis</i> IP 32953	Yerps	4 744 671	3 901
<i>Yersinia pestis</i> str. CO92	YerpeC	4 653 728	3 885
<i>Yersinia pestis</i> KIM	YerpeK	4 600 755	4 086
<i>Yersinia pestis</i> biovar <i>Mediaevails</i> str. 91001	YerpeM	4 595 065	3 895
<i>Yersinia pestis</i> <i>Antiqua</i>	Yerpa	4 702 289	4 167
<i>Yersinia pestis</i> Nepal516	Yerpn	4 534 590	3 981

O-4 The family O_9F_1 (*Pseudomonadaceae*), represented by $Pseae(II+2+2+3)=Pseae(9)$, gets into the cluster made of 3 families F_2 (*Alcanivoraceae*), F_3 (*Hahellaceae*) and F_4 (*Chromohalobacter*) of order O_8 (*Oceanospirillales*), preventing the latter to form a monophyletic cluster for $K = 5, 6$, see Fig. 11. This figure also shows *Sacd2* is closer to order O_8 than O_{10} , see [F-3].

Compare Note 237 on p. 90 of Bergey’s *Outline*: “The position of the *Oceanospirillales* within the ARB tree is ambiguous.”

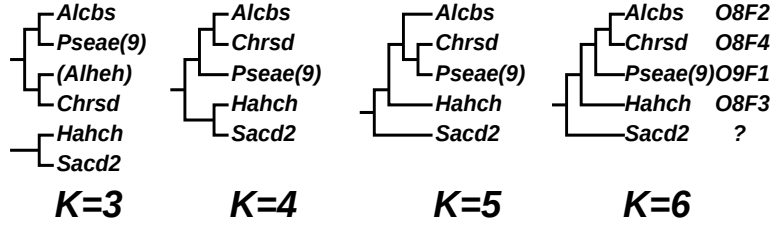
With most of the notations fixed, we are now in a position to describe how the B12 Beta group gets inserted into the Gamma group, see Fig. 12. This may lead to taxonomic revisions at the class level:

C-3 The insertion of the Beta group into the Gamma group is a phenomenon common to the CVTrees and 16S rRNA trees, but not reflected in the Bergey’s Manual. As seen from Fig. 12 with respect to the monophyletic cluster of Beta group, members of the Gamma group may be divided into 3 subgroups:

- An upper subgroup consists of the O_8 , O_9 , and the $O_{10} - O_{14}$ cluster that includes the upper part of $O_{13}(28/36)$;

Table 24: The 8 organisms in the lower group of order O_{13}

Name	Abbr.	Genome Size	Gene Number
<i>Baumannia cicadellincola</i>	Bauch	686 194	595
<i>C. Blochmannia floridanus</i>	Blofl	705 557	583
<i>C. Blochmannia pennsylvanicus</i> BPEN	Blopb	791 654	610
<i>Buchnera aphidicola</i> Sg	Bucap	641 454	546
<i>Buchnera aphidicola</i> (<i>Baizongia pistaciae</i>)	Bucbp	615 980	504
<i>Buchnera aphidicola</i> Cc <i>Cinara cedri</i>	Bucac	416 380	357
<i>Buchnera</i> sp. APS	Bucal	640 681	564
<i>Wiggelsworthia brevipalpis</i>	Wigbr	697 724	611

Figure 11: The family O_9F_1 gets into the order O_8 . Pseae(II+2+2+3) is written as Pseae(9).

- A lower subgroup consists of O_5F_2 (Fratt(5)) and the lower part of $O_{13}(8/36)$.
- A middle subgroup whose members jump around the Beta group at $K = 5$ and 6. This includes O_3 , O_6 , the O_1/O_7 cluster and the (Rutma, Thicr) pair.

All the 8 organisms in the lower part of O_{13} are endocellular symbionts of insects^{[13]–[20]}. Their genomes have undergone a reductive evolution and now have very small size, less than 0.8M bp and 615 genes, as compared to the upper group with more than 4M bp and 2400 genes, see Tables 23 and 24. Therefore, it is a common problem of CVTrees and the 16S rRNA trees that they could not distinguish early evolved genomes from those resulted by reductive evolution simply from their being located on lower part of a branch.

B12 Delta Group

The 13 organisms in the Delta group and their convergence at species level in the CVTrees are given in Table 25.

Since there are only 13 organisms represented in this class we show their related branches in CVTrees in Fig. 13.

Genus Convergence:

The 2 genera G_1 (*Desulfurovibrio* represented by Desvh(II)) and G_3 (*Lawsonia* represented by Lawip) converge to family O_2F_1 (*Desulfurovibrionaceae*) at all $K = 3 \sim 6$.

Family Convergence:

1. The two families F_1 (*Desulfuromonaceae*, represented by Pelpr and Pelcd) and F_2 (*Geobacteraceae* represented by Geosl(II)) in the Order O_5 (*Desulfuromonales*) form a monophyletic cluster at all $K = 3$ to 6, see Fig. 13.
2. The two families F_1 (*Syntrophobacteraceae* represented by Synfu) and F_2 (*Syntrophaceae* represented by Synas) converge to order O_6 at $K = 3, 5, 6$.

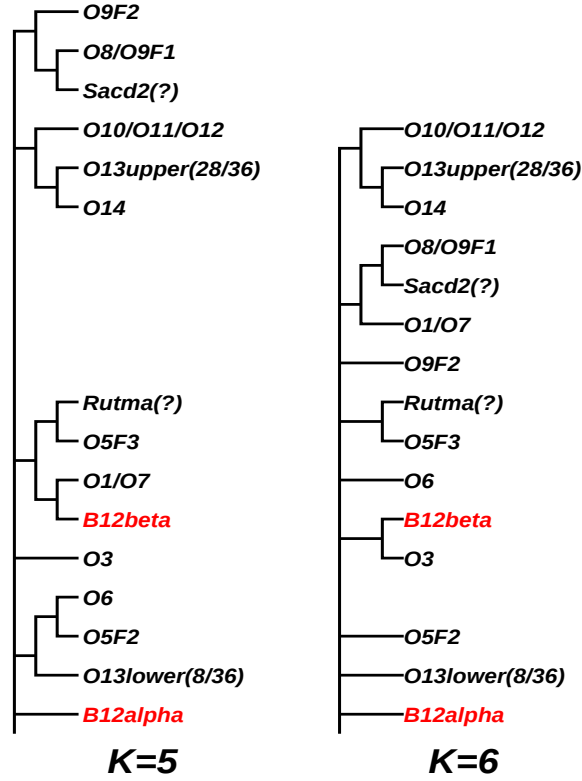


Figure 12: The insertion of the *Betaproteobacteria* group into the *Gammaproteobacteria* group. Only orders or order/family in the Gamma group are indicated.

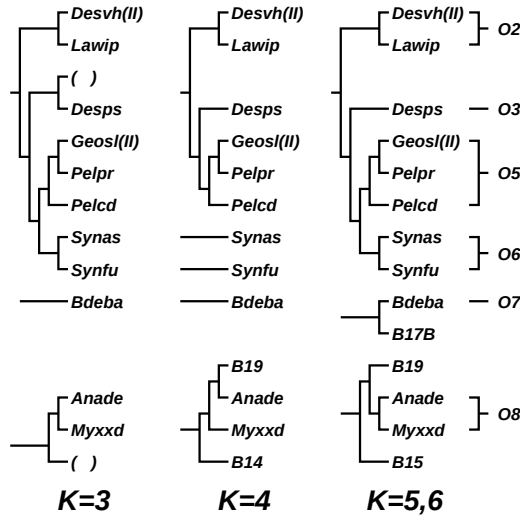
3. The two families F_1 (*Cystobacteraceae* represented by Anade) and F_2 (*Myxococcaceae* represented by Myxxd) from suborder *Cystobaterineae* of order O_8 (*Mycococcales*) converge to order O_8 at $K = 3, 5, 6$. However, see [C-4] below.

Order Convergence:

From Fig. 13 it is clearly seen that the orders O_2 (*Desulfovibrionales*), O_3 (*Desulfobacterales* represented by Desps only), . At $K = 4$ the 2 families of Order O_5 are separated. Note that for $K = 5$ and 6 there exists the same monophyletic cluster formed by 5 orders; at $K = 6$ all the 6 orders form a monophyletic cluster.

Table 25: The 13 organisms in Delta group of Phylum B12.

Bergey's Taxonomy			CVTrees			
Order	Family	Genus	Species	Strain	Grouping	K
O_2	F_1	G_1	2	2	Desvh(II)	3,4,5,6
		G_3	1	1	Lawip	
O_3	F_1	G_5	1	1	Desps	
O_5	F_1	G_4	2	2	Pelcd,Pelpr	3,4,5,6
	F_2	G_1	2	2	Geosl(II)	
O_6	F_1	G_1	1	1	Synfu	
	F_2	G_1	1	1	Synas	
O_7	F_1	G_1	1	1	Bdeba	
$O_{8.1}$	F_1	G_2	1	1	Anade	
	F_2	G_1	1	1	Myxxd	

Figure 13: The CVTree branchings for the 13 members of the Delta class (*Deltaproteobacteria*).**Difference between CVTrees and Taxonomy:**

G-7 The 2 species Pelcd and Pelpr from genus $O_5F_1G_4$ (*Pelobacter*) never get together in all CVTrees from $K = 3$ to 6. However, this does not prevent them from joining Geosl(II) to form a properly defined family as described above. The fact that Pelpr joins Geosl(II) was observed in 16S rDNA analysis (see Footnote 296 on p. 133 of Bergey's *Outline*). As regarding Pelcd, Footnote 294 says "By 16S rDNA analysis, this species groups with species of the *Desulfuromonas*". For the time being this could not be checked in the CVTrees as there was no genome from the latter genus. However, the branching in Fig. 13 does not contradict the aforementioned observation in 16S rRNA tree.

C-4 It is seen from Fig. 13 that the four orders O_2 , O_3 , O_5 and O_6 form a monophyletic cluster at $K = 3, 5, 6$. This cluster is the unquestionable core of the class *Deltaproteobacteria* in CVTrees. However, order O_7 (*Bdellovibrionales* represented by Bdeba) and order O_8 (*Myxococcales* represented by Anade and Myxxd) escape from the main cluster of the Delta group. For the former case we cannot say anything until more related genomes become available. For the latter case we note that the taxonomic position of the *Myxococcales* has

been a long-standing problem. Some years ago there was even suspicion that these species might not belong to bacteria at all, see [21].

B12 Epsilon Group

The 9 organisms in the Epsilon group and their convergence at the strain and species levels are given in Table 26. The corresponding CVTree branches are shown in Fig. 14. We have included *Thiomicrospira denitrificans* (Thidn) into this class as mentioned in [G-4] before.

Table 26: The 9 organisms in Epsilon group of Phylum B12.

Bergey's Taxonomy			CVTrees			
Order	Family	Genus	Species	Strain	Grouping	K
O_1	F_1	G_1	2	3	Camje(1+2)	3,4,5,6
	F_2	G_1	3	5	Helpy(3)	3,4,5,6
					Helac,Helhp	?
		G_4	1	1	Wolsu	

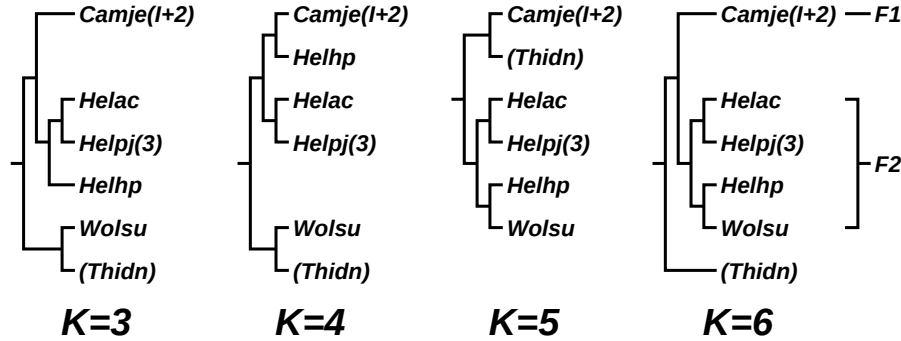


Figure 14: The CVTree branch for the class *Epsilonproteobacteria*. Note that Thidn joins this group for all $K = 3 \sim 6$ as mentioned before in [G-4].

Family Convergence:

The 2 families F_1 (*Campylobacteraceae*) and F_2 (*Helicobacteraceae*) form a monophyletic cluster at $K = 6$. Since order O_1 (*Campylobacterales*) is the only order listed under the Epsilon group in the Bergey's Manual there is no family convergence problem up to the uncertain placement of Thidn.

Difference between CVTrees and Taxonomy:

- G-8 The 3 species in the genus *Helicobacter* including Helpj(3) converge only at $K = 3$ as Heplj(II+3). The $K = 5$ and 6 trees in Fig. 14 may hint on that the problem comes from improper assignment of Wolsu to G_4 other than keeping it in G_1 the Helpj(II+3) strains do.
- F-5 The 2 genera G_1 (Helpj(II'+3) at $K = 5, 6$) and G_4 (Wolsu) form a monophyletic cluster at $K = 5$ and 6, although there might be problem with genus assignment of Wolsu, see [G-8] above.

Before concluding the discussion of phylum B12 we look at the difference between CVTrees and Bergey's taxonomy at the highest taxonomic rank, namely, the convergence of classes into phylum:

P-1 The full convergence of the 5 classes from phylum B12 is challenged by four outliers:

- Carru escapes from the whole B12 clad. However, this tiny genome of bacterial symbiont should be discarded in studying the phylogeny of free-living bacteria.
- Anade and Myxxd escape from the Delta group. As we pointed out before in [C-4], the placement of *Mycococcales* has been known to biologists for yeras.
- The position of Bdeba may be clarified when more genomes of related taxa become available, see [C-4] too.

The presence of only 4 outliers among a total of 208 organisms in B12 should be considered as a remarkable agreement of CVTrees with the taxonomy.

3.2.8 Phylum B13 (*Firmicutes*)

The 96 organisms from Phylum B13 and their convergence in CVTrees at the strain and species levels are given in Table 27. The *Firmicutes* are a very diverse group. "Hugenholz recognizes at least four other phyla within the *Firmicutes*." (Footnote 3 on p. 2 of the *Outline*^[2]). Therefore, we analyze the three classes of B13 separately.

B13 Class 1 (*Clostridia*)

There are 11 organisms represented by complete genomes in this class, see the upper part of Table 27. The branchings of these 11 organisms in CVTrees are shown in Fig. 15.

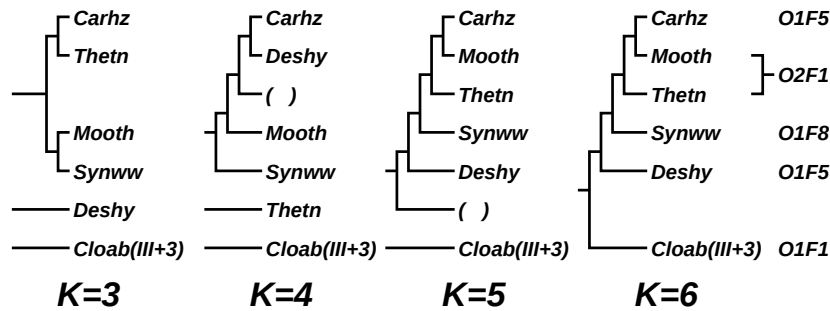


Figure 15: Convergence of the 11 organisms of Phylum B13 Class 1. Note the monophyletic grouping of the 11 organisms at $K = 6$.

Family Convergence:

The 3 families F_1 (*Clostridiaceae*), F_5 (*Peptococcaceae*), and F_8 (*Syntrophomonadaceae*) in O_1 (*Clostridiales*) form a monophyletic cluster at $K = 6$ although the assignment of orders and families may have to be adjusted, see [O-5] below.

Table 27: The 96 organisms in Phylum B13.

