ERRATUM

Impact of Culture-Independent Studies on the Emerging Phylogenetic View of Bacterial Diversity

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Volume 180, no. 18, p. 4765–4774, 1998. Page 4767, column 1: Table 1 should appear as shown below.

TABLE 1 Summary of 16S rRNA-based clonal analyses of diversity of uncultivated bacteria[a]

Habitat type	No. of studies	No. of sequences[c]	Bacterial divisions[b]																																		
			Proteobacteria[d]																																		
			α[c]	β	γ	δ[d]	ε[e]	*Cytophagales*	*Actinobacteria*	Low-G+C gram positives[e]	*Acidobacterium*	*Verrucomicrobia*	Spirochetes	*Nitrospira*	GNS	OP11	*Plantomycetes*	Green sulfur	TM7	TM6	*Thermus/Deinococcus*	Cyanobacteria[c]	*Synergistes*	OP8	Termite group I	OS-K	*Chlamydia*	OP3	OP10	WS1	OP5	Marine group A	*Fibrobacter*	*Flexistipes*	*Dictyoglomus*	*Thermotogales*	*Thermodesulfobacterium*	*Aquificales*
Geothermal	10	212	○	○	√	○	√	○	√		○	√	○	○	○	√	○	○			○	√		√		○		√	√		√				√	○	√	○
Soil	16	743	●	○	○	○		○	●	○	●	●	√	√	○	√	○	√	√	√							√			√								
Marine	23	687	●	○	●	○	√	○	○	○	√	○			√	√	○	√	√			○				√						√						
Freshwater	4	107	●	○	√			√	○		○	√				√																						
Wastewater	5	430	●	●	●	○	√	○	●	○	√	○	√	√	○		○		√	√			√				√							√				
Pollutant associated	7	202	○	○	○	○	○	○	○	○	○	√	√	√	√	√								√	√				√	√	√							
Acid metal leaching	2	2	●	○	●			○	○	○	○			●																								
Subsurface	6	229	○	●	●	○	○	√	○	●			√	○	○	○	√	√			√								○									
Symbionts and commensals	10	280	√	√	●	√		○	√	○			○										√		√								√					
Disease associated	3	7		○	○			○		○			○																									
Totals	86	2,918																																				

[a] An expanded version of this table detailing individual studies is available at http://crab2.berkeley.edu/~pacelab/176.htm.
[b] Incidence of division-level representatives in studies of particular habitat types ranked from most represented to least represented divisions: >75% (●), 25 to 75% (○) or <25% (√) of studies have representatives of division. No symbol indicates division not detected.
[c] Excluding organelles.
[d] *Proteobacteria* are presented at the subdivision level due to the extensive sequence representation of this division.
[e] Cannot establish as a monophyletic gorup in all analyses.