

Table 1: Classification of 16S rRNA sequences obtained from isolates of onshore fine (n = 56), onshore coarse (n = 126), offshore coarse (n = 84), and surface water (n = 117) libraries. Classification based on Ribosomal Database Project classifier tool at 95% confidence unless otherwise noted by footnote.

Phylum	Family	Genus	% of Onshore fine	% of Onshore coarse	% of Offshore coarse	% of Surface water
<i>Proteobacteria</i>	<i>Sphingomonadaceae</i>	<i>Sphingomonas</i>	8.93	11.9	4.76	0.85
		<i>Sphingobium</i>				5.98 ^a
		<i>Novosphingobium</i>	3.57	0.79		
		<i>Sphingorhabdus</i>				0.85
	<i>Pseudomonadaceae</i>	<i>Pseudomonas</i>	5.36	2.38	5.95	18.8 ^b
		unclassified				0.85
	<i>Oxalobacteraceae</i>	<i>Massilia</i>	1.79	8.73	7.14	
		<i>Noviherbaspirillum</i>	5.36	5.56 ^b		0.85
		unclassified		0.79		
	<i>Moraxellaceae</i>	<i>Acinetobacter</i>	1.79	8.73	3.57	5.13
		<i>Psychrobacter</i>				4.27
		<i>Paraperlucidibaca</i>				0.85
		unclassified			1.19	
	<i>Campylobacteraceae</i>	<i>Arcobacter</i>				10.26
	<i>Comamonadaceae</i>	<i>Hydrogenophaga</i>				1.71
		<i>Acidovorax</i>				0.85
		<i>Simplicispira</i>				0.85
		<i>Variovorax</i>		0.79		
		unclassified				1.71
	<i>Caulobacteraceae</i>	<i>Brevundimonas</i>	1.79	0.79	2.38	0.85
		<i>Caulobacter</i>				0.85
	<i>Acetobacteraceae</i>	<i>Roseomonas</i>		0.79	3.57	
	<i>Shewanellaceae</i>	<i>Shewanella</i>				3.42
	<i>Aeromonadaceae</i>	<i>Aeromonas</i>				2.56
	<i>Methylobacteriaceae</i>	<i>Methylobacterium</i>	1.79	0.79		
		<i>Microvirga</i>	1.79			
	<i>Rhizobiaceae</i>	<i>Rhizobium</i>				1.71
	<i>Rhodospirillaceae</i>	<i>Azospirillum</i>				0.85
		<i>Skermanella</i>	1.79			
	<i>Xanthomonadaceae</i>	<i>Stenotrophomonas</i>				0.85
		unclassified		0.79		
	<i>Chromatiaceae</i>	<i>Rheinheimera</i>				0.85
<i>Enterobacteriaceae</i>	<i>Escherichia/Shigella</i>				0.85	
<i>Erythrobacteraceae</i>	<i>Erythrobacter</i>				0.85	
<i>Ferrimonadaceae</i>	unclassified				0.85	
<i>Rhodobacteraceae</i>	unclassified				0.85	
<i>Actinobacteria</i>	<i>Microbacteriaceae</i>	<i>Microbacterium</i>	1.79	5.56 ^b	13.1	

		<i>Agrococcus</i>	4.76	2.38	
		<i>Curtobacterium</i>	1.59	2.38	
		<i>Amnibacterium</i>	0.79 ^a		
		<i>Cryobacterium</i>	0.79		
		<i>Labedella</i>	1.79		
		<i>Mycetocola</i>		1.19	
		unclassified		1.19	
	<i>Streptomycetaceae</i>	<i>Streptomyces</i>	21.43	7.94	14.29
	<i>Micrococcaceae</i>	<i>Arthrobacter</i>		4.76	5.95
		<i>Kocuria</i>		2.38	3.57
		<i>Micrococcus</i>	1.79	1.59	
		unclassified			1.19
	<i>Pseudonocardiaceae</i>	<i>Saccharothrix</i>	1.79	0.79	
		<i>Amycolatopsis</i>	1.79		
		<i>Lentzea</i>			1.19 ^a
		<i>Umezawaea</i>	1.79 ^a		
		unclassified			1.19
	<i>Nocardioideae</i>	<i>Nocardioides</i>	1.79	0.79	1.19
		<i>Aeromicrobium</i>	1.79		
	<i>Cellulomonadaceae</i>	<i>Cellulomonas</i>		0.79	
		unclassified	1.79		
	<i>Intrasporangiaceae</i>	<i>Terrabacter</i>	1.79	0.79	
	<i>Nocardiaceae</i>	<i>Rhodococcus</i>	1.79	0.79	
	<i>Promicromonosporaceae</i>	<i>Cellulosimicrobium</i>		1.59	
	<i>Bogoriellaceae</i>	<i>Georgenia</i>			1.19
	<i>Corynebacteriaceae</i>	<i>Corynebacterium</i>			1.19
	<i>Dermabacteraceae</i>	<i>Brachybacterium</i>			0.85
	<i>Dietziaceae</i>	<i>Dietzia</i>		0.79	
	<i>Geodermatophilaceae</i>	<i>Modestobacter</i>		0.79	
	<i>Sanguibacteraceae</i>	<i>Sanguibacter</i>			0.85
<i>Bacteroidetes</i>	<i>Flavobacteriaceae</i>	<i>Flavobacterium</i>			14.53
		<i>Chryseobacterium</i>		2.38	0.85
		<i>Cloacibacterium</i>			0.85
		<i>Epilithonimonas</i>			0.85
		unclassified		1.19	2.56
	<i>Cytophagaceae</i>	<i>Hymenobacter</i>	5.36	3.17	
		<i>Adhaeribacter</i>			1.19
		<i>Dyadobacter</i>		0.79	
		<i>Fluviimonas</i>			0.85
		<i>Pontibacter</i>			1.19
		<i>Siphonobacter</i>		0.79	
	<i>Chitinophagaceae</i>	<i>Flaviumibacter</i>			0.85
		unclassified		4.76	

	<i>Cyclobacteriaceae</i>	unclassified				4.27
	<i>Sphingobacteriaceae</i>	<i>Pedobacter</i>			1.19	
<i>Firmicutes</i>	<i>Bacillaceae</i>	<i>Bacillus</i>	16.07	11.9	3.57	
	<i>Carnobacteriaceae</i>	<i>Trichococcus</i>			1.19	1.71
		<i>Desemzia</i>		0.79		
	<i>Planococcaceae</i>	<i>Chryseomicrobium</i>			2.38	
		<i>Planomicrobium</i>				0.85
	<i>Paenibacillaceae</i>	<i>Brevibacillus</i>			1.19	
		<i>Paenibacillus</i>	1.79			
	<i>Bacillales Incertae Sedis XII</i>	<i>Exiguobacterium</i>		0.79		
<i>Deinococcus- Thermus</i>	<i>Deinococcaceae</i>	<i>Deinococcus</i>	1.79	1.59		

^aIndicates that one of the sequences was classified with 85-95% confidence; ^bindicates that two of the sequences were classified with 85-95% confidence. Any sequence with a confidence level less than 85% for classification at the level of genus is listed as 'unclassified' in the table.