

Actinobacteria Specific Inserts in 23s rRNA

B. Gao and R.S. Gupta (2005) IJSEM 55: 2401-2412

Roller, C. et al. (1992) J. Gen. Microbiol. 138:167-175

Actinobacteria	Trichotomospora caesia	AY956800	CGGTAGTCGATGGA-CAACCGGTTGA-TATTCGGTACCCGCTTTGAAACGCCCAATATTGAATCCTCTGATGCTAAGTCCGTGAA----
	Thermomonospora chromogena	AF116563	CGGTAGTCGATGGA-TAACGGGTTGA-TATTCGGTACCCGCGTGTGCGCCA-CGTCGAGGCGGTTGATGCTAACCCGTCGAG----
	Pseudonocardia halophobica	AY956793	CGGTAGGCGATGGA-TAACGGGTTGA-TATTCGGTACCCGCGTGTGCGCCA-TGCCGAGGCGTGTGATGCTAACCATCCGAA----
	Saccharopolyspora erythraea	AY956803	CGGTAGGCGATGGA-TAACGGGTTGA-TATTCGGTACCCGCGTGTGCGCCA-TGGTGAACCGGTTGAGACTAACCATCCG----
	Tsukamurella paurometabola	AY956797	CGGTAGTCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGTGTGCGCCA-TGATGAATCAGTTG-TACTAACCGTCTGTA----
	Gordonia rubripertincta	AY956799	CGGTAGTCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGTGTGCGCCA-TGATGAATCAGTTG-TACTAACCGTCTGTA----
	Streptomycoideus glaucoflavus	AY956805	CGGTAGGCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGTGTGCGCCA-TGCTGAATCAGTTG-TACTAACCATCCGAA----
	Williamsia murale	AY956801	CGGTAGGCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGTGTGCGCCA-TGATGAATCAGTTG-TACTAACCATCCGTA----
	Micromonospora chersina	AY956804	CGGTAGTCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGAAGAGACCGACC-TGACGAACCTCGTTGCTAACACCCAA----
	Kocuria rhizophila	AY956795	CGGTAGGCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGAAGAGACCGACC-TACTGA-GCCGGGACTACTAACCCAGCCAC
	Renibacterium salmoninarum	AF143477	CGGTAGTCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGAAGAGACCGCCA-TACTGA-GCAGGTGATACTAACCCGCGA--AG
	Microbacterium oxydans	AY956796	CGGTAGTCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGAAGAGACCGCCA-AGCTAA-TCCAGTAGTCTAAGTGTCTGA--AT
	Leifsonia xyli	AB016822	CGGTAGTCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGAAGAGACCGCCA-AGCTAA-TCCAGTGGTCTAAGAGTCTTA--AT
	Oerskovia turbata	AY956798	CGGTAGGCGATGGA-CAACGGGTTGA-TATTCCTACCCGCGAAGAGACCGCCA-TACCAGAACCCGCGTGTGCTAAGCGCCCTT--AA
	Kribbella sandramycini	AY956794	CGGTAGTCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGAAGAGACCGACC-GACCGAACCTGCTGATGCTAAGTCTTCGA----
Other Bacteria	Tropheryma whippelii	AB016850	CGGTAGTCGATGGA-CAACGGGTTGA-TATTCGGTACCCGCGAAGAGACCGCCA-TATT--CCGCGTAGT-----
	Microbispora bispora	U83912	CGGTAGTCGATGG-CAACGGGTTGA-TATTCGGTACCCGCGTGTGCGGCTTCT-G-----
	Rubrobacter radiotolerans	AY956802	CGGTAGGCGATGGA-AAACAGGTTAA-TATTCCTGTACTTCAGTTATTGGTCGCT-----
	Symbiobacterium thermophilum	AP006840	CGGTAGGCGATGG-AAACAGGTTAA-TATTCCTGTACTTCAGTTATTGGTCGCT-----
	Mycoplasma penetrans	NC_000912	CGGTAGTCGATGGA-TAACAGGTTAA-TATTCCTGTACTTCAGTTATTGGTCGCT-----
	Listeria innocua	X92949	CGGTAGGCGATGGA-CAACAGGTAA-GATTTCCTGTACTTCAGTTATTGGTCGCT-----
	Bacillus subtilis	Z99104	CGGTAGGCGATGGA-CAACAGGTTGA-TATTCCTGTACTTCAGTTATTGGTCGCT-----
	Lactococcus lactis	X64887	CGGTAGTCGATGGA-CAACAGGTTGA-TATTCCTGTACTTCAGTTATTGGTCGCT-----
	Staphylococcus aureus	BA000017	CGGTAGGCGATGGA-TAACAGGTTGA-TATTCCTGTACTTCAGTTATTGGTCGCT-----
	Clostridium tetani	NC_004557	CGGTAGTCGATGGA-CAACAGGTTGA-TATTCCTGTACTTCAGTTATTGGTCGCT-----
	Symeohocystis sp.	BA000022	CGGTAGTCGATGGA-CAACAGGTTGA-TATTCCTGTACTTCAGTTATTGGTCGCT-----
	Thermus thermophilus	X12612	CGGTAGGCGAAGGG-CAGCGGTTAA-TATTCGGGCTTCCCGCAGT-----
	Chlamydia muridarum	U68437	CGGTAGACGATGGAGCAGAGTTAAATATTCCGACCACTAAACTAT-----