Bergey's Taxonomy				CVTrees			
Class	Order	Family	Genus	Species	Strain	Grouping	K
C_1	O_1	F_1	G_1	4	6	Cloab(III+3)	3,4,5,6
		F_5	G_2	1	1	Carhz	
			G_4	1	1	Deshy	
		F_8	G_1	1	1	Synww	
	O_2	F_1	G_7	1	1	Mooth	
			G_{11}	1	1	Thetn	
C_2	O_1	F_1	G_1	10	12	Mychj(3')	3,4,5,6
			G_4	1	1	Urepa	
	O_2	F_1	G_2	1	1	Mesfl	
	O_3	F_1	G_2	1	2	Onype(II)	3,4,5,6
C_3	O_1	F_1	G_1	7	13	Bacli(2),Bacan(3)	3,4,5,6
						Bachk(2'),Baccr(3')	4,5,6
			G_6	1	1	Geoka	
			G_{12}	1	1	Oceih	
						Bacillaceae(V+2+2'+3+3')	3,4,5,6
		F_4	G_1	3	4	Lismo(II+2)	3,4,5,6
		F_8	G_1	4	13	Staeq(2)	3,4,5,6
						Staaau(9)	5,6
						Staaau(II+2+9)	5,6
						Lacda(2)	3,4,5,6
	O_2	F_1	G_1	9	10		
			G_3	1	1	Pedpe	
		F_4	G_1	1	1	Entfa	
		F_5	G_1	1	1	Leume	
			G_2	1	1	Oenoe	
		F_6	G_1	5	21	Strpm(I+3+3+3+11)	3,4,5,6
			G_2	1	2	Lacla(2)	4,5,6

Difference between CVTrees and Taxonomy:

- F-6 The 2 genera G_2 (*Carboxydotherrmus*, represented by Carhz) and G_4 (*Desulfitobacterium*, represented by Deshy) in the Family $C_1O_1F_5$ (*Peptococcaceae*) do not get together for all K except for $K = 4$.
- F-7 The 2 genera G_7 (*Moorella*, represented by Mooth) and G_{11} (*Thermoanaerobacter*, represented by Thetn) in the Family $C_1O_2F_1$ (*Thermoanaerobacteriaceae*) do not get together for all K .
- O-5 The 2 genera from two different orders, namely, $O_1F_5G_2$ represented by Carhz and $O_2F_1G_7$ represented by Mooth, get together for $K = 5$ and 6. Their clustering causes the non-convergence indicated in [F-6] and [F-7]. This may hint on the necessity to redefine the families and genera within the orders O_1 and O_2 .
- C-5 All the 11 organisms from $B_{13}C_1$ form a monophyletic group at $K = 6$, see Fig. 15. This fact indicates that indeed they belong to the same class C_1 (*Clostridia*), but there might be taxonomic problems in assigning order and family thereunder.

B13 Class 2 (*Mollicutes*)

The 16 organisms and their convergence in CVTrees at strain and species levels are given in the middle part of Table 27. Their CVTrees are shown in Fig. 16. The 16 organisms in C_2 , including

all three orders, appear as a monophyletic clad for $K = 4$ to 6, but internal relationship vary slightly.

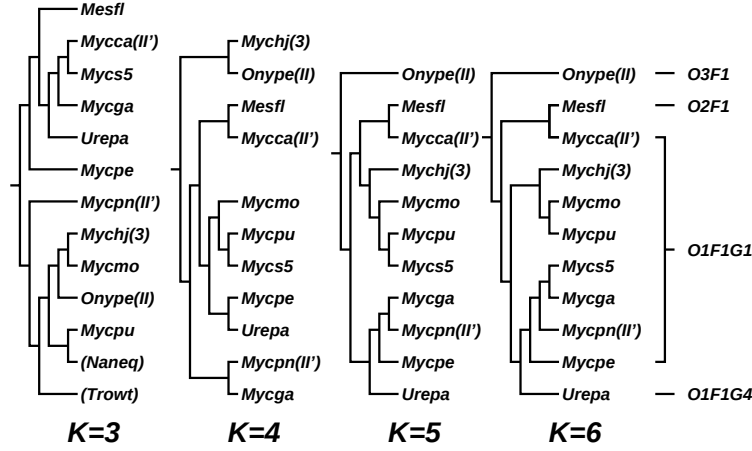


Figure 16: The CVTrees for the 16 organisms in the class $B_{13}C_2$ (*Mollicutes*).

Species Convergence:

Among the 10 species in the genus *Mycoplasma* Mycca and Mycms always group together for $K = 3 \sim 6$, we denote them conditionally as Mycca(II'). The two species Mycge and Mycnpn always group together for $K = 3 \sim 6$, we denote them conditionally as Mycnpn(II'). This notation is only used to simplify the branching picture.

Order Convergence:

The 3 orders of *Mollicutes* form a monophyletic cluster at $K = 4$ to 6 despite problems in designation of orders, see [O-6] below.

Difference between CVTrees and Taxonomy:

- S-3 The 3 strains of *Mycoplasma hyopneumoniae* do form a monophyletic cluster at all $K = 3$ to 6. There are variations of their mutual placement at different K : (Mychj, (Mych2, Mych7)) at $K = 3$, (Mych2, (Mychj, Mych7)) at $K = 4$ and 6, ((Mych2, Mychj), Mych7) at $K = 5$. That is why we denote it as Mychj(3') in species trees and in Table 27. Though a minor problem, we list this as one of the different cases. However, see [F-8] for the overall convergence of the *Mycoplasmataceae* family.
- G-9 The 12 species/strains in the genus *Mycoplasma* do not form a monophyletic cluster due to the insertion of Urepa (see [F-8]) and Metfl (see [O-6]). However, this does not prevent the proper definition of the family *Mycoplasmataceae*.
- F-8 The mixing up of Urepa with *Mycoplasma* makes the division of G_1 (*Mycoplasma*) and G_4 (*Ureaplasma*) within the family O_1F_1 questionable. We note that this mixing of Urepa into *Mycoplasma* has been observed in the 16S rRNA trees as well, see, e.g., [22].
- O-6 The mixing up of Mesfl from O_2 (*Entomoplasmatales*) with members of O_1 (*Mycoplasmatales*) makes the division of O_1 and O_2 questionable. However, there does exist a larger monophyletic cluster consisting of O_1 and O_2 at $K = 5$ and 6 beside the O_3 (*Acholeplasmatales*). An alternative solution for the time being would be assigning Mycca(II') to order O_2 . We have to await opinion of bacteriologists.

B13 Class 3 ('Bacilli')

There are 69 organisms represented in the class '*Bacilli*'. Their taxonomic distribution and convergence in CVTrees at strain and species levels are given in the lower part of Table. 27.

Strain Convergence:

In Bergey's taxonomy "species" are the lowest rank. However, the high resolution power of the CVTree method may reveal information on evolutionary relationship of various strains of one and the same species. Since in class C_3 several species have many strains sequenced, we describe two of them (most of these converging cases are simply summarized in Table 27).

1. The nine strains in the species *Staphylococcus aureus* always form a monophyletic group from $K = 3 \sim 6$. Within this group there are 5 strings that group as
 $(((\text{Staas}, \text{Staaw}), (\text{Staa3}, \text{Staac})), \text{Staaau})$ at $K = 3$,
 $(((\text{Staas}, \text{Staaw}), \text{Staa3}), (\text{Staac}, \text{Staaau}))$ at $K = 4$,
 $((\text{Staas}, \text{Staaw}), ((\text{Staa3}, \text{Staac}), \text{Staaau}))$ at $K = 5, 6$. If we denote this monophyletic subgroup by 5strs, then the convergence of all 9 strains is shown in Fig. 17. These nine strains are denoted as Staau(9) in a species tree and in Table 27.

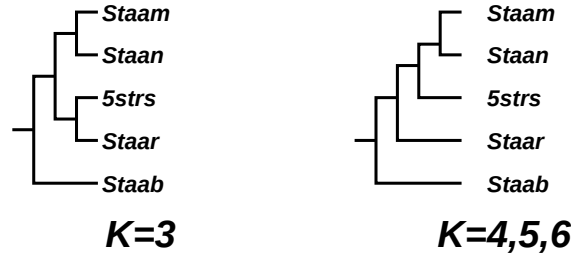


Figure 17: Convergence of the nine strains in the species *Staphylococcus aureus*. For the monophyletic subgroup 5strains see text.

2. The 11 strains in the species *Streptococcus pyogenes* always form a monophyletic group and converge for $K = 3 \sim 6$ as shown in Fig. 18. These 11 strains are denoted as strpm(11) in a species tree and in Table 27.

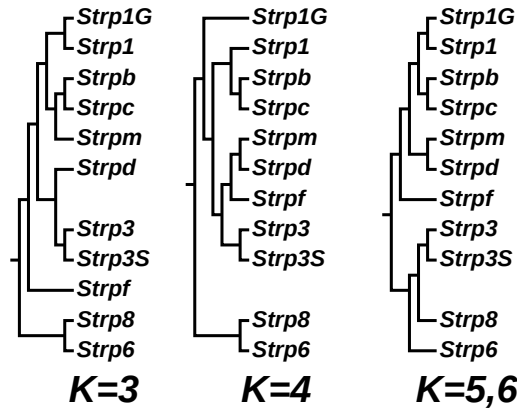


Figure 18: The convergence of the 11 strains in the species *Streptococcus pyogenes*.

Species Convergence:

1. The 12 strains from the 4 species in the genus *Staphylococcus*, including Staes(2) and Staa(9), form a monophyletic group for $K = 3 \sim 6$. The convergence with K is shown in Fig. 19. This group is denoted as Staa(II+2+9) in genus trees and in Table 27.

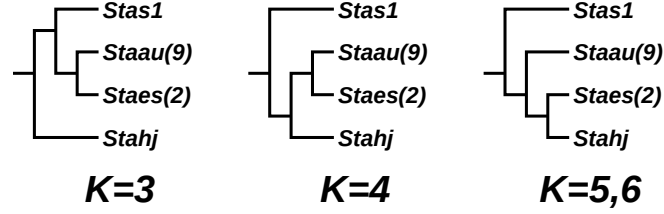


Figure 19: The convergence of the 4 species in genus *Staphylococcus*.

2. The 5 species in the genus *Streptococcus* including Strpn(3), Strth(3), Stra1(3) and Strpm(11), converge for $K = 3 \sim 6$. Denoted as Strpy(I+3+3+3+11) in a genus tree. The convergence of these 21 organisms is shown in Fig. 20

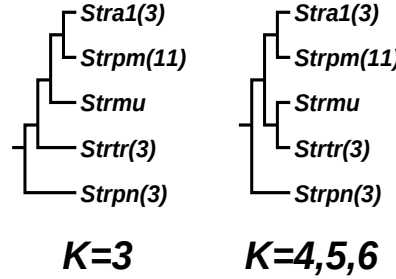


Figure 20: The convergence of the 5 species (21 strains) in the genus *Streptococcus* to be denoted as Strpy(I+3+3+3+11) in a genus tree.

Genus Convergence:

1. The 2 genera G_1 (*Lacobacillus*) and G_3 (*Pediococcus*) form a monophyletic cluster of the family O_2F_1 (*Lactobacillaceae*) at $K = 5,6$ in spite of the mixing of Pedpe into G_1 , see [G-11].
2. The 2 genera G_1 (*Leuconostoc*, represented by Leume) and G_2 (*Oenococcus*, represented by Oenoe) form a monophyletic cluster of the family O_2F_5 (*Leuconostocaceae*) at $K = 3,5,6$.
3. The 2 genera G_1 (*Streptococcus*, represented by Strpy(I+3+3+3+11)) and G_2 (*Lactococcus*, represented by Lacla(2)) from the Family O_2F_1 (*Streptococcaceae*) form a monophyletic group for $K = 4 \sim 6$, but not at $K = 3$.

Family Convergence:

1. The 3 families F_1 (*Bacillaceae*), F_4 (*Listeriaceae*), and F_8 (*Staphylococcaceae*) in C_3O_1 (*Bacillales*) form a monophyletic cluster at $K = 6$, but there is mixing-up with O_2 at $K = 3 \sim 5$.
2. The 4 families F_1 (*Lactobacillaceae*), F_4 (*Enterococcaceae*), F_5 (*Leuconostoc*), and F_6 (*Streptococcaceae*) in O_2 (*'Lactobacillales'*) form a monophyletic cluster at $K = 6$, but mix with O_1 at $K = 4$ and 5.

Order Convergence:

All the 69 organisms of the class C_3 , containing 2 orders, form a monophyletic cluster for $K = 3 \sim 6$, see Fig. 21 for their mutual relationship.

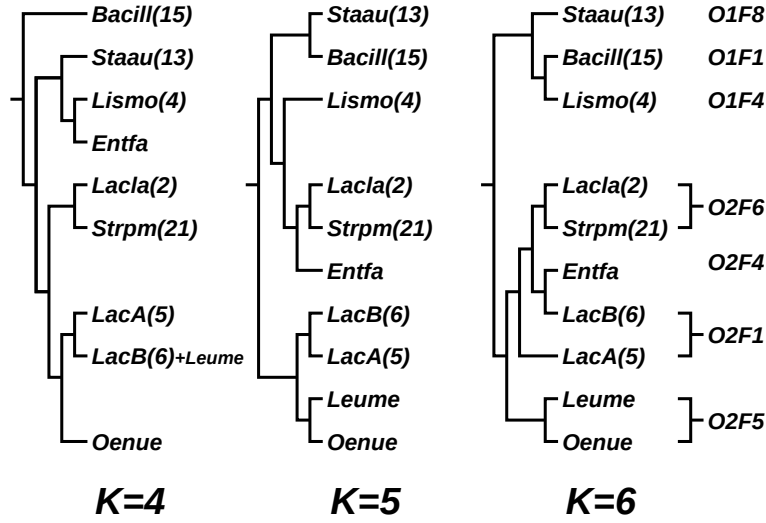


Figure 21: Monophyletic cluster formed by the 69 organisms of $B_{13}C_3$.

Difference between CVTrees and Taxonomy:

- S-4 The 3 strains Baccz, Baccr and Bacc1 in the species *Bacillus cereus* do not form a monophyletic group at all K , but they stay close to each other. In Fig. 22 the abbreviations of these strains are suffixed by a “*”.
- S-5 The 2 strains Bachk and BacthA in the species *Bacillus thuringiensis* stay close but not together at all K . In Fig. 22 these strain names are suffixed by a “#”.
- G-10 As seen from Fig. 22 the 13 strains from the genus *Bacillus* do not form a monophyletic group in CVTrees. However, if we include another two genera from the same Family *Bacillaceae*, G_6 (*Geobacillus* represented by Geoka) and G_{12} (*Oceanobacillus* represented by Oceih), the 15 organisms do form a monophyletic cluster for $K = 3 \sim 6$. This shows that the Family *Bacillus* is properly defined, but not the genera thereunder.

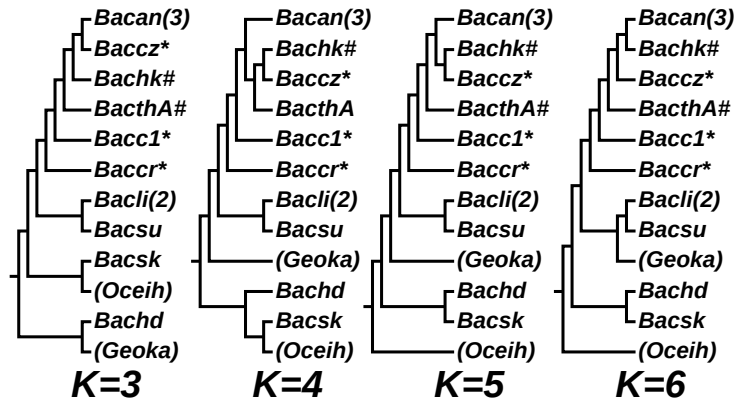


Figure 22: The 15 organisms in the Family *Bacillaceae* form a monophyletic group for $K = 3 \sim 6$.

We note that an inspection of the Bergey's *Outline* shows that at least 6 species in the genus *Geobacillus* have been moved out from *Bacillus* to this genus in different time.

- G-11 The 9 species of the genus F_1G_1 (*Lactobacillus*), including Lacda(2), clearly form two clusters. Cluster LacA consists of (Lacda(2), (Lacac, (Lacga, Lacjo))) for all $K = 3 \sim 6$. Cluster LacB consists of the other 5 species plus a species Pedpe from another genus F_1G_3 (*Pediococcus*) firmly mixed in, see Fig. 23.

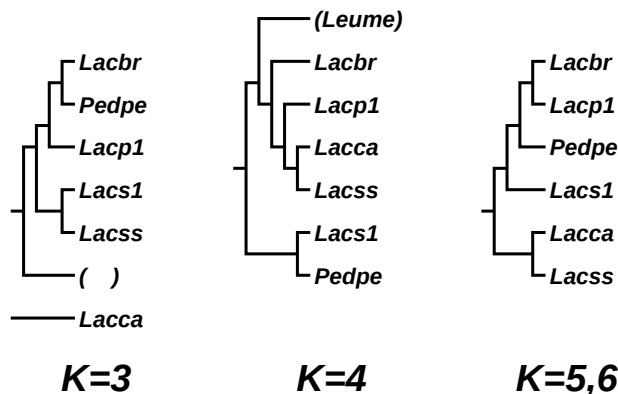


Figure 23: The LacB cluster of genus *Lactobacillus* with Pedpe from genus *Pediococcus* mixed in.

Now consider the relationship of the 3 classes in phylum B13:

- P-2 At $K = 6$ the two branches of class *Clostridia* (11 organisms) and class *Bacilli* (69 organisms) form a monophyletic cluster, while the class *Mollicutes* with 16 organisms stands out as a separate cluster. This situation hints on the necessity of dividing B13 at least into 2 phyla. At $K = 5$ the classes *Bacilli* and *Mollicutes* preserve their identity, but the class *Clostridia* splits into two, see Fig. 26 at the end of this Supplement.

