

ADDITIONAL FILE 1

Table S1. Taxonomic Distribution of Organisms Possessing AHL Lactonase and AHL Acylase with Respect to the Amino Acid Sequences of the Enzyme Present in the Reference Organisms: *Bacillus* sp. SB4 (GenBank [AAR85482.1](#)), *Ralstonia* sp. XJ12B (GenBank [AAO41113.1](#))

AHL-Lactonase	AHL-Acylase
Reference Organism	
<i>Bacillus</i> sp. SB4 (GenBank AAR85482.1)	<i>Ralstonia</i> sp. XJ12B (GenBank AAO41113.1)
Actinobacteria	
<i>Arthrobacter chlorophenolicus</i> A6	<i>Actinoplanes utahensis</i>
<i>Frankia</i> sp. EAN1pec	<i>Arthrobacter viscosus</i>
<i>Mycobacterium</i> sp. MCS	<i>Nocardioides</i> sp. JS614
<i>Mycobacterium smegmatis</i> str. MC2 155	<i>Streptomyces</i> sp. FERM BP-5809
<i>M. marinum</i> M	<i>Streptomyces</i> sp. M664
<i>Streptomyces clavuligerus</i> ATCC 27064	<i>Streptomyces</i> sp. Mg1
<i>Rubrobacter xylanophilus</i> DSM 9941	<i>S. ambofaciens</i> ATCC 23877
<i>Rhodococcus</i> sp. RHA1	<i>S. griseus</i> subsp. <i>griseus</i> NBRC 13350
	<i>S. lavendulae</i> subsp. <i>lavendulae</i>
	<i>S. mobaraensis</i>
	<i>S. sviceps</i> ATCC 29083
	<i>Symbiobacterium thermophilum</i> IAM 14863
Acidobacteria	
<i>Candidatus Koribacter versatilis</i> Ellin345	<i>Solibacter usitatus</i> Ellin6076
<i>Uncultured Acidobacteria bacterium</i>	
Cyanobacteria	
	<i>Cyanothece</i> sp. ATCC 51142
	<i>Cyanothece</i> sp. CCY0110
	<i>Cyanothece</i> sp. PCC 7424
	<i>Cyanothece</i> sp. PCC 7822
	<i>Cyanothece</i> sp. PCC 8801
	<i>Cyanothece</i> sp. PCC 8802
	<i>Gloeobacter violaceus</i> PCC 7421
	<i>Microcoleus chthonoplastes</i> PCC 7420
	<i>Nostoc punctiforme</i> PCC 73102
	<i>Synechocystis</i> sp. PCC 6803
Bacteroidetes	
<i>Cellulophaga</i> sp. MED134	<i>Algoriphagus</i> sp. PR1
<i>Croceibacter atlanticus</i> HTCC2559	<i>Microscilla marina</i> ATCC 23134
<i>Flavobacteria</i>	<i>Pedobacter</i> sp. BAL39
	<i>Polaribacter irgensii</i> 23-P
	<i>Robiginitalea biformata</i> HTCC2501
	<i>Salinibacter ruber</i> DSM 13855

Table S1. Contd....

