Table 2: Consensus Phylogenetic Groups

Clade	Species in RecA Consensus Clade[6]	Comprable SS-RNA Consensus ?[1,2,3]	RecA Bootstrap[4]			sRNA Bootstrap[5]		
			PP	NJ	FM	DP	NJ	FM
Proteobacteria - γ1[7]	*Escherichia coli, Shigella flexneri, Yersinia pestis, Erwinia carotovara, Serratia marcescens, Enterobacter agglomerans, Proteus vulgaris, Pr. mirabilis, Vibrio cholerae, V. anguillarum, Haemophilus influenzae*	YES	78	91	100	100	100	100
Proteobacteria - γ2	*Azotobacter vinelandii, Pseudomonas aeruginosa, Ps. putida, Ps. fluorescens*	YES	100	100	100	100	100	100
Proteobacteria - γ	γ1, γ2, *Acinetobacter calcoaceticus*	YES (+ *Legpn*)	33	63	75	48	85	92
Proteobacteria - β1	*Methylobacillus flagellatum, Methylomonas clara, Methylophilus methylotrophus, Burkholderia cepacia, Bordetella pertussis*	YES (+ *Neigo*)	74	84	88	100	100	100
Proteobacteria - β2	*Thiobacillus ferrooxidans, Acidiphilium facilis*	No	100	100	100	*	*	*
Proteobacteria - βγ	γ, β1, β2, *Xanthomonas oryzae, Neisseria gonorrhoeae, Legionella pneumophila*	YES (-*Acifa*)	53	86	95	90	94	95
Proteobacteria - α	*Rhodobacter capsulatus, Rho. sphaeroides, Rhizobium meliloti, Rhi. viciae, Rhi. phaseoli, Acetobacter polyoxogenes, Magnetospirillum magnetotacticum, Brucella abortus, Agrobacterium tumefaciens, Rickettsia prowazekii*	YES (+*Acifa*)	14	68	72	100	100	100
Proteobacteria - αβγ	α, β, γ	YES	10	57	58	93	96	96
Proteobacteria - δ	*Myxococcus xanthus* 1, *M. xanthus* 2	YES	43	71	42	*[8]	*	*
Proteobacteria - ε	*Campylobacter jejuni, Helicobacter pylori*	YES	100	100	100	100	100	100
Proteobacteria	γ, β, α, δ, ε	NO	14	38	49	*	*	36
Gram "+" High GC	*Corynebacterium glutamicum, Streptomyces ambofaciens, S. violaceus, S. lividans, Mycobacterium tuberculosis, Myb. leprae*	YES	97	100	100	100	100	100
Gram "+" Low GC	*Bacillus subtilis, Lactococcus lactis, Streptococcus pneumoniae, Staphylococcus aureus, Acholeplasma laidlawii*	YES (+ *Mycpn, Mycge*)	27	59	63	50	56	80
Mycoplasmas	*Mycoplasma mycoides, Myp. pulmonis*	YES (+ *Achla)*	88	100	98	71	88	84
Cyanobacteria	*Arabidopsis thaliana, Anabaena variabilis, Synechococcus* sp. PCC7942, *Syn.* sp. PCC7002	YES	100	96	91	100	100	100
Deinococcus-Thermus	*Deinococcus radiodurans, Thermus aquaticus, T. thermophilus*	NO	95	96	95	*	*	*

[1]For those groups which have 1 or 2 additional species in the SS_rRNA tree, the extra species are listed
[2]Groups found in trees generated by neighbor-joining, Fitch-Margoliash, De Soete and *dnapars.*
[3]Abbreviations are for *Legionella pneuomnphila, Neisseria gonorrhoeae, Acidiphilium facilis, Mycosplasma pneumonia, M. genitalium, and Acholeplasma laidlawii*
[4]PP = protein parsimony, NJ = neighbor-joining, FM = Fitch-Margoliash, DP = DNA parsimony
[5]Bootstrap values are shown for comprable clade
[6]Groups found in trees generated by neighbor-joining, Fitch-Margoliash, De Soete, *protpars* and PAUP
[7]Not applicable.
[8]Bootstraps were only calculated for trees with the one δ sequence (see Methods)