3.2.9 Phylum B14 (*Actinobacteria*)

In the first edition of the *Bergey's Manual of Systematic Bacteriology* (1986) *Actinobacteria* were an order within the phylum of *Firmicutes*. In the forthcoming second edition of the *Bergey's Manual* they make a separate Phylum B14. The 35 organisms representing Phylum B14 in the dataset and their convergence in the CVTrees at the strain and species levels are shown in Table 28.

Species Convergence:

The 9 “species” of the genus *Mycobacterium* including Mycav(2) and Myctu(I+2') (see [S-6] below) form the same monophyletic cluster at $K = 4 \sim 6$, see Fig. 24. These 11 organisms are denoted as Myctu(VII+2+2') or Myctu(11) in a genus tree. Since Myckm and Mycss always stay together they are conditionally denoted as Myckm(II) in Table 28 and Fig. 24.

Genus Convergence:

The 2 genera G_1 (*Nocardia*) and G_2 (*Rhodococcus*) stay in the same family $O_{1,10}F_5$ (*Norcardiaceae*) at $K = 5$ and 6.

Family Convergence:

The 3 families F_1 (*Corynebacteriaceae*, represented by Corgl(III+2)), F_4 (*Mycobacteriaceae*, represented by Myctu(VII+2+2')) and F_5 (*Nocardiaceae*, represented by Nocfa and Rhosr) form a monophyletic cluster at $K = 5$ and 6.

Order Convergence:

Now we can summarize the order convergence in Phylum B14. We abbreviate the order notation $O_{1,i}$ to O_i . There are 35 organisms in 8 orders represented in Table 28. There is one undefined order represented by the only species Synth that never gets into the cluster of the other 34 organisms, see Fig. 25.

Table 28: The 35 organisms in Phylum B14.

Bergey's Taxonomy				CVTrees			
Class	Order	Family	Genus	Species	Strain	Grouping	K
$C_{1.2}$	$O_{1.5}$	F_1	G_1	1	1	Rubxd	
$C_{1.5}$	$O_{1.9}$	F_1	G_2	2	2	Artau(II)	3,4,5,6
		F_6	G_3	1	2	Trowt(2)	3,4,5,6
		F_{12}	G_{10}	1	1	Leixx	
	$O_{1.10}$	F_1	G_1	4	5	Corgl(III+2)	4,5,6
		F_4	G_1	8	11	Mycav(2),Myckm(II)	3,4,5,6
						Myctu(I+2')	3,4,5,6
		F_5	G_1	1	1	Nocfa	
			G_2	1	1	Rhosr	
	$O_{1.12}$	F_1	G_1	1	1	Proac	
		F_2	G_1	1	1	Nocjs	
	$O_{1.14}$	F_1	G_1	1	2	Straw(II)	3,4,5,6
	$O_{1.15}$	F_2	G_3	1	1	Thefy	
	$O_{1.16}$	F_1	G_1	2	2	Frasc(II)	3,4,5,6
		F_5	G_1	1	1	Acice	
	O_2	F_1	G_1	2	2	Biflo(II)	3,4,5,6
$C_?$	$O_?$	$F_?$	$G_?$	1	1	Symth	

On the Placement of Symth:

The genome of *Symbiobacterium thermophilum* IAM 14863 was submitted by a Japanese group on 7 September 2004 and resubmitted on 3 December 2005 with the number of nucleotides unchanged. The authors only indicated it as “Bacteria, Actinobacteria, Symbiobacterium”. There is no such entry in Bergey’s Manual. From our result it seems that the placement is questionable. At $K = 3$ and 4 it gets into a mixed group from various phyla. At $K = 5, 6$ it appears as a close neighbor of $B_{13}C_1$. This hints on the possibility that Symth is actually a member of $B_{13}C_1$ (*Firmicutes*).

Remark: We recollect Footnote 424 on p. 205 of the Bergey’s *Outline*:

“The *Actinobacteria* are a unique line of descent. The lineage of *Coriobacteridae*, *Rubrobacteridae*, and *Acidimicrobiidae* are deep branching and well separated in the PCA plots, with the former appearing embedded in the outlying regions of *Clostridia*. Ludwig notes support for the separation of the *Kineosporiaceae* (sic *Kineococcaceae*) as we have noted with our own unpublished sequence data. The lack of stable branching pattern within the major taxa of the *Actinobacteria* is borne out by the incredibly tight clustering in the PCA plots. While the 16S rRNA data might suggest that the taxa of *Actinobacteria* are overclassified, there is ample support for the current scheme based on other features.

“Ludwig has also called into question the separation of *bifidobacteria* into a separate class. Although he notes some peculiarities in the sequences, he has not recognized these as a separate lineage. PCA plots clearly demonstrate a separation of this group from the main line of descent. More importantly, the adjacent groups in the plots are consistent with the adjacent groups in the RDP tree. While this can be argued as an artifact of the treeing, it might also indicate some additional support for the separation proposed by Stackebrandt et al. This will likely be resolved as work on Volume IV progresses.”

Difference between CVTrees and Taxonomy:

S-6 Although the 2 strains MyctuH and MyctuC of the species *Mycobacterium tuberculosis* (human tuberculosis) stay together for $K = 3 \sim 6$, they do not form a monophyletic cluster, as

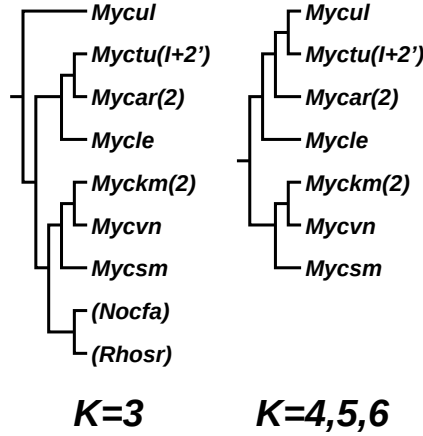


Figure 24: The 11 organisms in genus *Mycobacterium* for a monophyletic cluster at $K = 4$ to 6. At $K = 3$ two species from family *Nocardiaceae* get mixed in.

another species *M. bovin* (Mycbo for bovin tuberculosis) always cuts in and forms a cluster as (MyctuC, (MyctuH, Mycbo)) for $K = 3 \sim 6$. All these organisms belong to the “*Mycobacterium tuberculosis* complex” according to the NCBI taxonomy. The nucleotide identity of the Mycbo to the Myctu genomes is more than 99.95%^[23]. Yet their pathogenic behavior is different: Myctu is human-specific while Mycbo has a wider infectious range. There is good reason to keep Mycbo as another species although at genomic level it is closer to one of the strain H of Myctu than the other strain C. We denote these 3 strains conditionally as Myctu(I+2’).

- O-7 The 2 Families F_1 (*Micrococcaceae*, represented by Artau(II)) and F_{12} (*Microbacteriaceae*, represented by Leixx) stay together for $K = 3 \sim 6$, the third family F_6 (*Cellulomonadaceae*, represented by Trowt(2)) does not join the former to form a monophyletic cluster for the suborder $O_{1,9}$ (*Micrococcacineae*). Apparently this is a problem with the designation of F_6 to this suborder.
- O-8 The 2 families F_1 (*Propionibacteriaceae*, represented by Proac) and F_2 (*Nocardoidaceae*, represented by Nocjs) do not form the Bergey’s suborder $O_{1,12}$ (*Propionibacterineae*) at all K .
- O-9 The 2 families F_1 (*Frankiaceae*, represented by Frasc(II)) and F_5 (*Acidothermaceae*, represented by Acice) do not form the Bergey’s suborder $O_{1,16}$ (*Frankineae*) at all K .

Now the convergence of classes in phylum B14:

- P-3 As seen from Fig. 25 at $K = 5$ and 6 the 33 organisms from the subclass $C_{1,5}$ do form a monophyletic cluster, but Rubxd from $C_{1,2}$ and Symth from an unspecified lineage stand out.

This means 33 out of 35 organisms unambiguously form the core of phylum B14.

3.2.10 Phylum B15 (*Planctomycetes*)

The Phylum B15 is represented by a single genome in the dataset. Therefore, no discussion until the phylum level.

3.2.11 Phylum B16 (“*Chlamydia*”)

According to the Bergey’s *Outline* in the phylum B16 there is only one class containing one order. The 11 organisms of phylum B16 and their convergence at the strain and species levels are given

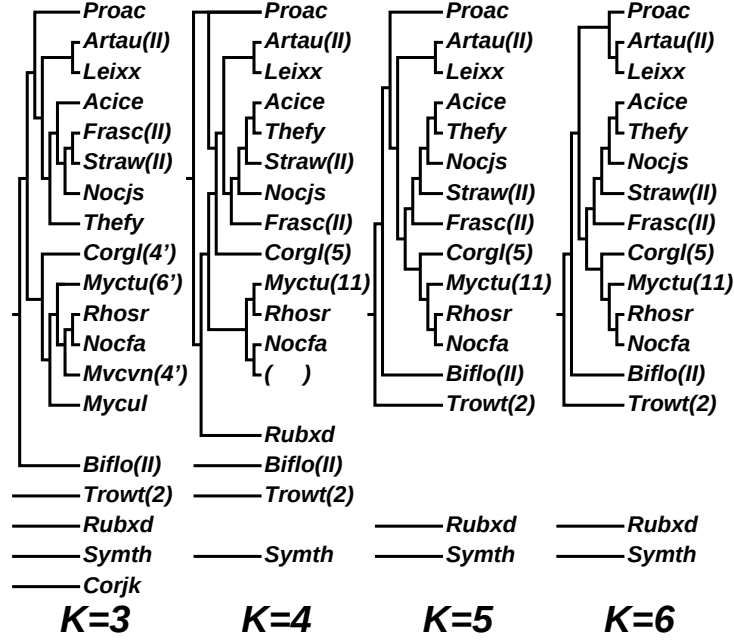


Figure 25: Monophyletic cluster of all but two species in the Phylum B14 for $K = 5 \sim 6$.

in Table 29.

Table 29: The 11 organisms in Phylum B16.

Bergey's Taxonomy				CVTrees			
Class	Order	Family	Genus	Species	Strain	Grouping	K
C_1	O_1	F_1	G_1	2	3	Chlta(I+2)	3,4,5,6
			G_2	4	7	Chlpn(4')	?
						Chlpn(III+4')	4,5,6
		F_2	G_1	1	1	Paruw	

Genus Convergence:

The 2 genera G_1 (*Chlamydia*, represented by Chlta(I+2)) and G_2 (*Chlamydophila*, represented by Chlpn(III+4')) in the family F_1 (*Chlamydiaceae*) form a monophyletic group for $K = 3 \sim 6$.

Family Convergence:

The two families F_1 (*Chlamydiaceae*) and F_2 (*Parachlamydiaceae* represented by Paruw) form a monophyletic group for $K = 3 \sim 6$. In fact, this is the monophyletic cluster of the whole phylum B16.

Difference between CVTrees and Taxonomy:

S-7 Although the 4 strains in the species *Chlamydophila pneumoniae* form a monophyletic cluster for $K = 3 \sim 6$, there are variations in their mutual relationship: (ChlpnT, (ChlpnA, (ChlpnC, ChlpnJ))) at $K = 3$ and 5; (ChlpnJ, (ChlpnT, (ChlpnA, ChlpnC))) at $K = 4$, and (ChlpnA, (ChlpnT, (ChlpnC, ChlpnJ))) at $K = 6$. This was why we use 4' in the notations Chlpn(4') and Chlpn(III+4').

3.2.12 Phylum B17 (*Spirochaetes*)

The 9 organisms of phylum B17 and their convergence at the strain and species levels are given in Table 30.

Table 30: The 9 organisms of Phylum B17.

Bergey's Taxonomy				CVTrees			
Class	Order	Family	Genus	Species	Strain	Grouping	K
C_1	O_1	F_1	G_2	3	3	Borbu(III)	3,4,5,6
			G_9	2	2	Trepa(II)	4,5,6
		F_3	G_1	2	4	Lepin(2),Lepbo(2)	3,4,5,6
						Lepin(2+2)	3,4,5,6

Genus Convergence:

The two genera G_2 (*Borrelia*) and G_9 (*Treponema*) in the family F_1 (*Spirochaetaceae*) converge for $K = 5$ and 6.

Difference between CVTrees and Taxonomy:

O-10 The two families F_1 (*Spirochaetaceae*) and F_3 (*Leptospiraceae*) in phylum B17 never get together for all $K = 3 \sim 6$.

“*Treponema* and *Leptospira* are assigned to the same order due to their common spirochete-like morphology” — a recent paper [24] cited the 1st Ed. of the *Bergey's Manual of Systematic Bacteriology* (1984) as saying so.

The two families O_1F_1 and O_1F_3 may well belong to two separate phyla.

3.2.13 Phylum B19 (*Acidobacteria*)

For the time being the Bergey's *Outline* only lists 3 species belonging to 3 genera under the same lineage $C_1O_1F_1$. Though the two sequenced genomes (Acibl and Solus) are not among the listed three they always stay together in the CVTrees. Therefore, assigning a Bergey's code B19.1.1.1.1 to Acibl and another unspecified genus $G_?$ to Solus does not lead to any problem at present time.

Table 31: The 2 species in Phylum B19.

Bergey's Taxonomy				CVTrees			
Class	Order	Family	Genus	Species	Strain	Grouping	K
C_1	O_1	F_1	G_1	1	1	Acibl	
			$G_?$	1	1	Solus	

3.2.14 Phylum B20 (*Bacteroidetes*)

The 7 organisms in phylum B20 and their convergence in CVTrees at the strain and species levels are given in Table 32.

Family Convergence:

The 2 families F_1 (*Bacteroidaceae*, represented by Bacfn(I+2)) and F_3 (*Porphyromonadaceae*, represented by Porgi) in the order $B_{20}C_1O_1$ (*Bacteroidales*) form a monophyletic cluster for all $K = 3 \sim 6$.

Table 32: The 7 organisms in Phylum B20.

Bergey's Taxonomy				CVTrees			
Class	Order	Family	Genus	Species	Strain	Grouping	K
C_1	O_1	F_1	G_1	2	3	Bacfn(I+2)	3,4,5,6
		F_3	G_1	1	1	Porgi	
C_2	O_1	F_1	$G_?$	1	1	Grafo	
C_3	O_1	F_3	G_4	1	1	Cyth3	
		F_5	G_4	1	1	Salrd	

Difference between CVTrees and Taxonomy:

O-11 The two families F_3 (*Flexibacteriaceae*, represented by Cyth3) and F_5 (*Crenotrichaceae*, represented by Salrd) in the order C_3O_1 (*Sphingobacteriales*) of phylum B20 never get together for all $K = 3 \sim 6$. This is caused by Salrd escaping from the monophyletic cluster formed by the other 8 organisms of B20 at all $K = 3$ to 6. All the other 8 organisms form a monophyletic cluster of B20.

We note that the position of Salrd is the most unstable among all 432 organisms under study. At $K = 3$ it clusters with the 4 Archaea of the family *Halobacteriaceae*. At $K = 4$ it pairs with the only species Rhoba of B15. At $K = 5$ it groups with the 4 organisms of B4 (*Deinococcus-Thermus*) and an outlier Rubxd from B14 (*Actinobacteria*). At $K = 6$ it forms a cluster with the 4 organisms from B11 (*Chlorobi*).

Class convergence in phylum B20:

P-4 The escape of Salrd (see [O-11] above) prevents the 3 classes of phylum B20 from forming a monophyletic cluster. However, excluding Salrd from this phylum would resolve the problem.

3.2.15 Phylum B21 (*Fusobacteria*)

The Phylum B21 is represented by a single genome in the dataset. Therefore, no discussion until the phylum level.

4 Placement of Highest Taxa

Taking into account the preceding analysis of the convergent and non-convergent cases in all branches we obtain the CVTrees of the highest taxonomic ranks from the original organism trees. The best convergent $K = 6$ CVTree is given in the main text of the paper. The $K = 5$ tree is shown in Fig. 26 below.

From Fig. 26 and that for $K = 6$ in the main text we have some observationd on the relationships at the highest taxonokic level:

1. The two Phyla B1 and B2 get together for $K = 5, 6$ as if they form a single taxon. Furthermore, they join B6 to form a monophyletic cluster.
2. The phylum B17 (*Spirochaetews*) should be split into two phyla. This is mainly caused by the problematic placement of *Leptospiraceae* in this phylum, see [O-10] above.
3. The phylum *Firmicutes* should be split at least into two phyla by making the *Mollicutes* a separate phylum.