AHL-Lactonase	AHL-Acylase
Reference Organism	
<i>Bacillus</i> sp. SB4 (GenBank AAR85482.1)	<i>Ralstonia</i> sp. XJ12B (GenBank AAO41113.1)
Chloroflexi	
<i>Dehalococcoides</i> sp. VS	<i>Chloroflexus aggregans</i> DSM 9485
	<i>C. aurantiacus</i> J-10-fl
	<i>Herpetosiphon aurantiacus</i> ATCC 23779
	<i>Roseiflexus</i> sp. RS-1
	<i>Roseiflexus castenholzii</i> DSM 13941
Deinococcus-Thermus	
<i>Deinococcus radiodurans</i> R1	<i>Deinococcus radiodurans</i> R1
<i>D. geothermalis</i> DSM 11300	<i>Thermus aquaticus</i> Y51MC23
Firmicutes	
<i>Bacillus</i> sp.	<i>Bacillus</i> sp. B14905
<i>Bacillus</i> sp. 240B1	<i>Bacillus anthracis</i> str. A0488
<i>Bacillus</i> sp. 42	<i>B. badius</i>
<i>Bacillus</i> sp. 91	<i>B. cereus</i> B4264
<i>Bacillus</i> sp. A24	<i>B. coahuilensis</i> m4-4
<i>Bacillus</i> sp. B14905	<i>B. thuringiensis</i> serovar konkukian str. 97-27
<i>Bacillus</i> sp. COT1	<i>Oceanobacillus iheyensis</i> HTE831
<i>Bacillus</i> sp. CSX-1	
<i>Bacillus</i> sp. SB4	
<i>Bacillus anthracis</i> str. Ames	
<i>B. cereus</i>	
<i>B. cereus</i> 03BB108	
<i>B. cereus</i> AH1134	
<i>B. cereus</i> AH187	
<i>B. cereus</i> AH820	
<i>B. cereus</i> AH820	
<i>B. cereus</i> ATCC 10987	
<i>B. cereus</i> ATCC 14579	
<i>B. cereus</i> B4264	
<i>B. cereus</i> E33L	
<i>B. cereus</i> G9241	
<i>B. cereus</i> G9842	
<i>B. cereus</i> NVH0597-99	
<i>B. cereus</i> W	
<i>B. licheniformis</i> ATCC 14580	
<i>B. subtilis</i>	
<i>B. thuringiensis</i> serovar galleriae	
<i>B. thuringiensis</i> serovar kim	
<i>B. thuringiensis</i> serovar konkukian str. 97-27	

Table S1. Contd....

AHL-Lactonase	AHL-Acylase
Reference Organism	
<i>Bacillus</i> sp. SB4 (GenBank AAR85482.1)	<i>Ralstonia</i> sp. XJ12B (GenBank AAO41113.1)
Firmicutes	
<i>B. thuringiensis</i> serovar kurstaki	
<i>B. thuringiensis</i> serovar ostrinae	
<i>B. thuringiensis</i>	
<i>B. thuringiensis</i> serovar alesti	
<i>B. thuringiensis</i> serovar canadensis	
<i>B. thuringiensis</i> serovar israelensis ATCC 35646	
<i>B. thuringiensis</i> serovar japonensis	
<i>B. thuringiensis</i> serovar jinhongiensis	
<i>B. thuringiensis</i> serovar kyushuensis	
<i>B. thuringiensis</i> serovar oswaldocruzi	
<i>B. thuringiensis</i> serovar pakistani	
<i>B. thuringiensis</i> serovar toumanoffi	
<i>B. thuringiensis</i> str. Al Hakam	
<i>B. weihenstephanensis</i> KBAB4	
<i>Caldicellulosiruptor saccharolyticus</i> DSM 8903	
<i>Clostridium beijerinckii</i> NCIMB 8052	
<i>C. boltea</i> ATCC BAA-613	
<i>C. kluyveri</i> DSM 555	
<i>C. scindens</i> ATCC 35704	
<i>Dorea longicatena</i> DSM 13814	
<i>Geobacillus</i> sp. WCH70	
<i>Lysinibacillus sphaericus</i> C3-41	
<i>Moorella thermoacetica</i> ATCC 39073	
<i>Pelotomaculum thermopropionicum</i> SI	
<i>Staphylococcus aureus</i> RF122	
<i>S. aureus</i> subsp. <i>aureus</i> MW2	
<i>S. aureus</i> subsp. <i>aureus</i> MSSA476	
<i>S. aureus</i> subsp. <i>aureus</i> Mu50	
<i>S. saprophyticus</i> subsp. <i>saprophyticus</i> ATCC 15305	
<i>Thermosinus carboxydvorans</i> Nor1	
Alpha-Proteobacteria	
<i>Acidiphilium cryptum</i> JF-5	<i>Brevundimonas diminuta</i>
<i>Agrobacterium tumefaciens</i>	<i>Caulobacter crescentus</i> CB15
<i>A. tumefaciens</i> str. C58	<i>Caulobacter</i> sp. K31
<i>Bradyrhizobium</i> sp. ORS278	<i>Erythrobacter</i> sp. NAP1
<i>Bradyrhizobium japonicum</i> USDA 110	<i>Erythrobacter</i> sp. SD-21

Table S1. Contd....

