

The Phylogenetic Systematics Of Freelifing Nematodes

Mode of living	Organism or host	Proteobacterial subdivision	% Identity ^b
Surface attached	<i>Thiothrix nivea</i>	γ	86.4
Endosymbiotic ^c	<i>Agrobacterium tumefaciens</i>	α	81.0
	<i>Rickettsia rickettsii</i>	α	77.8
	<i>Neisseria gonorrhoeae</i>	β	80.9
	<i>Calyptogenia magnifica</i> ^d	γ	85.6
	<i>Lucinoma aequizonata</i> ^d	γ	90.5
	<i>Riftia pachyptila</i> ^d	γ	92.7
	<i>Solemya reidi</i> ^d	γ	91.9
	<i>Solemya velum</i> ^d	γ	90.2
	<i>Thyasira flexuosa</i> ^d	γ	90.3
	<i>Vesicomya cordata</i> ^d	γ	85.2
Free living	<i>Pseudomonas testosteroni</i>	β	79.5
	<i>Chromatium vinosum</i>	γ	90.2
	<i>Escherichia coli</i>	γ	82.0
	<i>Oceanospirillum linum</i>	γ	87.1
	<i>Pseudomonas aeruginosa</i>	γ	89.5
	<i>Pseudomonas mendocina</i>	γ	88.4
	<i>Thiobacillus hydrothermalis</i>	γ	86.6
	<i>Thiomicrospira</i> sp. strain L12	γ	87.1
	<i>Thiomicrospira thyasirae</i>	γ	86.4
	<i>Vibrio harveyi</i>	γ	84.0

^a All of the sequences used were obtained from the alignment published by the Ribosomal Database Project (18).

^b Identity values were calculated by using an alignment containing 895 sequence positions.

^c Bacteria are listed as symbiotic if they have the potential to spend at least portions of their lives as symbionts.

^d For chemoautotrophic symbionts the names of the hosts are given.

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