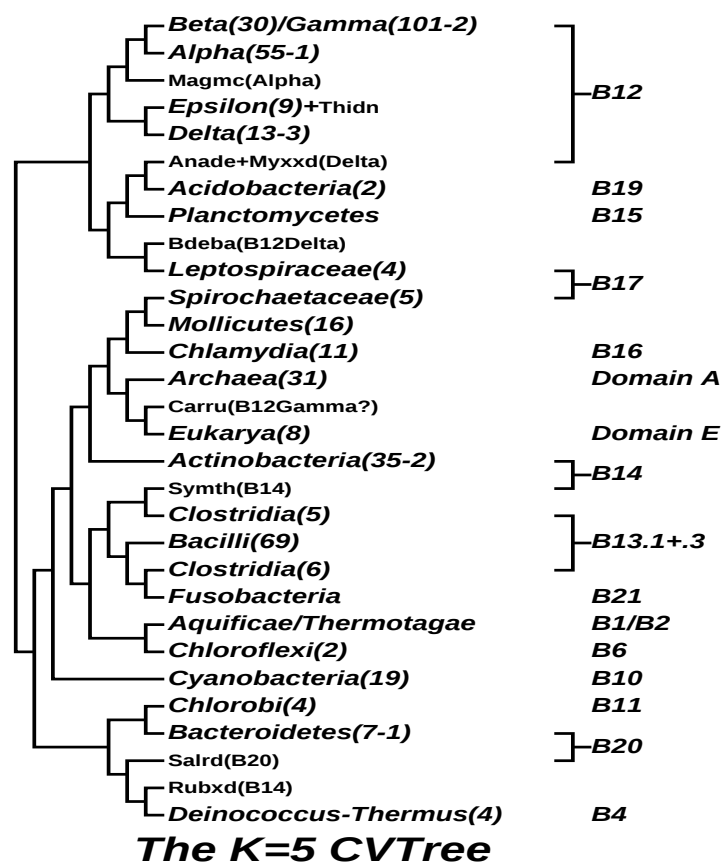


Figure 26: The highest rank CVTree at $K = 5$. A taxon name represents a monophyletic cluster with the number of organisms given in parentheses. For example, Gamma(101-2) is the cluster for Gammaproteobacteria made of 99 organisms, the 2 outliers, Garru and Thidn, appear elsewhere in the tree. Note that this is an unrooted tree and the branches are not to scale.

5 The CVTrees for K=3 to 6

Using the collection of all translated amino acid sequences of the 440 organisms as input, the CVTree program^[3, 4] produces a distance matrix at a fixed K . Then the Neighbor-Joining program in the PHYLIP package^[5] is used to generate a tree. The four original CVTrees are given below. These are the raw material upon which this study is based.

5.1 The K=3 CVTree

440 Populations

Neighbor-Joining/UPGMA method version 3.6a2.1

```

      +---Psyar
+----122
!      +---Psyck
!
!      +-----Aerhy
!      !
!      !      +-----Vibch
!      !      !      +-----Vibpa
!      !      !      !      +-----Vibvu
!      !      !      !      +-----Vibvy
!      !      !      !      +-----Vibf1
!      !      !      !      +-----Colp3
!      !      !      !      +-----Pseht
!      !      !      !      +-----Psea6
!      !      !      !      +-----Sheam
!      !      !      !      +-----Shean
!      !      !      !      +-----Shesm
!      !      !      !      +-----Shesr
!      !      !      !      +-----Sheon
!      !      !      !      +-----Shedo
!      !      !      !      +-----Shefn
!      !      !      !      +-----Psyin
!      !      !      !      +-----Phopr
!
!      !      !      !      +-----Ecoli5
!      !      !      !      +-----EcoliA
!      !      !      !      +-----EcoliU
!      !      !      !      +-----EcoliC
!      !      !      !      +-----EcoliK
!      !      !      !      +-----EcoliW
!      !      !      !      +-----EcoliE

```

```

!           !           ! +-73
!           !           +-168 +-----Ecoli0
!           !           ! !
!           !           ! ! +-----Salch
!   +-388      !           ! ! +-103
!           ! !           ! ! ! +-Salpa
!           ! !           ! ! ! +-100
!           ! !           +-258 +-114 +-Salty
!           ! !           ! ! !
!           ! !           ! ! ! +-----Salti
!           ! !           ! ! +59
!           ! !           ! ! +-----SaltyT
!           ! !           ! !
!           ! !           ! +-----Erwct
!           ! !           +-270
!           ! !           ! ! +---Yerpa
!           ! !           ! ! +-15
!           ! !           ! ! +-17 +---YerpeC
!           ! !           ! !
!           ! !           ! ! +-53 +-----Yerpn
!           ! !           +-307 ! ! !
!           ! !           ! ! ! +-----YerpeK
!           ! !           ! ! +-142 +-16
!   +-389 !           ! !           +-----YerpeM
!           ! !           +-318 !
!           ! !           ! ! +-----Yerps
!           ! !           ! !
!           ! !           ! ! +-----Pholl
!           ! !           ! !
!           ! !           ! ! +-----Sodgl
!           ! !           +-369
!           ! !           ! +-----Haedu
!           ! !           ! !
!           ! !           ! ! +-Haei8
!           ! !           ! ! +---66
!           ! !           +-224 +-173 +-Haein
!           ! !           ! !
!           ! !           ! +187 +-----Pasmu
!           ! !           ! !
!           ! !           +-196 +-----Mansm
!           ! !           !
!           ! !           +-----Haes1
!           ! !
!           ! +-----Idilo
!           !
!           ! +-----Hahch
!           ! +-332
!           ! ! +-----Sacd2
!           ! !
!           ! !           +-----Acibl
!           ! !           +-266
!           ! !           +-353 +-----Solus
!           ! !           ! !
!           ! !           ! +-----Rhoba
!           ! !           !
!           ! !           ! +---Bacfn
!           ! !           +-430 +-80
!           ! !           ! ! +-172 +---Bacfr
!           ! !           ! !
!           ! !           ! +331 +-----Bactn
!           ! !           ! !
!           ! !           ! +387 +-----Porgi
!           ! !           !
!           ! !           ! +-----Cyth3
!           ! !           +-298
!           ! !           +-----Grafo
!           ! !

```

357-407! !

[illegible]

```

!      !      !      !      !      +-398 !      !      + -264 +-----Ralme
!      !      !      !      !      !      !      !      !
!      !      !      !      !      !      !      !      +-----Ralso
!      !      !      !      !      !      !      !      !
!      !      !      !      !      !      !      !      +-----Polsj
!      !      !      !      !      !      !      +-245
!      !      !      !      !      !      !      +-----Rhofd
!      !      !      !      !      !      !      !
!      !      !      !      !      !      !      +-----Metca
!      !      !      !      !      !      !      !
!      !      !      !      !      !      !      +-----Metfl
!      !      !      !      !      !      !      +-352
!      !      !      !      !      !      !      +-----Thida
!      !      !      !      !      !      !      +-378
!      !      !      !      +-426 !      !      +-----Niteu
!      !      !      !      !      !      !      +-211
!      !      !      !      !      !      +306 +-----NiteuC
!      !      !      !      !      !      !
!      !      !      +-435 !      !      +-----Nitmu
!      !      !      !      !      !      !
!      !      !      !      !      !      +---Xanac
!      !      !      !      !      !      +-118
!      !      !      !      !      !      !      +---Xanc5
!      !      !      !      !      !      +---129
!      !      !      !      !      !      !      +Xanc8
!      !      !      !      !      !      !      +-58
!      !      !      !      !      !      +-247 +Xancp
!      !      !      !      !      !      !      !
!      !      !      !      !      !      !      +Xanom
!      !      !      !      !      +-337 +-----4
!      !      !      !      !      !      +Xanor
!      !      !      !      !      !      !
!      !      !      !      !      !      +---Xylfa
!      !      !      !      !      +-----85
!      !      !      !      !      +---Xylft
!      !      !      !      !      !
!      !      !      !      !      !      +-Anasp
!      !      !      !      !      !      +---120
!      !      !      !      !      !      +255 +---Anava
!      !      !      !      !      !      !
!      !      !      !      !      +276 +-----Triei
!      !      !      !      !      !      !
!      !      !      !      !      +-288 +-----Syny3
!      !      !      !      !      !      !
!      !      !      !      !      !      +-----Synel
!      !      !      !      !      !      +-248
!      !      !      !      !      +-321 !      +Synp6
!      !      !      !      !      !      !      +-----25
!      !      !      !      !      !      !      +Synp7
!      !      !      !      !      !      !
!      !      !      !      !      !      +-----Synja
!      !      !      !      !      !      +---137
!      !      !      !      !      !      +-----Synjb
!      !      !      !      !      !      !
!      !      !      !      !      +-367 +-----Prom9
!      !      !      !      !      !      +---102
!      !      !      !      !      !      +-178 +---Promp
!      !      !      !      !      !      !      !
!      !      !      !      !      !      +-181 +-----Promt
!      !      !      !      !      !      !      !
!      !      !      !      !      !      !      +-----Proma
!      !      !      !      !      !      +-250
!      !      !      !      !      !      +-----Promm
!      !      !      !      !      !      !
!      !      !      !      +-403 !      !
!      !      !      !      !      !      !      +-----Synpx
!      !      !      !      !      +-182 +---131
!      !      !      !      !      !      !      +-133 +-----Synsc

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!      +-431 !      !      !      !
!      !      !      !      +-166 +----Syns9
!      !      !      !      !
!      !      !      !      +----Syns3
!      !      !      !
!      !      !      !      +-----Glovi
!      !      !      +-363
!      !      !      !      +-----Nitoc
!      !      !
!      !      !      +-----Acice
!      !      !      !
!      !      !      !      +----Fraal
!      !      !      +-279      +-151
!      !      !      !      !      +----Frasc
!      !      !      !      !      +-249
!      !      !      !      !      !      +---Straw
!      !      !      +-294 +-263 +-145
!      !      !      !      !      +---Strco
!      !      !      !      !
!      !      !      !      !      +-----Nocjs
!      !      !      !      !
!      !      !      +-341 +-----Thefy
!      !      !      !      !
!      !      !      !      !      +-----Artau
!      !      !      !      !      +-154
!      !      !      +-351 +-328 +-----Artfb
!      !      !      !
!      !      !      !      +-----Leixx
!      !      !      !
!      !      !      !      +-----Proac
!      !      !      !
!      !      !      !      +-----Cordi
!      !      !      !      +-256
!      !      !      !      !      +-----Coref
!      !      !      !      !      +-197
!      !      !      +-384 !      !      +Corgl
!      !      !      !      !      +-----34
!      !      !      !      !      +CorglB
!      !      !      !      !
!      !      !      !      !      +---Mycav
!      !      !      !      !      +-98
!      !      !      !      !      !      +---Mycpa
!      !      !      !      !      !      +-186
!      !      !      !      !      !      +Mycbo
!      !      !      !      !      !      +-21
!      !      !      !      +-383      +-206 +-----24      +MyctuH
!      !      !      !      !      !
!      !      !      !      !      !      +MyctuC
!      !      !      !      !      !
!      !      !      !      !      !      +-----Mycle
!      !      !      !      !
!      !      !      !      !      +-397
!      !      !      !      !      !      +-268      +Myckm
!      !      !      !      !      !      +-46
!      !      !      !      !      !      +-150      +Mycss
!      !      !      !      !      !      !
!      !      !      !      !      !      +-176 +---Mycvn
!      !      !      !      !      !      !
!      !      !      !      !      +-303 +-238 +-----Mycsm
!      !      !      !      !      !
!      !      !      !      !      !      +-----Nocfa
!      !      !      !      !      !      +-188
!      !      !      !      !      !      +-----Rhosr
!      !      !      !      !
!      !      !      !      !      +-----Mycul
!      !      !      +-427 !
!      !      !      !      !      +-----Bifad
!      !      !      !      !      +-164

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!      !      !      !      +-----Biflo
!      !      !      !      +-----Anade
!      !      !      !      +-284
!      !      !      !      +-376 +-----Myxxd
!      !      !      !      !      +-----Symth
!      !      !      !      !      +-----Deigd
!      !      !      !      !      +207
!      !      !      !      !      !      +-----Deira
!      !      !      !      +-404      +-289
!      !      !      !      !      !      +-Thet2
!      !      !      !      !      +-391 +-----20
!      !      !      !      !      !      +-Thet8
!      !      !      !      !      !      +-----Rubxd
!      !      !      !      !      !      +-----Halma
!      !      !      !      +-396      +-----Halma
!      !      !      !      !      +180
!      !      !      !      !      +204 +-----Natpd
!      !      !      !      !      !      +-----Halsa
!      !      !      !      !      +-214 +-----Halsa
!      !      !      !      !      !      +-----Halwd
!      !      !      !      !      +-377 +-----Halwd
!      !      !      !      !      !      +-----Salrd
!      !      !      !      !      +-----Aerpe
!      !      !      !      !      +296
!      !      !      !      !      !      +-----Thepe
!      !      !      !      !      !      +-----Pyrab
!      !      !      !      !      !      +322      +-117
!      !      !      !      !      !      !      +127 +-----Pyrho
!      !      !      !      !      !      !      !      +-----Pyrfu
!      !      !      !      !      !      !      !      +314 +-----Pyrko
!      !      !      !      !      !      !      !      +-----Pyrae
!      !      !      !      !      !      !      !      +-346      +--141
!      !      !      !      !      !      !      !      !      +-----Pyris
!      !      !      !      !      !      !      !      !      +-----Picto
!      !      !      !      !      !      !      !      !      +213
!      !      !      !      !      !      !      !      !      !      +-----Theac
!      !      !      !      !      !      !      !      !      !      +136
!      !      !      !      !      !      !      !      !      !      +-----Thevo
!      !      !      !      !      !      !      !      !      !      +324
!      !      !      !      !      !      !      !      !      !      +-----Sulac
!      !      !      !      !      !      !      !      !      !      +140
!      !      !      !      !      !      !      !      !      !      +189 +-----Sulto
!      !      !      !      !      !      !      !      !      !      !      +-----Sulso
!      !      !      !      !      !      !      !      !      !      !      +-371
!      !      !      !      !      !      !      !      !      !      !      !      +-----Metac
!      !      !      !      !      !      !      !      !      !      !      !      +147
!      !      !      !      !      !      !      !      !      !      !      !      +155 +-----Metbf
!      !      !      !      !      !      !      !      !      !      !      !      !      +274 +-----Metma
!      !      !      !      !      !      !      !      !      !      !      !      !      +325 +-----Metbu
!      !      !      !      !      !      !      !      !      !      !      !      !      +-----MetthP
!      !      !      !      !      !      !      !      !      !      !      !      !      +-393
!      !      !      !      !      !      !      !      !      !      !      !      !      !      +-364      +-----Metja

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!      !      !      !      !      +-193
!      !      !      !      !      !      +-----Metmp
!      !      !      !      !      !      +-297
!      !      !      !      !      !      !      +-----Metst
!      !      !      !      !      !      !      +-344 +-233
!      !      !      !      !      !      !      +-----Metth
!      !      !      !      !      !      !      +-----Metka
!      !      !      !      !      !      !      +-415 +-----Methj
!      !      !      !      !      !      !      +-----Aqua
!      !      !      !      !      !      !      +-366
!      !      !      !      !      !      !      !      +-----Arcfu
!      !      !      !      !      !      !      !      +-336
!      !      !      !      !      !      !      !      +-----Thema
!      !      !      !      !      !      !      !      +-381
!      !      !      !      !      !      !      !      +-----Carhz
!      !      !      !      !      !      !      !      +-350
!      !      !      !      !      !      !      !      +-----Thetn
!      !      !      !      !      !      !      !      +-356
!      !      !      !      !      !      !      !      +-433 ! +-410 ! +-----Mooth
!      !      !      !      !      !      !      !      !      +-334
!      !      !      !      !      !      !      !      !      +-----Synww
!      !      !      !      !      !      !      !      !      +----Dehe1
!      !      !      !      !      !      !      !      !      +-----91
!      !      !      !      !      !      !      !      !      +----Dehsc
!      !      !      !      !      !      !      !      !      +-----Anamm
!      !      !      !      !      !      !      !      !      +-185
!      !      !      !      !      !      !      !      !      !      +-----Anapz
!      !      !      !      !      !      !      !      !      !      +-----Ehrch
!      !      !      !      !      !      !      !      !      !      +-61
!      !      !      !      !      !      !      !      !      !      !      +-----Ehrcj
!      !      !      !      !      !      !      !      !      !      !      +-105
!      !      !      !      !      !      !      !      !      !      !      +Ehrrg
!      !      !      !      !      !      !      !      !      !      !      +-235 +-----5
!      !      !      !      !      !      !      !      !      !      !      !      +Ehrru
!      !      !      !      !      !      !      !      !      !      !      !      +-2
!      !      !      !      !      !      !      !      !      !      !      !      +Ehrrw
!      !      !      !      !      !      !      !      !      !      !      +-292 !
!      !      !      !      !      !      !      !      !      !      !      +-----Wolpm
!      !      !      !      !      !      !      !      !      !      !      +-124
!      !      !      !      !      !      !      !      !      !      !      +-----Woltr
!      !      !      !      !      !      !      !      !      !      !      +-----Neosm
!      !      !      !      !      !      !      !      !      !      !      +-----Ricbr
!      !      !      !      !      !      !      !      !      !      !      +-----126 +-----Riccn
!      !      !      !      !      !      !      !      !      !      !      !      +-79
!      !      !      !      !      !      !      !      !      !      !      !      +-374 ! ! +-----Ricfe
!      !      !      !      !      !      !      !      !      !      !      !      !      +-108
!      !      !      !      !      !      !      !      !      !      !      !      !      +-Ricpr
!      !      !      !      !      !      !      !      !      !      !      !      !      +-19
!      !      !      !      !      !      !      !      !      !      !      !      !      +-401 !      +---Ricty
!      !      !      !      !      !      !      !      !      !      !      !      !      +-----Pelub
!      !      !      !      !      !      !      !      !      !      !      !      !      +-----Barhe
!      !      !      !      !      !      !      !      !      !      !      !      !      +-409 +-----113
!      !      !      !      !      !      !      !      !      !      !      !      !      +-----Barqu
!      !      !      !      !      !      !      !      !      !      !      !      !      +Lepbl
!      !      !      !      !      !      !      !      !      !      !      !      !      +-----1

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!           !           !           !           !           !           +-----Entfa
!           !           !           !           !           !           !
!           !           !           !           !           !           +-309      +---Lisin
!           !           !           !           !           !           !           +-77
!           !           !           !           !           !           !           !   +-Lismf
!           !           !           !           !           !           !           +-----86  +-55
!           !           !           !           !           !           !           !   +-Lismo
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +---Liswe
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +-----Lacac
!           !           !           !           !           !           !           +-179
!           !           !           !           !           !           !           !   +-329  !   +-----Lacga
!           !           !           !           !           !           !           !   +-123
!           !           !           !           !           !           !           !   +-234  +-----Lacjo
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +-Lacda
!           !           !           !           !           !           !           +-----48
!           !           !           !           !           !           !           +-Lacde
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +-----Lacbr
!           !           !           !           !           !           !           +-210
!           !           !           !           !           !           !           !   +-311  +222 +-----Pedpe
!           !           !           !           !           !           !           !   !
!           !           !           !           !           !           !           !   +-272 +-----Lacpl
!           !           !           !           !           !           !           !   !
!           !           !           !           !           !           !           !   !   +-----Lacs1
!           !           !           !           !           !           !           !   +-300 +-236
!           !           !           !           !           !           !           !   +-----Lacss
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +-304 +-----Lacla
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           !   +-----Lacca
!           !           !           !           !           !           !           !   +-241
!           !           !           !           !           !           !           !   !   +-----Leume
!           !           !           !           !           !           !           !   +-199
!           !           !           !           !           !           !           !   +-----Oenoe
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           !   +-Stra1
!           !           !           !           !           !           !           !   +-54
!           !           !           !           !           !           !           !   +---81  +-Stra5
!           !           !           !           !           !           !           !   !
!           !           !           !           !           !           !           !   +---Stra3
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           !   +Strp1
!           !           !           !           !           !           !           !   +-32
!           !           !           !           !           !           !           !   !   +Strp1G
!           !           !           !           !           !           !           !   +-42
!           !           !           !           !           !           !           !   !   +Strpb
!           !           !           !           !           !           !           !   !   +-26
!           !           !           !           !           !           !           !   !   +-192  !   +-39  +Strpc
!           !           !           !           !           !           !           !   !
!           !           !           !           !           !           !           !   +-45  +-Strpm
!           !           !           !           !           !           !           !   !
!           !           !           !           !           !           !           !   !   +Strp3
!           !           !           !           !           !           !           !   !   +-18
!           !           !           !           !           !           !           !   +-47  +-43  +Strp3S
!           !           !           !           !           !           !           !   !
!           !           !           !           !           !           !           !   +-221  !   !   +Strpd
!           !           !           !           !           !           !           !   !   +-----56  !
!           !           !           !           !           !           !           !   !   +Strpf
!           !           !           !           !           !           !           !   !
!           !           !           !           !           !           !           !   !   +Strp6
!           !           !           !           !           !           !           !   +-33
!           !           !           !           !           !           !           !   +-229  !   +Strp8
!           !           !           !           !           !           !           !   !
!           !           !           !           !           !           !           !   +-----Strmu

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60

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! ! ! ! ! +-----Lawip
! ! ! ! !
! ! ! ! ! +-----Deshy
+-438 ! ! ! ! ! +-425 +-411
! ! ! ! ! +-----Desps
! ! ! ! !
! ! ! ! ! +-----Geomg
! ! ! ! ! +-416 +-202
! ! ! ! ! +-333 +-----Geosl
! ! ! ! !
! ! ! ! ! +-355 +-----Pelpr
! ! ! ! !
! ! ! ! ! +-399 +-----Pelcd
! ! ! ! !
! ! ! ! ! +-----Synas
! ! ! ! ! +-354
! ! ! ! ! +-----Synfu
! ! ! ! !
! ! ! +-----Bdeba
! ! ! ! !
! ! ! ! ! +-----Camfe
! ! ! ! ! +-190
! ! ! ! ! +-Camje
! ! ! ! ! +-37
! ! ! ! ! +-Camjr
! ! ! ! !
! ! ! ! ! +-281 +---Helac
! ! ! ! ! +-420 ! ! !
! ! ! ! ! +-----68 +Helph
! ! ! ! ! ! +-28
! ! ! ! ! +35 +Helpy
! ! ! ! ! +-287 +-230 !
! ! ! ! ! +-Helpj
! ! ! ! !
! ! ! ! ! +-----Helhp
! ! ! ! !
! ! ! ! ! +-408 ! +-----Thidn
! ! ! ! ! +-261
! ! ! ! ! +-----Wolsu
! ! ! ! !
! ! ! ! ! +-----Corjk
! ! ! ! ! +-340
! ! ! ! ! +-----Trede
! ! ! ! ! +-290
! ! ! ! ! +-----Enccu
! ! ! ! !
! ! ! ! ! +-----Coxbu
! ! ! ! !
! ! ! ! ! +Frat1
! ! ! ! ! +-3
! ! ! ! ! +-358 +-23 +Fratt
! ! ! ! !
! ! ! ! ! +-27 +---Frath
! ! ! ! !
! ! ! ! ! +---107 +-Frato
! ! ! ! !
! ! ! ! ! +-412 +---Fratn
! ! ! ! !
! ! ! ! ! +-Legpa
! ! ! ! ! +-----95
! ! ! ! ! ! +---Legph
! ! ! ! ! +-90
! ! ! ! ! +-422 +-406 +-Legpl
! ! ! ! !
! ! ! ! ! +-----Rutma
! ! ! ! ! +-368
! ! ! ! ! +-----Thicr

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!           ! ! !
!           ! ! ! +----Neig1
!           ! ! +-----110
!           +-424 ! +-Neima
!           !     +-78
!           !     +-Neimb
!           !
!           ! +-----Paruw
!           ! !
!           ! !     +-Shibs
!           ! !     +-44
!           +-405 ! +Shifl5
!           !     +-69
!           !     ! ! +Shifl
!           !     +-82 +-22
!           !     ! ! +ShiflT
!           +-----130 !
!           ! +---Shiss
!           !
!           +-----Shids
!
+-----Aciad

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5.2 The K=4 CVTree

440 Populations

Neighbor-Joining/UPGMA method version 3.6a2.1