	Aquifex aeolicus	AB000751	CGGTAGGCGATGG-AGCGGGTCAA-TATTCGGGCGCAGTCCGTTGG-----
	Escheriachia coli	NC_000913	CGGTAGTCGATGGA-AAACAGGTTAA-TATTCCTGTACTTCAGTTATTGGTCGCT-----
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Actinobacteria	Trichotomospora caesia	GCCGCCCTGATCTCTTCGGAG--TGAGGGGAGTGGTGGAGCCGACGCCGA-GTGGTA---GTAGGTAAGCGA--TGGGTGACGCGAGGAAGTA	
	Thermomonospora chromogena	TCCGGCCACTCTCTTCTTGGAG--GGGGTGTGTGGAGAGCCGGGACCCGA-GCGGTA---GTAGGCGAGCGA--TGGGTGACGCGAGGAAGTA	
	Pseudonocardia halophobica	-CCGCGCTCTGAGTCTCTTCGG-ACGAGGGGAGTGGGGGACCGTGGGTCGA-TTCGCG---GTAGGCAAGCGA--TGGGTGACGCGAGGAAGTA	
	Saccharopolyspora erythraea	--TGSGCTGTGTAGTCTTCGG-ACGAGGCTAGTTGCT--GCATGGACCTGA-TTCCGCG---GTAGTCAAGTGA--TGGGTGACGCGAGGAAGTA	
	Tsukamurella paurometabola	-AGCACCTTGATCACCTTCGGG-TGACGGTGTGTGGAT--GCACGGACCTCG-GCTGGTA---GTAGTCAAGCGA--TGGGTGACGCGAGGAAGTA	
	Gordonia rubripertincta	-AGCACCTTGATCACCTTCGGG-TGACGGTGTGTGGAT--GCACGGACCTCG-GCTGGTA---GTAGTCAAGCGA--TGGGTGACGCGAGGAAGTA	
	Streptomycoideus glaucoflavus	-TCCCCAGGAGCACCTTCGGG-TCCCGGTTGGGTGAT--GCATGGACCTTG-GCTGGTA---GTAGGCAAGCGA--TGGGTGACGCGAGGAAGTA	
	Williamsia murale	-AGATCAAGGTTACCTTCGGG-TTCTGTTGGTTGGAT--GCATGGACCTTT-GCTGGTA---GTAGTCAAGCGA--TGGGTGACGCGAGGAAGTA	
	Micromonospora chersina	-CCAGCCAAGGT--CTTCGGA-CTGAGTTGGGA---GCGTGGAACTCG-GCGGTA---GTAGTCAAGCGA--TGGGTGACGCGAGGAAGTA	
	Kocuria rhizophila	CATGACCGTGACCCCTTGTGGTCTCGGGGTTGTGGTAGGC-TGGACCTGATCCGGGGA--GTTAAAGCTTTAACAGGTTGACGCGAGGAAGTA	
	Renibacterium salmoninarum	CATGATCGATCACCTTGTGG--TGTGAGTTTTTGTGGATCGCGGACCTTATCCTGGGA--GTTAAAGCTTTAACAGGTTGACGCGAGGAAGTA	
	Microbacterium oxydans	CCGAGTACTGATCCCTTCGGG--GTACGCTCTGGGCTAGCGCAGACCCCATTTCTGTGC--GTTAAGCTTTAACAGGTTGACGCGAGGAAGTA	
	Leifsonia xyli	CCTGGACCCGATCCCTTCGGG--GTACGCTCTGGGCTAGCGCAGACCCCATTTCTGTGC--GTTAAGCTTTAACAGGTTGACGCGAGGAAGTA	
	Oerskovia turbata	CCCC--CACCGTCTCTTCGGG--A-GACATCGGGGAGCGGCGGACCCGA-ACCGTACTAGTATTAAAGGTTGACGCGAGGAAGTA	
	Kribbella sandramycini	-----AACCATGAGGCTTCGGTGTAGTGGCGAGCAGACGGCCGA-GTGGTA---GTAGGTCATTTG--AGAGTGAACGCGAGGAAGTA	
Tropheryma whippelii	-----TTCGTTCAGC--ATTTTG--CTGTGTTACGGTAC--CCCTTTTACGGTGT--GCAGGTAAGCGA--TGGGGGACGCGAGGAAGTA		
Microbispora bispora	-----CCGA--TGGGGGACGCGAGGAAGTA		
Rubrobacter radiotolerans	-----TGACCGA--TCCGGGACGCGAGGAAGTA		
Symbiobacterium thermophilum	-----AATGA--TGGAGTGAACGAGGATTA		
Mycoplasma penetrans	-----ACGA--TGGGTGACACGAGGATA		
Listeria innocua	-----AGCAA--TGGGGGACGCGAGGATA		
Bacillus subtilis	-----GA--TGGAGGACGCGAGTGGTA		
Lactococcus lactis	-----AATCGA--TGGGGGACGCGTAGGATA		
Staphylococcus aureus	-----ACAAA--TGGGTGACACGAGGATA		
Clostridium tetani	-----GG--CG--GGACGCGAGGATA		
Symeohocystis sp.	-----GCCA--TGGGGGACGCTTAGGATA		
Thermus thermophilus	-----AGCAA--AGGAATGACGGATAGGATA		
Chlamydia muridarum	-----AGCCGG--TCTCGTACGCGAGGATA		
Aquifex aeolicus	-----GCGA--AGGGGGACGCGAGGATA		
Escheriachia coli	-----		
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Note: Dashes (-) in this particular alignment indicate sequence gap. The positions which are conserved in all sequences are denoted by the asterisks (*)

Fig. 4 Partial alignment of 23S rRNA sequences showing a large insert (99~110nt) specific for Actinobacteria. Dashes in the alignment represent lack of nucleotide at that position. The sequences in the braces are from different actinobacterial strains and the left sequences are from representatives of other bacterial groups.