```

+----Psyar
+-----126
!     +----Psyck
!
!           +-----Alcbs
!           +-318
!           ! +-----Chrsd
!           !
!           !     +-----Pse14
!           +-334 +-121
!           ! ! +---132 +-----Pseu2
!           ! ! !
!           ! ! ! +-----Psesm
!           ! ! !
!           ! ! +-207 +Pseae
!           ! ! ! +-----42
!           ! ! ! +PseaeU
!           ! ! !
!           ! +-372 +-195 +-----Pseen
!           ! ! ! ! +-140
!           ! ! ! ! +-----Psepk
!           ! ! ! +---171
!           ! ! ! ! +-----Psef5
!           ! ! ! +---145
!           ! ! ! +-----Psepf
!           ! ! !
!           ! ! ! +-----Hahch
!           ! ! +-370
!           ! ! +-----Sacd2
!           !
!           !           +-----Aerhy
!           !           !
!           !           +-299 +-----Phopr
!           !           ! ! !
!           !           ! ! ! +-----Vibch
!           !           ! +-251 +-199
!           !           ! ! ! +-----Vibpa
!           !           ! ! ! +-170

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! !      +-328    +-218    !    +--Vibvu
! !      ! !      !    +----89
! !      ! !      !    +--Vibvy
! !      ! !      !
! !      ! !      +-----Vibf1
! !      ! !      +-----Psyin
! !      !
! !      +-338      +-----Colp3
! !      ! !      +-295
! !      ! !      +-298 +-----Pseht
! !      ! !      ! !
! !      ! !      +-312 +-----Psea6
! !      ! !      !
! !      ! !      +-----Idilo
! !      ! !      !
! !      ! +-327 +-----Sheam
! !      ! !
! !      ! !      +--Shean
! !      ! !      +-96
! !      ! +-221      ! ! +Shesm
! !      ! !      +-134 +-65
! !      ! !      ! ! +Shesr
! !      ! !      +-192 !
! !      ! !      ! ! ! +----Sheon
! !      ! +-198 !
! !      ! !      +-----Shefn
! !      ! !
! !      ! +-----Shedo
! !      !
! !      ! +--Ecoli5
! !      ! !
! !      ! +--94      +-EcoliA
! !      ! !      +-71
320-385 ! !      ! +-91 +-EcoliU
! !      ! !
! !      ! +-113      +--EcoliC
! !      ! !
! !      ! !      +EcoliE
! !      ! !      +-40
! !      ! !      +EcoliO
! !      ! +-106
! !      ! !      +EcoliK
! !      ! !      +--27
! !      ! +-125      +EcoliW
! !      ! !
! !      +-371      ! !      +---Shibs
! !      ! !      ! !      +-97
! !      ! !      ! !      +---Shiss
! !      ! !      ! !      +-98
! !      ! !      ! !      +Shifl
! !      ! !      ! !      +-36
! !      ! !      ! +-108 +-47 +ShiflT
! !      ! !      ! !      +-154      ! !
! !      ! !      ! !      +-Shifl5
! !      ! !      !
! !      ! !      +----Shids
! !      ! !
! !      ! !      +---Salch
! !      ! !      +-76
! !      ! !      ! +--Salty
! !      ! !      +---92
! !      ! !      +-230      ! +-Salpa
! !      ! !      +-75
! !      ! !      ! +Salti
! !      ! !      +-26
! !      ! !      +SaltyT

```

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! ! ! ! ! ! !
! ! ! ! ! ! ! +-----Erwct
! ! ! ! ! ! !
! ! ! ! ! ! ! +Yerpa
! ! ! ! ! ! ! +-24
! ! ! ! ! ! ! +-264 +-214 +33 +Yerpn
! ! ! ! ! ! ! ! !
! ! ! ! ! ! ! +-34 +YerpeK
! ! ! ! ! ! ! ! !
! ! ! ! ! ! ! ! ! +YerpeC
! ! ! ! ! ! ! +-----68 +-32
! ! ! ! ! ! ! +-279 ! ! +YerpeM
! ! ! ! ! ! ! ! !
! ! ! ! ! ! ! +-Yerps
! ! ! ! ! ! ! +-----Sodgl
! ! ! ! ! ! !
! ! ! ! ! ! ! +-347 +-----Pholl
! ! ! ! ! ! !
! ! ! ! ! ! ! +-----Haedu
! ! ! ! ! ! !
! ! ! ! ! ! ! +-Haei8
! +-398 ! ! ! +-----61
! ! ! +-239 +-182 +-Haein
! ! ! ! !
! ! ! ! +-205 +-----Pasmu
! ! ! ! !
! ! ! +-210 +-----Haes1
! ! ! !
! ! ! +-----Mansm
! ! !
! ! ! +-----Neig1
! ! ! +-101
! ! ! ! +-Neima
! ! ! ! +-78
! ! ! ! +-Neimb
! ! !
! ! ! +-----Xanac
! ! ! +-114
! ! ! ! +-----Xanc5
! ! ! +-135
! ! ! ! ! +Xanc8
! ! ! ! +-13
! ! ! +-151 +Xancp
! ! ! ! !
! ! ! ! ! +-Xanom
! ! ! +-282 +-----41
! ! ! ! ! +-Xanor
! ! ! ! !
! ! ! ! ! +-----Xylfa
! ! ! ! ! +-----99
! ! ! ! ! +-----Xylft
! ! ! ! !
! ! ! ! ! +-----Coxbu
! ! ! ! !
! ! ! ! ! +Frat1
! ! ! ! ! +-367 +6
! ! ! ! ! ! +Fratt
! ! ! ! ! ! +-25
! ! ! ! ! ! ! +Frath
! ! ! ! ! ! +-----50 +-19
! ! ! ! ! ! ! +Frato
! ! ! ! ! +-392
! ! ! ! ! !
! ! ! ! ! ! +---Fratn
! ! ! ! ! !
! ! ! ! ! ! +---Legpa
! +-408 ! ! ! +49

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!      !      !      +-----58  +---Legph
!      !      !      !
!      !      !      +---Legpl
!      !      !
!      !      !      +---Agrt5
!      !      !      +-----37
!      !      !      !      +---Agrt5W
!      !      !      +---211
!      !      !      !      +-----Rhiet
!      !      !      !      !      +---122
!      !      !      !      !      +---191  +-----Rhil3
!      !      !      !      !      !
!      !      !      !      !      +-----Rhime
!      !      !      +---265
!      !      !      !      +Brua2
!      !      !      !      +---16
!      !      !      !      !      +---35  +Bruab
!      !      !      !      !      !
!      !      !      +---275 +-----52  +-Brusu
!      !      !      !      !
!      !      !      !      +---Brume
!      !      !      !      !
!      !      !      !      +-----Messb
!      !      !      !      +---267
!      !      !      !      +-----Rhilo
!      !      !      !
!      !      !      +---330  +-----Braja
!      !      !      !      !
!      !      !      !      !      +-----Rhop2
!      !      !      !      !      +---216  +---136
!      !      !      !      !      !      +---142  +-----Rhops
!      !      !      !      !      !      !
!      !      !      !      !      +---164  +-----Rhopa
!      !      !      !      !      !
!      !      !      !      +---235  !      +-----Rhopa3
!      !      !      !      !      +---150
!      !      !      +---358  !      +-----Rhopb
!      !      !      !      !
!      !      !      !      !      +-----Nithx
!      !      !      !      !      +---152
!      !      !      !      !      +-----Nitwn
!      !      !      !      !
!      !      !      !      !      +-----Jansc
!      !      !      !      !      !
!      !      !      !      !      +---237  +---Rosdo
!      !      !      +---379  !      !      +---193
!      !      !      !      !      +---213  +---Silpo
!      !      !      !      !      +---261  !
!      !      !      !      !      +-----Silst
!      !      !      !      !      !
!      !      !      !      !      +-----Parde
!      !      !      !      !      +---227
!      !      !      !      !      +-----Rhos4
!      !      !      !      !
!      !      !      +---389  !      +-----Magsa
!      !      !      !      !      +---288
!      !      !      !      !      +-----Rhoru
!      !      !      !      !
!      !      !      !      !      +-----Caucr
!      !      !      !      !      +---303
!      !      !      !      !      +---317  +-----Hypna
!      !      !      !      !      !
!      !      !      !      !      +-----Marmm
!      !      !      +---399  +---348
!      !      !      !      !      +-----Eryli
!      !      !      !      !      +---262
!      !      !      !      !      +-----Novad

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!           !           !           !           +-244
!           !           !           !           +-----Sphal
!           !           !           !           +-----Gluox
!           !           !           !           +-319
!           !           !           !           +-374 +-----Grabc
!           !           !           !           !
!           !           !           !           +-----Zymmo
!           !           !           !           +-----Anamm
!           !           !           !           +-208
!           !           !           !           ! +-----Anapz
!           !           !           !           !
!           !           !           !           +-234 +-----Ehrch
!           !           !           !           ! ! +-129
!           !           !           !           ! ! ! +-----Ehrcj
!           !           !           !           ! +-143
!           !           !           !           ! ! +Ehrrg
!           !           !           !           ! +-----7
+-413 !           !           !           !           ! +Ehrru
!           !           !           !           !           +-1
!           !           !           !           !           +Ehrrw
!           !           !           !           !
!           !           !           !           +-272 !
!           !           !           !           ! ! +-----Wolpm
!           !           !           !           ! ! +-146
!           !           !           !           ! ! +-----Woltr
!           !           !           !           ! !
!           !           !           !           +-305 +-----Neosm
!           !           !           !           ! !
!           !           !           !           ! ! +-----Ricbr
!           !           !           !           ! ! !
!           !           !           !           ! +-148 +-----Riccn
!           !           !           !           ! ! +-117
!           !           !           !           ! ! +-390 ! ! +-----Ricfe
!           !           !           !           ! ! +-137
!           !           !           !           ! ! +-----Ricpr
!           !           !           !           ! ! +-82
!           !           !           !           ! +-395 ! +-----Ricty
!           !           !           !           !
!           !           !           !           +-----Pelub
!           !           !           !           !
!           !           !           !           +-----Barhe
!           !           !           !           +-----131
!           !           !           !           +-----Barqu
!           !           !           !           !
!           !           !           !           +-----Anasp
!           !           !           !           +-----111
!           !           !           !           +-257 +-----Anava
!           !           !           !           ! !
!           !           !           !           ! +-----Triei
!           !           !           !           !
!           !           !           !           +-297 +-----Synel
!           !           !           !           ! ! +-263
!           !           !           !           ! ! ! +-----Synja
!           !           !           !           ! ! ! +-----115
!           !           !           !           ! ! ! +-----Synjb
!           !           !           !           ! +-281
!           !           !           !           ! +-323 ! +Synp6
!           !           !           !           ! ! +-----10
!           !           !           !           ! +-269 +Synp7
!           !           !           !           ! !
!           !           !           !           ! +-----Syny3
!           !           !           !           !
!           !           !           !           +-----Glovi
!           !           !           !           +-364
!           !           !           !           +-----Prom9
!           !           !           !           +-128

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!      !      !      !      !      +-----Promp
!      !      !      !      +-197
!      !      !      !      !      +-----Proma
!      !      !      !      !      +-179
!      !      !      !      !      +-----Promt
!      !      !      +-225
!      !      !      !      +-----Promm
!      !      !      !      !      +-----Synpx
!      !      !      +-189      +-149
!      !      !      !      +-153 +-----Synsc
!      !      !      !      !      !
!      !      !      +-176 +-----Syns9
!      !      !      !
!      !      !      +-----Syns3
!      !      !
!      !      !      +-----Acice
!      !      !      +-296
!      !      !      !      +-----Thefy
!      !      !      +-325
!      !      !      !      !      +-----Straw
!      !      !      +-337 +-161
!      !      !      !      !      +-----Strco
!      !      !      !      !
!      !      !      +-342 +-----Nocjs
!      !      !      !      !
!      !      !      !      !      +-----Fraal
!      !      !      !      +-178
!      !      !      +-369      +-----Frasc
!      !      !      !      !
!      !      !      !      !      +-----Artau
!      !      !      !      !      +-169
!      !      !      !      !      +-315 +-----Artfb
!      !      !      !      !
!      !      !      +-396      +-----Leixx
!      !      !      !      !
!      !      !      !      !      +-----Cordi
!      !      !      !      !      +-243
!      !      !      !      !      !      +-----Coref
!      !      !      !      !      !      +-175
!      !      !      !      !      +-268      !      +Corgl
+-424 !      !      !      !      !      +-----17
!      !      !      !      !      !      +CorglB
!      !      !      !      !
!      !      !      !      !      +-----Corjk
!      !      !      !
!      !      !      !      +---Mycav
!      !      !      !      +---85
!      !      !      !      !      +---Mycpa
!      !      !      !      !
!      !      !      +-403      +-177      +Mycbo
!      !      !      !      !      !      +-9
!      !      !      !      !      !      +-----14 +MyctuH
!      !      !      !      !      !      !
!      !      !      !      !      +-206 +-167      +MyctuC
!      !      !      !      !      !      !
!      !      !      !      !      !      +-----Mycul
!      !      !      !      !      !
!      !      !      !      !      !      +-----Mycle
!      !      !      !      !      +-242
!      !      !      !      !      !      +Myckm
!      !      !      !      !      !      +-----12
!      !      !      +-425 !      !      !      +-147      +Mycss
!      !      !      !      !      !      +-277 !      !
!      !      !      !      !      !      !      +-165 +-----Mycvn
!      !      !      !      !      !      !
!      !      !      !      !      !      +-----Mydsm

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68

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!           !           !           !           +-----Entfa
!           !           !           !           !
!           !           !           !           +---Lisin
!           !           !           !           +---102
!           !           !           !           !           +-Lismf
!           !           !           !           +-----112 +-67
!           !           !           !           !           +-Lismo
!           !           !           !           !           !
!           !           !           !           +----Liswe
!           !           !           !           !
!           !           !           !           !           +Staa3
!           !           !           !           !           +-38
!           !           !           !           !           !           +Staas
!           !           !           !           !           !           +-23
!           !           !           !           !           !           +Staaaw
!           !           !           !           !           !           !
!           !           !           !           !           !           +Staac
!           !           !           !           !           !           +-53 +-43
!           !           !           !           !           !           +Staaau
!           !           !           !           !           !           !
!           !           !           !           !           !           +-57 ! +Staam
!           !           !           !           !           !           !           +-22
!           !           !           !           !           !           !           +Staan
!           !           !           !           !           !           !           !
!           !           !           !           !           !           +---77 !
!           !           !           !           !           !           !           +-Staar
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +-155 +--Staab
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +Staeq
!           !           !           !           !           !           +---158 +----56
!           !           !           !           !           !           !           +Staes
!           !           !           !           !           !           +---168 !
!           !           !           !           !           !           !           +-----Stahj
!           !           !           !           !           !           !           !
!           !           !           !           !           !           +-----Stas1
!           !           !           !           !           !           !
!           !           !           !           !           !           +-----Lacac
!           !           !           !           !           !           +-172
!           !           !           !           !           !           !           +-----Lacga
!           !           !           !           !           !           !           +-127
!           !           !           !           !           !           +---246 +-----Lacjo
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +---Lacda
!           !           !           !           !           !           !           +-----55
!           !           !           !           !           !           !           +---Lacde
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +-----Lacbr
!           !           !           !           !           !           !           !
!           !           !           !           !           !           !           +-306
!           !           !           !           !           !           !           !           +-241 +----Lacca
!           !           !           !           !           !           !           !           !           +-223
!           !           !           !           !           !           !           !           +---228 +-----Lacss
!           !           !           !           !           !           !           !           !           +-273
!           !           !           !           !           !           !           !           !           +-----Lacpl
!           !           !           !           !           !           !           !           !           !
!           !           !           !           !           !           !           !           !           +---331
!           !           !           !           !           !           !           !           !           +---285 +-----Leume
!           !           !           !           !           !           !           !           !           !
!           !           !           !           !           !           !           !           !           +-----Lacs1
!           !           !           !           !           !           !           !           !           +-250
!           !           !           !           !           !           !           !           !           +-----Pedpe
!           !           !           !           !           !           !           !           !           !
!           !           !           !           !           !           !           !           !           +-----Oenoe
!           !           !           !           !           !           !           !           !           !
!           !           !           !           !           !           !           !           !           +-----Lac1a
!           !           !           !           !           !           !           !           !           +---138
!           !           !           !           !           !           !           !           !           +-----Lac1c
!           !           !           !           !           !           !           !           !           !
!           !           !           !           !           !           !           !           !           +-341 !
!           !           !           !           !           !           !           !           !           +---Stra1

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```

!                                     +-64
!                                     +-----88 +-Stra5
!                                     !
!                                     +---Stra3
!                                     !
!                                     !                                     +---Strp1
!                                     !                                     +-70
!                                     !                                     ! ! +-Strpb
!                                     !                                     ! +-48
!                                     !                                     ! +-Strpc
!                                     !                                     !
!                                     !                                     +212      +-83
!                                     !                                     ! !      +Strp3
!                                     !                                     ! !      +-29
+-300                                !                                     ! !      +Strp3S
!                                     !                                     ! +73
!                                     !                                     ! +86      !      +Strpd
!                                     !                                     ! !      +-44
!                                     !                                     ! !      +-69 +Strpm
!                                     !                                     !
!                                     ! +226 +-----93 !      +-Strpf
!                                     ! !
!                                     ! !      +---Strp1G
!                                     ! !
!                                     ! !      +-Strp6
!                                     ! !      +-74
!                                     ! !      +---Strp8
!                                     ! !
!                                     ! !      +-----Strmu
+-248                                ! !
!                                     ! +203      +-Strt1
!                                     ! !      +-60
!                                     !      +-----103 +-Strt2
!                                     !
!                                     !      +---Strtr
!
!                                     !      +---Strpn
!                                     +-----79
!                                     !      +StrpnD
!                                     +28
!                                     !      +Strr6
!
!                                     +-----Alheh
!                                     +359
!                                     !      +-----Metca
!
!                                     !      +-----Niteu
+-380                                ! !      +-166
!                                     ! !      +-255 +-----NiteuC
!                                     ! !      !
!                                     ! +346 +-----Nitmu
!                                     !
!                                     !      +-----Nitoc
!
!                                     !      +-----Azobh
!                                     !      +-224
!                                     !      +266 +-----Azose
!                                     ! !
!                                     !      +322 +-----Decar
!                                     ! !
!                                     ! +345 +-----Thida
!                                     !
!                                     !      +-----Chrvo
!
!                                     !      +-Borbr
!                                     !      +-63
+-387                                !      +-----105 +-Borpa
!                                     !
!                                     !

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```

! ! ! ! ! +---Borpe
! +-437 ! ! ! ! !
! ! ! ! ! +Burca
! ! ! ! ! +--30
! ! ! ! ! +-124 +Burch
! ! ! ! ! +-351 ! !
! ! ! ! ! +-133 +----Burce
! ! ! ! ! ! !
! ! ! ! ! +-314 ! +-----Burs3
! ! ! ! ! ! !
! ! ! ! ! +-174 +----Burma
! ! ! ! ! ! ! +-100
! ! ! ! ! ! ! +-Burp1
! ! ! ! ! ! ! +-120 +-81
! ! ! ! ! ! ! +-220 ! +-Burps
! ! ! ! ! ! ! !
! ! ! +-397 ! ! ! ! ! +----Burth
! ! ! ! ! ! ! !
! ! ! ! ! +-373 +-321 ! ! +-----Burxl
! +-426 ! ! ! ! ! +-274
! ! ! ! ! ! ! +----Ralej
! ! ! ! ! ! ! +-144
! ! ! ! ! ! ! +-173 +----Raleu
! ! ! ! ! ! ! ! !
! ! ! ! ! ! ! +-233 +-----Ralme
! ! ! ! ! ! ! !
! ! ! ! ! ! ! +-----Ralso
! ! ! +-401 ! ! !
! ! ! ! ! ! ! +-----Polsj
! ! ! ! ! ! ! +-231
! ! ! ! ! ! ! +-----Rhofd
! ! ! ! ! ! !
! ! ! ! ! ! ! +-----Metfl
! ! ! ! ! ! !
! ! +-415 ! ! +-----Rutma
! ! ! ! ! +-339
! ! ! ! ! +-----Thicr
! ! ! ! !
! ! ! ! ! +-----Magmc
! ! ! ! !
! ! ! ! ! +-----Rhoba
! ! +-375
! ! ! ! ! +-----Salrd
! ! ! ! !
! ! ! ! ! +-----Aerpe
! ! ! ! !
! ! ! ! ! +-----Picto
! ! ! ! ! +-247
! ! ! ! ! ! ! +-----Theac
! ! ! ! ! ! ! +-157
! ! ! ! ! ! ! +-----Thevo
! ! ! ! ! ! !
! ! ! +-356 ! ! +-----Pyrab
! ! ! ! ! +-324 +139
! ! ! ! ! ! ! +-159 +-----Pyrho
! ! ! ! ! ! !
! ! ! ! ! ! ! +-184 +-----Pyrfu
! ! ! ! ! ! ! +-309 +-----Pyrko
! ! ! ! ! ! !
! ! ! ! ! +-353 ! +-----Sulac
! ! ! ! ! +-180
! ! ! ! ! ! +-----Sulso
! ! ! ! ! ! ! +-162
! ! ! ! ! ! ! +-----Sulto
! ! ! +-402 !
! ! ! ! ! +-----Pyrae

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72

73

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! ! ! +-304
! +-438 ! ! ! ! +-----Mycge
! ! ! ! +-187
! ! ! ! +-----Mycpn
! ! ! ! +---Borap
! ! ! ! +-59
! ! ! ! +-----80 +---Borga
! ! ! ! !
! ! ! +-407 +---Borbu
! ! ! !
! ! ! ! +-----Trede
! ! ! ! +-316
! ! ! ! +-----Tropa
! ! ! !
! ! ! ! +-----Bauch
! ! ! ! +-254
! ! ! ! ! +-----Blofl
! ! ! ! +-260 +-185
! ! ! +-419 ! ! ! +-----Blop
! ! ! ! !
! ! ! ! ! +-----Wigbr
! ! ! ! +-270
! ! ! ! ! +-----Bucac
! ! ! ! !
! ! ! ! ! +-229 +-----Bucal
! ! ! ! +-349 ! +-156
! ! ! ! ! +-209 +-----Bucap
! ! ! ! !
! ! ! ! ! +-----Bucbp
! ! ! ! +-391 !
! ! ! ! ! +-----Carru
! ! ! ! !
! ! ! ! ! +Trow8
! ! ! ! ! +-----8
! ! ! ! ! +Trowt
! ! ! ! !
! ! ! ! ! +-----Chlab
! ! ! ! ! +-118
! ! ! ! ! ! +-----Chlcv
! ! ! ! ! ! +-110
! ! ! ! ! ! +-----Chlff
! ! ! ! ! +-433 +-410 !
! ! ! ! ! +-188
! ! ! ! ! ! +ChlpnA
! ! ! ! ! ! +-2
! ! ! ! ! ! +-3 +ChlpnC
! ! ! ! ! !
! ! ! ! ! +-202 +-----4 +ChlpnT
! ! ! ! ! !
! ! ! ! ! ! +ChlpnJ
! ! ! ! !
! ! ! ! ! ! +-----Chlmu
! ! ! ! ! +-362 +-----119
! ! ! ! ! ! +Chlta
! ! ! ! ! ! +-----5
! ! ! ! ! ! +Chltr
! ! ! ! !
! ! ! ! ! +-----Paruw
! ! ! ! !
! ! ! ! ! +-----Cloab
! ! ! ! ! +-289
! ! ! ! ! ! +-----Clono
! ! ! ! ! +-236
! ! ! ! ! ! +-----Clote
! ! ! ! ! +-435 +-311
! ! ! ! ! +-Clopl
! ! ! ! ! +-54

```

```

!               !      +-----95  +---Clope
!               !               !
!               !               +---Clops
!               !               !
!               !               +-----Bifad
!               !               +-194
!               !               ! +-----Biflo
!               !               +-417
!               !               ! ! +-----Fusnn
!               !               ! ! !
!               !               ! +404          +Lepbl
!               !               !               ! +-----18
!               !               !               ! +Lepbo
!               !               !               ! +---141
!               !               !               ! +---Lepic
!               !               !               ! +---66
!               !               !               ! +---Lepin
!               !               !               !
!               !               ! +-----Naneq
!               !               !
!               +-432          +-----Arath
!               !               +-280
!               !               ! ! +-----Drome
!               !               ! +232
!               !               ! +-----Worm
!               !               ! +-326
!               !               ! ! ! +-----Ashgo
!               !               ! ! ! +-219
!               !               ! ! +-291 +-----Yeast
!               !               +-393 !
!               !               +-----Schpo
!               !               !
!               !               +-----Enccu
!               !               +-366
!               !               +-----Plafa
!
+-----Aciad

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5.3 The K=5 CVTree

440 Populations

Neighbor-Joining/UPGMA methodStrp1 version 3.6a2.1

```

+-----Psyar
+-----117
!   +-----Psyck
!
!       +-----Alcbs
!       !
!       ! +-----Chrsd
!       ! !
!       ! +330 !           +-----Pse14
!       ! ! !           +-113
!       ! ! !           +---122 +-----Pseu2
!       ! ! !           ! !
!       ! +317 !           +-----Psesm
!       !       ! +188
!       !       ! ! !           +-----Pseen
!       !       ! ! ! +139
!       !       ! ! ! ! +-----Psepk
!       +347 ! ! +172
!       ! ! +205 ! +-----Psef5
!       ! !       ! +145
!       ! !       ! +-----Psepf
!       ! !       !
!       +351 !       !           +-----Pseae

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! ! ! ! +-----42
! ! ! ! +-PseaeU
! ! ! !
! ! ! ! +-----Hahch
! ! ! !
! ! ! +-----Sacd2
! ! !
! ! ! +-----Aerhy
! ! ! !
! ! ! +282 +-----Phopr
! ! ! ! ! !
! ! ! ! ! ! +-----Vibch
! ! ! ! +231 +-183
! ! ! ! ! ! +-----Vibpa
! ! ! ! ! ! +-160
! ! ! ! +214 ! +---Vibvu
! ! ! ! ! +----81
! ! ! ! ! +---Vibvy
! ! ! +298 !
! ! ! +-----Vibf1
! ! ! !
! ! ! ! +-----Sheam
! ! ! ! !
! ! ! ! +184 +---Shean
! ! ! ! ! +94
! ! ! ! ! ! +-Shesm
! ! ! +307 ! ! +-123 +-57
! ! ! +201 ! ! +-Shesr
! ! ! ! !
! ! ! ! +-----Sheon
! ! ! ! !
! ! ! ! ! +-----Shedo
! ! ! ! +180
! ! ! ! +-----Shefn
! ! ! +322 !
! ! ! ! +-----Psyin
! ! ! !
! ! ! ! +-----Colp3
! ! ! ! +283
! ! ! ! +287 +-----Pseht
! ! ! ! ! !
! ! ! +295 +-----Psea6
! ! ! !
! ! ! ! +-----Idilo
! ! ! !
! ! ! ! +-Ecoli5
! ! ! ! +84
! ! ! ! ! ! +-EcoliA
! ! ! ! +86 +-59
! ! ! ! ! ! +-EcoliU
! ! ! ! ! !
! ! ! ! ! +---EcoliC
! ! ! ! !
! ! ! ! ! +EcoliE
! ! ! ! +-111 +-30
! ! ! ! ! ! +EcoliO
! ! ! ! ! ! +96
! ! ! ! ! ! ! +EcoliK
! ! ! ! ! ! ! +---16
! ! ! ! ! ! ! +EcoliW
! ! ! ! ! +-105
! ! ! ! ! +---Shibs
! ! ! ! +-116 ! +-97
! ! ! ! ! ! +---Shiss
! ! ! ! ! ! +-101
! ! ! ! ! ! +Shifl
299-378 +-348 ! ! ! ! +37

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77

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!      !      !      !
!      !      +-377      !      !      +---Borbr
!      !      !      !      !      +---56
!      !      !      !      !      +-----107 +---Borpa
!      !      !      !      !      !
!      !      !      !      !      +-----Borpe
!      !      !      !      !
!      !      !      !      +-344      !      !      +Burca
!      !      !      !      !      !      +-----20
!      !      !      !      !      !      +-118      +Burch
!      !      !      !      !      !      !      !
!      !      !      !      !      !      +-128 +-----Burce
!      !      !      !      !      !      !      !
!      !      !      !      !      !      +-301      !      +-----Burs3
!      !      !      !      !      !      !
!      !      !      !      !      !      !      +-164      +-----Burma
!      !      !      !      !      !      !      !      +-99
!      !      !      !      !      !      !      !      !      +-Burp1
!      !      !      !      !      !      !      !      +-114 +-67
!      !      !      !      !      !      !      +-206      !      +---Burps
!      !      !      !      !      !      !      !      !
!      !      !      !      !      !      !      !      +-----Burth
!      !      !      !      !      !      !      !
!      !      +-382 +-355 +-311 !      !      +-----Burxl
!      !      !      !      !      !      +-261
!      !      !      !      !      !      +-----Ralej
!      !      !      !      !      !      +-143
!      !      !      !      !      !      +-159 +-----Raleu
!      !      !      !      !      !      !      !
!      !      !      !      !      !      +-216 +-----Ralme
!      !      !      !      !      !      !
!      !      !      !      !      !      +-----Ralso
!      !      !      !      !      !
!      !      !      !      !      !      +-----Polsj
!      !      !      !      !      +-221
!      !      !      !      !      +-----Rhofd
!      !      !      !      !
!      !      !      !      !      +-----Chrvo
!      !      !      !      +-319
!      !      !      !      !      +-----Neig1
!      !      !      !      +-----109
!      !      !      !      !      +---Neima
!      !      !      !      +-91
!      !      !      !      +---Neimb
!      !      !      !
!      !      !      !      +-----Rutma
!      !      !      +-345
!      !      !      +-----Thicr
!      !      !
!      !      !      +-----Xanac
!      !      !      +-104
!      !      !      !      +-----Xanc5
!      !      !      +-127
!      !      !      !      !      +Xanc8
!      !      !      !      +-----19
!      !      !      +-136      +Xancp
!      !      !      !      !
!      !      !      !      !      +-Xanom
!      !      !      +-234      +-----44
!      !      !      !      +Xanor
!      !      !      !
!      !      !      !      +-----Xylfa
!      !      !      !      +-----98
!      !      !      !      +-----Xylft
!      +-387 !
!      !      !
!      !      !      +-----Bauch
!      !      !      +-263

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!      !      !      !      +-----Blofl
!      !      +-277 +-197
!      !      !      !      +-----Blop
!      !      !      !
!      !      !      +-----Wigbr
!      !      +-289
!      !      !      !      +-----Bucac
!      !      !      !
!      !      !      +-247      +-----Bucai
!      !      !      !      +-156
!      !      !      +-226 +-----Bucap
!      !      !      !
!      !      !      +-----Bucbp
!      !      +-402
!      !      !      !      +-----Coxbu
!      !      !      !
!      !      !      !      +-369      +---Legpa
!      !      !      !      +-82
!      !      !      !      +-----88      +---Legph
!      !      !      !      !
!      !      !      !      +---Legpl
!      !      !      +-386
!      !      !      !      +Frat1
!      !      !      !      +-1
!      !      !      !      !      +Fratt
!      !      !      !      +-49
!      !      !      !      !      +Frath
!      !      !      +-----90 +-36
!      !      !      !      +Frato
!      !      !      !
!      !      !      +---Fratn
!
!      !      !
!      !      !      +Agrt5
!      !      !      +-----29
!      !      !      !      +Agrt5W
!      !      !      +-211
!      !      !      !      +-----Rhiet
!      !      !      !      +-130
!      !      !      !      +-199 +-----Rhil3
!      !      !      !      !
!      !      !      !      +-----Rhime
!      !      !      !      +-246
!      !      !      !      +Brua2
!      !      !      !      +-18
!      !      !      !      +41 +Bruab
!      !      !      !      !
!      !      !      !      +-259 +-----54 +-Brusu
!      !      !      !      !
!      !      !      !      +---Brume
!      !      !      !
!      !      !      +-310 !      +-----Messb
!      !      !      !      +-250
!      !      !      !      +-----Rhilo
!      !      !      !
!      !      !      !      +-----Barhe
!      !      !      !      +-349 +-----135
!      !      !      !      +-----Barqu
!      !      !      !
!      !      !      !      +-----Braja
!      !      !      !      !
!      !      !      !      +-----Nithx
!      !      !      !      +-229 +-147
!      !      !      !      +-----Nitwn
!      !      !      !
!      !      !      !      +-218      +---Rhop2
!      !      !      !      +-133
!      !      !      !      +-142 +---Rhops

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80

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!           !           !           !   +----Ricpr
!           !           !           +--100
!           !           !           +----Ricty
!           !           !           !
!           !           +-----Pelub
!           !           !
!           !           +-----Magmc
!           !           !           !
!           !           !           +-----Camfe
!           !           !           +--240
!           !           !           !           +---Camje
!           !           !           +--293 +-----70
!           !           !           !           +---Camjr
!           !           !           !           !
!           !           !           !           +-----Thidn
!           !           !           !           !
!           !           !           +--306           +-----Helac
!           !           !           !           !
!           !           !           !           +-----121           +----Helph
!           !           !           !           !           +--87
!           !           !           !           !           +--93           +----Helpy
!           !           !           !           +--286           !
!           !           !           !           !           +----Helpj
!           !           !           !           !
!           !           !           !           +-----Helhp
!           !           !           !           +--424 !           +--429           +--274
!           !           !           !           +-----Wolsu
!           !           !           !           !
!           !           !           !           +-----Desdg
!           !           !           !           +--241
!           !           !           !           +--336 +-----Desvh
!           !           !           !           !
!           !           !           !           +-----Lawip
!           !           !           !           !
!           !           !           !           +--408 +-----Desps
!           !           !           !           !
!           !           !           !           !           +-----Geomg
!           !           !           !           !           +--176
!           !           !           !           +--406           +--269           +-----Geosl
!           !           !           !           !           !
!           !           !           !           !           +--332 +-----Pelpr
!           !           !           !           !           !
!           !           !           !           +--401 +-----Pelcd
!           !           !           !           !
!           !           !           !           !           +-----Synas
!           !           !           !           +--381
!           !           !           !           +-----Synfu
!           !           !           !           !
!           !           !           !           +-----Acibl
!           !           !           !           +--342
!           !           !           !           !           +-----Solus
!           !           !           !           +--413
!           !           !           !           !           +-----Anade
!           !           !           !           +--422 +--350
!           !           !           !           !           +-----Myxxd
!           !           !           !           !
!           !           !           !           +-----Rhoba
!           !           !           !           +--431
!           !           !           !           !           +-----Bdeba
!           !           !           !           !           !
!           !           !           !           +--423           +Lepbl
!           !           !           !           !           +-----11
!           !           !           !           !           +Lepbo
!           !           !           !           +--140
!           !           !           !           !           +Lepic
!           !           !           !           +-----31
!           !           !           !           +Lepin

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```

!                                     +-----Aerpe
!                                     +-362
!                                     ! ! +-----Pyræ
+-430 !                               +-366 +-179
!                                     ! ! +-----Pyris
!                                     ! !
!                                     ! +-----Thepe
!                                     +-379
!                                     ! ! +-----Sulac
!                                     ! ! +-204
!                                     ! +-212 +-----Sulto
!                                     +-394 !
!                                     ! ! +-----Sulso
!                                     ! !
!                                     ! ! +-----Picto
!                                     ! +-258
!                                     ! ! +-----Theac
!                                     ! +-169
!                                     ! +-----Thevo
!                                     !
!                                     ! +-----Arcfu
!                                     !
!                                     ! +-----Metac
!                                     +-407 ! +-157
!                                     ! ! +-374 +-166 +-----Metma
!                                     ! ! ! !
!                                     ! ! ! ! +-270 +-----Metbf
!                                     ! ! ! !
!                                     ! ! +-384 +-339 +-----Metbu
!                                     ! ! ! !
!                                     ! ! ! ! +-----MetthP
!                                     ! ! ! !
!                                     ! ! ! ! +-----Methj
!                                     ! ! ! !
!                                     ! ! ! ! +-----Metja
!                                     ! +-400 ! +-242
!                                     ! ! +-----Metmp
!                                     +-411 ! +-340
!                                     ! ! ! ! +-----Metst
!                                     ! ! ! ! +-367 +-284
!                                     ! ! ! ! +-----Metth
+-433 ! ! ! !
!                                     ! ! ! ! +-----Metka
!                                     ! ! ! ! +-388
!                                     ! ! ! ! +-----Pyrab
!                                     ! ! ! ! +-141
!                                     ! ! ! ! +-152 +-----Pyrho
!                                     ! ! ! !
!                                     ! ! ! ! +-192 +-----Pyrfu
!                                     ! ! ! !
!                                     ! ! ! ! +-----Pyrko
!                                     ! ! ! !
!                                     ! ! ! ! +-----Naneq
!                                     ! ! ! !
!                                     ! ! ! ! +-----Halma
!                                     ! ! ! ! +-230
!                                     ! ! ! ! +-239 +-----Natpd
!                                     ! ! ! !
!                                     ! ! +-420 +-248 +-----Halsa
!                                     ! ! ! !
!                                     ! ! ! ! +-----Halwd
!                                     ! ! ! !
!                                     ! ! ! ! +-----Carru
!                                     ! ! ! !
!                                     ! ! ! ! +-----Arath
!                                     ! ! ! ! +-372
!                                     ! ! ! ! +-----Drome

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85


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! ! ! ! ! +232 +-----Lacjo
! ! ! ! ! ! !
! ! ! ! ! ! ! +---Lacda
! ! ! ! ! ! ! +-----53
! ! ! ! ! +415 ! ! +---Lacde
! ! ! ! ! ! !
! ! ! ! ! +313 +-----Lacbr
! ! ! ! ! ! ! +252
! ! ! ! ! ! ! +268 +-----Lacpl
! ! ! ! ! ! ! ! !
! ! ! ! ! ! ! +273 +-----Pedpe
! ! ! ! ! ! ! ! !
! ! ! ! ! +338 +279 +-----Lacs1
! ! ! ! ! ! !
! ! ! ! ! ! ! +-----Lacca
! ! ! ! ! ! ! +271
! ! ! ! ! ! ! +-----Lacss
! ! ! ! ! ! !
! ! ! ! ! ! ! +-----Leume
! ! ! ! ! +280
! ! ! ! ! +-----Oenoe
! ! ! ! ! ! !
! ! ! ! ! +-----Cloab
! ! ! ! ! !
! ! ! ! ! +417 ! +285 +-----Clono
! ! ! ! ! ! ! +249
! ! ! ! ! ! ! +-----Clote
! ! ! ! ! ! ! +272
! ! ! ! ! ! ! +---Clop1
! ! ! ! ! +395 ! +71
! ! ! ! ! ! ! +-----92 +---Clope
! ! ! ! ! ! !
! ! ! ! ! ! ! +---Clops
! ! ! ! ! ! !
! ! ! ! ! +-----Fusnn
! ! ! ! ! +438 !
! ! ! ! ! ! ! +-----Carhz
! ! ! ! ! ! ! +335
! ! ! ! ! ! ! +368 +-----Mooth
! ! ! ! ! ! ! ! !
! ! ! ! ! ! ! +383 +-----Thetn
! ! ! ! ! ! ! ! !
! ! ! ! ! ! ! +399 +-----Synww
! ! ! ! ! ! !
! ! ! ! ! +409 +-----Deshy
! ! ! ! ! !
! ! ! ! ! +-----Symth
! ! ! ! ! !
! ! ! ! ! ! ! +-----Anasp
! ! ! ! ! ! ! +-----110
! ! ! ! ! ! ! +260 +-----Anava
! ! ! ! ! ! ! ! !
! ! ! ! ! ! ! +-----Triei
! ! ! ! ! ! !
! ! ! ! ! +276 +-----Synel
! ! ! ! ! ! ! +253
! ! ! ! ! ! ! +Synp6
! ! ! ! ! ! ! +267 +-----13
! ! ! ! ! +291 ! ! +Synp7
! ! ! ! ! ! !
! ! ! ! ! ! ! +-----Syny3
! ! ! ! ! ! !
! ! ! ! ! +316 ! +-----Synja
! ! ! ! ! ! ! +-----124
! ! ! ! ! ! ! +-----Synjb
! ! ! ! ! ! !
! ! ! ! ! ! ! +-----Glovi

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!           ! ! ! +-----Vibch
!           ! +-227 +-173
!           ! ! ! ! +-----Vibpa
!           ! ! ! +-154
!           ! +-205 ! +---Vibvu
!           ! ! +-----73
!           ! ! +---Vibvy
!           +-285 !
!           ! ! +-----Vibf1
!           ! !
!           ! ! +-----Sheam
!           ! ! !
!           ! ! +-189 +----Shean
!           ! ! ! ! +-95
!           ! ! ! ! ! ! +---Shesm
!           +-300 ! ! +---120 +-63
!           ! ! +-198 ! +---Shesr
!           ! ! ! !
!           ! ! ! +-----Sheon
!           ! ! !
!           ! ! ! +-----Shedo
!           ! ! +-179
!           ! ! +-----Shefn
!           +-311 !
!           ! ! +-----Psyin
!           ! !
!           ! ! +-----Colp3
!           ! ! +-276
!           ! ! +-284 +-----Pseht
!           ! ! ! !
!           ! +-293 +-----Psea6
!           !
!           ! +-----Idilo
!           !
!           !
!           ! +-Ecoli5
!           ! +-72
!           ! ! ! +-EcoliA
!           ! +-76 +-53
!           ! ! ! +-EcoliU
!           ! !
!           ! ! +-EcoliC
!           ! +-100
!           ! ! ! +EcoliE
!           ! ! ! +-33
!           ! ! ! ! +EcoliO
!           ! ! ! +-91
!           ! ! ! +EcoliK
!           ! +-108 +---19
!           ! ! ! +EcoliW
!           ! !
!           ! ! ! +---Shibs
!           ! ! ! +-94
!           ! ! ! ! +---Shiss
!           ! +-115 +-96
!           ! ! ! ! +Shif1
!           +-330 ! ! ! ! +-36
!           ! ! ! ! +-61 +Shif1T
!           ! ! ! !
!           ! ! ! ! +-Shif15
!           ! ! ! +-143 !
!           ! ! ! +-----Shids
!           ! !
!           ! ! ! +---Salch
!           ! ! ! +-67
!           ! ! ! ! +---Salty
!           ! ! ! ! +-----79
!           ! ! ! ! +-Salpa

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!      !      !      !      +-66
!      !      !      +--211      !      +Salti
!      !      !      !      !      +-18
!      !      !      !      !      +SaltyT
!      !      !      !      !      +-----Erwct
!      !      !      !      !      !
!      !      !      !      !      !      +Yerpa
!      !      !      !      !      !      +-26
!      !      !      !      +--196      +30 +Yerpn
!      !      !      +--217      !      !      !
!      !      !      !      !      !      +31 +YerpeK
!      !      !      !      !      !      !      !
!      !      !      !      !      !      !      +YerpeC
!      !      !      !      !      +-----54 +29
!      !      !      +--232      !      !      +YerpeM
!      !      !      !      !      !      !
!      !      !      !      !      !      +-Yerps
!      !      !      !      !      !      !
!      !      !      !      !      +-----Sodgl
!      !      !      !      !      !
!      !      +--288 +-----Pholl
!      !      !
!      +--369      !      +-----Haedu
!      !      !      !
!      !      !      !      +---Haei8
!      !      !      !      !      +-----85
!      !      !      +--215      +--174      +---Haein
!      !      !      !      !      !
!      !      !      !      +--182 +-----Pasmu
!      !      !      !      !      !
!      !      !      +--190 +-----Haes1
!      !      !      !
!      !      !      +-----Mansm
!      !      !
!      !      !      +-----Alcbs
!      !      !      +--315
!      !      !      !      +-----Chrzd
!      !      !      !
!      !      !      !      +-----Pse14
!      !      !      !      +--112
!      !      !      !      +---119 +-----Pseu2
!      !      !      +--324      !      !
!      !      !      !      !      +-----Psesm
!      !      !      !      !      +--186
!      !      !      !      !      !      +-----Pseen
!      !      !      !      !      !      +--138
!      !      !      !      !      !      +-----Psepk
!      !      !      !      !      !      +--171
!      !      !      +--334 +--208      !      +-----Psef5
!      !      !      !      !      +--147
!      !      !      !      !      +-----Psepf
!      !      !      !      !      !
!      !      !      !      !      +--Pseae
!      !      !      +--342      !      +-----44
!      !      !      !      !      +--PseaeU
!      !      !      !      !      !
!      !      !      !      !      +-----Hahch
287-370+-363      !
!      !      !      +-----Sacd2
!      !      !
!      !      !      +-----Alheh
!      !      +--333
!      !      !      +-----Metca
!      !      +--327
!      !      +-----Nitoc
!      !

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! ! +-----Rutma
! ! +-348
! ! ! +-----Thicr
! ! !
! ! ! +-----Coxbu
! ! ! !
! ! ! +-347 +---Legpa
! ! ! ! ! +-87
! ! ! ! +-----90 +---Legph
! ! ! ! !
! ! ! ! ! +---Legpl
! ! ! !
! ! ! ! +-----Azobh
! ! ! ! +-209
! ! ! ! +-260 +-----Azose
! ! ! ! !
! ! ! ! ! +-----Decar
! ! ! ! !
! ! ! ! +-309 +-----Metfl
! ! ! ! ! +-291
! ! ! ! ! +-----Thida
! ! ! ! ! +-301
! ! ! ! ! +-----Niteu
! ! ! ! ! +-336 ! +-150
! ! ! ! ! +-241 +-----NiteuC
! ! ! ! !
! ! ! ! ! +-----Nitmu
! ! ! ! !
! ! ! ! ! +-----Chrvo
! ! ! ! ! +-303
! ! ! ! ! +-----Neig1
! ! ! ! ! +-----104
! ! ! ! ! +-Neima
! ! ! ! ! +-81
! ! ! ! ! +-Neimb
! ! ! ! !
! ! ! ! ! +-Borbr
! ! ! ! ! +-341 +---57
! ! ! ! ! +-113 +-Borpa
! ! ! ! !
! ! ! ! ! +-----Borpe
! ! ! ! !
! ! ! ! ! +Burca
! ! ! ! ! +-----20
! ! ! ! ! +-123 +Burch
! ! ! ! !
! ! ! ! ! +-127 +-----Burse
! ! ! ! !
! ! ! ! ! +-----Burs3
! ! ! ! !
! ! ! ! ! +-165 +---Burma
! ! ! ! ! +-310 ! ! +-99
! ! ! ! ! +-382 ! ! ! ! +-Burp1
! ! ! ! ! +-117 +-74
! ! ! ! ! +-207 ! +-Burps
! ! ! ! !
! ! ! ! ! +-----Burth
! ! ! ! !
! ! ! ! ! +-----Burxl
! ! ! ! ! +-376 ! +-258
! ! ! ! ! +-----Ralej
! ! ! ! ! +-142
! ! ! ! ! +-159 +-----Raleu
! ! ! ! !
! ! ! ! ! +-302 +-220 +-----Ralme
! ! ! ! !
! ! ! ! ! +-----Ralso

```

```

!      !      !      !
!      !      !      ! +-----Polsj
!      !      !      +-219
!      !      !      +-----Rhofd
!      !      !
!      !      !      +----Xanac
!      !      !      +---101
!      !      !      ! +----Xanc5
!      !      !      +-128
!      !      !      ! !      +Xanc8
!      !      !      ! +-----17
!      !      !      +---134      +Xancp
!      !      !      !
!      !      !      !      +Xanom
!      !      !      +-226 +-----40
!      !      !      !      +Xanor
!      !      !      !
!      !      !      !      +---Xylfa
!      !      !      +-----92
!      !      !      +---Xylft
!      !      !
!      !      !      +Frat1
!      !      !      +1
!      !      !      ! +Fratt
!      !      !      +-55
!      !      !      ! !      +-Frath
!      !      !      +-----93 +-39
!      !      !      !      +-Frato
!      !      !      !
!      !      !      +---Fratn
!      !      !
!      !      !      +-----Bauch
!      +-386 !      +-270
!      !      !      ! !      +-----Blofl
!      !      !      +-312 +-206
!      !      !      ! !      +-----Blopb
!      !      !      ! !
!      !      !      ! +-----Wigbr
!      !      !      +-331
!      !      !      ! !      +-----Bucac
!      !      !      ! !
!      !      !      ! +305      +-----Bucai
!      !      !      !      +-185
!      !      !      +-261 +-----Bucap
!      !      !      !
!      !      !      +-----Bucbp
!      !      !
!      !      !
!      !      !      +Agrt5
!      !      !      +-----24
!      !      !      !      +Agrt5W
!      !      !      +-212
!      !      !      ! !      +-----Rhiet
!      !      !      ! !      +---129
!      !      !      ! +-201      +-----Rhil3
!      !      !      !
!      !      !      !      +-----Rhime
!      !      !      +-245
!      !      !      ! !      +Brua2
!      !      !      ! !      +-15
!      !      !      ! !      +-43 +Bruab
!      !      !      ! !
!      !      !      +-250 +-----45 +-Brusu
!      !      !      !
!      !      !      !      +-Brume
!      !      !
!      !      !      +-283 !      +-----Messb
!      !      !      ! !      +-247

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!           ! ! !           ! ! +-----Rhilo
!           ! ! !           ! !
!           ! ! !           ! ! +-----Barhe
!           ! ! !           +-337 +---130
!           +-392 !           ! ! +-----Barqu
!           ! !           ! !
!           ! !           ! ! +-----Braja
!           ! !           ! ! !
!           ! !           ! ! ! +-----Nithx
!           ! !           ! +-225 +-148
!           ! !           ! ! ! +-----Nitwn
!           ! !           ! ! !
!           ! !           ! +213 +---Rhop2
!           ! !           ! +135
!           ! !           ! +146 +---Rhops
!           ! !           +-354 ! ! !
!           ! !           ! ! +170 +-----Rhopa
!           ! !           ! !
!           ! !           ! ! +-----Rhopa3
!           ! !           ! +-152
!           ! !           ! ! +-----Rhopb
!           ! !           ! !
!           ! !           ! ! +-----Jansc
!           ! !           ! ! +235
!           ! !           ! ! ! +-----Rosdo
!           ! !           ! ! ! +216
!           ! !           +-361 ! ! ! +---Silpo
!           ! !           ! ! +252 +197
!           ! !           ! ! +---Silst
!           ! !           ! !
!           ! !           ! ! +-----Parde
!           ! !           ! ! +236
!           ! !           ! ! +-----Rhos4
!           ! !           ! !
!           ! !           ! ! +-----Gluox
!           ! !           ! ! +-280
!           ! !           ! ! ! +-----Grabc
!           ! !           +-362 +-353
!           ! !           ! ! +-----Magsa
!           ! !           ! ! +295
!           ! !           ! ! +-----Rhoru
!           ! !           ! !
!           ! !           ! ! +-----Caucr
!           ! !           ! ! +-316
!           ! !           ! ! ! +-----Hypna
!           ! !           ! ! ! +-314
!           ! !           +-404 ! ! +-----Marmm
!           ! !           ! ! +-359
!           ! !           ! ! +-----Eryli
!           ! !           ! ! +237
!           +-410 ! ! ! +244 +-----Novad
!           ! !           ! ! !
!           ! !           +-304 +-----Sphal
!           ! !           ! !
!           ! !           ! ! +-----Zymmo
!           ! !           ! !
!           ! !           +-----Magmc
!           ! !           ! !
!           ! !           ! ! +-----Anamm
!           ! !           ! ! +221
!           ! !           ! ! +-----Anapz
!           ! !           ! !
!           ! !           +-268 +-----Ehrch
!           ! !           ! ! +139
!           ! !           ! ! ! +-----Ehrcj
!           ! !           ! ! +167
!           ! !           ! ! +-----Ehrrg

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94

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!                                     +-320 +-----Nocjs
!                                     ! !
!                                     ! ! +-----Straw
!                                     +-326 +-162
!                                     ! ! +-----Strco
!                                     ! !
!                                     ! ! +-----Fraal
!                                     ! +-169
!                                     ! +-----Frasc
!                                     !
!                                     ! +-----Cordi
!                                     ! +-223
!                                     ! ! +-----Coref
!                                     ! ! +-160
!                                     ! +-243 ! +Corgl
!                                     +-351 ! ! +-----5
!                                     ! ! ! +CorglB
!                                     ! ! !
!                                     ! ! ! +-----Corjk
!                                     ! ! !
!                                     ! ! ! +---Mycav
!                                     ! ! ! +-----83
!                                     ! ! ! +---Mycpa
!                                     ! ! ! +-168
!                                     ! ! ! +Mycbo
!                                     ! ! ! +-13
!                                     ! +-325 +-177 +-----27 +MyctuH
!                                     ! ! !
!                                     ! ! ! +MyctuC
!                                     ! ! ! +-193 !
!                                     ! ! ! +-----Mycul
!                                     ! ! !
!                                     +-357 ! ! +-----Mycle
!                                     ! ! ! +-230
!                                     ! ! ! +Myckm
!                                     ! ! ! +-----2
!                                     ! ! ! +-163 +Mycss
!                                     ! ! !
!                                     ! ! +-264 +-178 +-----Mycvn
!                                     ! ! !
!                                     ! ! ! +-----Mydsm
!                                     ! ! !
!                                     ! ! ! +-----Nocfa
!                                     +-374 ! +-229
!                                     ! ! ! +-----Rhosr
!                                     ! ! !
!                                     ! ! ! +-----Artau
!                                     ! ! ! +-158
!                                     ! ! ! +-307 +-----Artfb
!                                     ! ! !
!                                     ! ! ! +-350 +-----Leixx
!                                     +-381 ! !
!                                     ! ! ! +-----Proac
!                                     ! ! !
!                                     ! ! ! +-----Bifad
!                                     ! ! +-164
!                                     ! ! +-----Biflo
!                                     ! !
!                                     ! ! +Trow8
!                                     ! ! +-----16
!                                     +-429 ! +-433 +Trowt
!                                     ! !
!                                     ! ! +-----Aquae
!                                     ! ! +-408
!                                     ! ! ! +-----Thema
!                                     ! ! +-422
!                                     ! ! ! ! +-----Dehe1

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! ! ! +---122
! ! ! +-----Dehsc
! ! !
! +-431 +-----Deigd
! ! +-191
! ! ! +-----Deira
! ! ! +-335
! ! ! ! +-Thet2
! ! ! ! +-----49
! ! ! +-406 +-Thet8
! ! !
! ! ! +-----Rubxd
! ! ! +-402
! ! ! +-----Synth
! ! +-434
! ! !
! ! ! +-----Anasp
! ! ! +-----109
! ! ! +-265 +-----Anava
! ! ! !
! ! ! ! +-----Triei
! ! ! !
! ! ! ! +-274 +-----Synel
! ! ! ! ! +-251
! ! ! ! ! ! +Synp6
! ! ! ! ! +-262 +-----10
! ! ! ! +-294 ! +Synp7
! ! ! ! !
! ! ! ! +-----Syny3
! ! ! !
! ! ! ! +-323 ! +-----Synja
! ! ! ! ! +-125
! ! ! ! ! +-----Synjb
! ! ! ! !
! ! ! ! +-----Glovi
! ! ! +-355
! ! ! ! +-----Prom9
! ! ! ! +-141
! ! ! ! ! +-----Promp
! ! ! !
! ! ! ! +-238 +-----Proma
! ! ! ! +-200
! ! ! ! ! +-----Promt
! ! ! !
! ! ! ! +-224 +-----Promm
! ! ! !
! ! ! ! ! +-----Synpx
! ! ! ! +-192 +-149
! ! ! ! ! +-151 +-----Synsc
! ! ! ! !
! ! ! ! +-181 +-----Syns9
! ! ! !
! ! ! ! +-----Syns3
! ! ! !
! ! ! !
! ! ! ! +-----Aerpe
! ! ! ! +-377
! ! ! ! ! +-----Pyrae
! ! ! ! +-379 +-187
! ! ! ! ! +-----Pyris
! ! ! !
! ! ! ! ! +-----Thepe
! ! ! ! +-390
! ! ! ! ! +-----Sulac
! ! ! ! ! +-228
! ! ! ! ! +-234 +-----Sulto
! ! ! ! +-401 !
! ! ! ! ! +-----Sulso
! ! ! !

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! ! +-----Picto
! +-277
! ! +-----Theac
! +172
! +-----Thevo
!
! +-----Arcfu
!
! +-----Metac
! +153
! +-366 +-166 +-----Metma
! ! !
! ! +269 +-----Metbf
! ! !
! +-412 +-383 +-338 +-----Metbu
! ! !
! ! +-----MetthP
! ! !
! ! +-----Methj
! ! !
! ! +-----Metja
! ! +396 +257
! ! ! +-----Metmp
! ! ! +367
! ! ! +-----Metst
! ! ! +380 +-306
! ! ! +-----Metth
! ! !
! ! ! +-----Metka
! ! ! +388
! +-415 ! ! +-----Pyrab
! ! ! +145
! ! +407 ! +157 +-----Pyrho
! ! !
! ! ! +202 +-----Pyrfu
! ! !
! ! ! +-----Pyrko
! ! !
! ! ! +-----Halma
! ! ! +239
! ! ! +246 +-----Natpd
! ! !
! +-420 ! +255 +-----Halsa
! ! !
! ! ! +-----Halwd
! ! !
! ! +-----Naneq
! !
! ! +-----Carru
! ! !
! ! ! +-----Arath
! ! ! +399
! ! ! +-----Drome
! ! ! +364
! ! ! +-----Worm
! +-416 !
! ! +400
! ! ! +-----Ashgo
! ! ! +240
! +-423 ! ! +405 +-343 +-----Yeast
! ! !
! ! ! +-----Schpo
! +-435 ! ! +409 !
! ! ! +-----Plafa
! ! !
! ! ! +-----Enccu
! ! !
! ! ! +-----Aywbp

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```

! ! ! ! ! +---124
! ! ! ! ! +-----Onype
! ! ! ! ! +-----Mesfl
! ! ! ! ! +-278
! ! ! ! ! +-----Mycca
! ! ! ! ! +-411 ! +-136
! ! ! ! ! +-----Mycms
! ! ! ! ! +-----Mycga
! ! ! ! ! +-297
! ! ! ! ! +-----Mycs5
! ! ! ! ! +398 +372
! ! ! ! ! +-----Mycge
! ! ! ! ! +387 +-199
! ! ! ! ! +-----Mycpn
! ! ! ! ! +-389 !
! ! ! ! ! +-----Mycpe
! ! ! +-427 ! ! !
! ! ! ! ! +-----Urepa
! ! ! ! ! +397 +--Mych2
! ! ! ! ! ! +-----50
! ! ! ! ! ! +--Mych7
! ! ! ! ! ! +-47
! ! ! ! ! +360 +--Mychj
! ! ! ! ! !
! ! ! ! ! +-----Mycmo
! ! ! ! ! +-346
! ! ! ! ! +-----Mycpu
! ! ! ! ! +-----Borap
! ! ! ! ! +-103
! ! ! ! ! +-----106 +-----Borga
! ! ! ! ! !
! ! ! ! ! +-403 +-----Borbu
! ! ! ! ! !
! ! ! ! ! ! +-----Trede
! ! ! ! ! ! +-322
! ! ! ! ! ! +-----TrepA
! ! ! ! ! !
! ! ! ! ! ! +-----Chlab
! ! ! ! ! ! +-133
! ! ! ! ! ! ! +-----Chlcv
! ! ! ! ! ! ! +-131
! ! ! ! ! ! ! +-----Chlff
! ! ! ! ! +-425 +-188
! ! ! ! ! ! ! +ChlpnA
! ! ! ! ! ! ! +-7
! ! ! ! ! ! ! ! +ChlpnC
! ! ! ! ! ! ! +-----8 +-6
! ! ! ! ! ! +-204 ! +ChlpnJ
! ! ! ! ! ! !
! ! ! ! ! ! +ChlpnT
! ! ! ! ! !
! ! ! ! ! ! +-----Chlmu
! ! ! ! ! +-352 +-132
! ! ! ! ! ! +Chlta
! ! ! ! ! ! +-----11
! ! ! ! ! ! +Chltr
! ! ! ! ! !
! ! ! ! ! +-----Paruw
! ! ! ! !
! ! ! ! ! +BacanE
! ! ! ! ! +-4
! ! ! ! ! +-22 +BacanM
! ! ! ! ! !

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