AHL-Lactonase	AHL-Acylase
Reference Organism	
<i>Bacillus</i> sp. SB4 (GenBank AAR85482.1)	<i>Ralstonia</i> sp. XJ12B (GenBank AAO41113.1)
Alpha-Proteobacteria	
<i>Granulibacter bethesdensis</i> CGDNIH1	<i>Erythrobacter litoralis</i> HTCC2594
<i>Hyphomonas neptunium</i> ATCC 15444	<i>Hoeflea phototrophica</i> DFL-43
<i>Jannaschia</i> sp. CCS1	<i>Hyphomonas neptunium</i> ATCC 15444
<i>Oceanicola granulosus</i> HTCC2516	<i>Paracoccus denitrificans</i> PD1222
<i>Mesorhizobium</i> sp. BNC1	<i>Parvibaculum lavamentivorans</i> DS-1
<i>Paracoccus denitrificans</i> PD1222	<i>Rhodospirillum rubrum</i> ATCC 11170
<i>Phenylobacterium zucineum</i> HLK1	<i>Sphingopyxis alaskensis</i> RB2256
<i>Rhizobium etli</i> CFN 42	
<i>R. leguminosarum</i> bv. <i>trifolii</i> WSM2304	
<i>Rhodobacteriales bacterium</i> HTCC2083	
<i>Rhodopseudomonas palustris</i> TIE-1	
<i>Roseobacter</i> sp. CCS2	
<i>Roseobacter litoralis</i> Och 149	
<i>R. denitrificans</i> OCh 114	
<i>Sagittula stellata</i> E-37	
<i>Sphingomonas wittichii</i> RW1	
<i>Stappia aggregata</i> IAM 12614	
Beta-Proteobacteria	
<i>Burkholderia cenocepacia</i> J2315	<i>Acidovorax avenae</i> subsp. <i>citrulli</i> AAC00-1
<i>B. graminis</i> C4D1M	<i>Alcaligenes faecalis</i>
<i>B. xenovorans</i> LB400	<i>Burkholderia</i> sp. H160
<i>Ralstonia solanacearum</i> GMI1000	<i>Burkholderia cepacia</i>
<i>Ralstonia eutropha</i> JMP134	<i>B. oklahomensis</i> C6786
	<i>B. pseudomallei</i> 14
	<i>B. pseudomallei</i> 305
	<i>B. pseudomallei</i> 668
	<i>B. pseudomallei</i> B7210
	<i>B. pseudomallei</i> DM98
	<i>B. pseudomallei</i> K96243
	<i>Comamonas testosteroni</i> KF-1
	<i>Cupriavidus taiwanensis</i>
	<i>Delftia acidovorans</i> SPH-1
	<i>Leptothrix cholodnii</i> SP-6
	<i>Limmobacter</i> sp. MED105
	<i>Methylbium petroleiphilum</i> PM1
	<i>Polynucleobacter</i> sp. QLW-P1DMWA-1
	<i>Ralstonia</i> sp. XJ12B

Table S1. Contd....

AHL-Lactonase	AHL-Acylase
Reference Organism	
<i>Bacillus</i> sp. SB4 (GenBank AAR85482.1)	<i>Ralstonia</i> sp. XJ12B (GenBank AAO41113.1)
Beta-Proteobacteria	
	<i>Ralstonia eutropha</i> H16
	<i>R. eutropha</i> JMP134
	<i>R. metallidurans</i> CH34
	<i>R. pickettii</i> 12J
	<i>R. solanacearum</i> GMI1000
Gamma-Proteobacteria	
<i>Acinetobacter</i> sp. ADP1	<i>Acinetobacter baumannii</i> AB0057
<i>A. baumannii</i> AB0057	<i>A. baumannii</i> ACICU
<i>A. baumannii</i> ACICU	<i>A. baumannii</i> AYE
<i>A. baumannii</i> AYE	<i>Alteromonas macleodii</i> 'Deep ecotype'
marine gamma proteobacterium HTCC2080	<i>Azotobacter vinelandii</i> AvOP
<i>Marinomonas</i> sp. MWYL1	<i>Cellvibrio japonicus</i> Ueda107
<i>Photorhabdus luminescens</i> subsp. <i>laumondii</i> TTO1	<i>Escherichia coli</i> KT 71
<i>Pseudomonas stutzeri</i> A1501	<i>Gamma proteobacterium</i> KT 71
<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	<i>Hahella chejuensis</i> KCTC 2396
<i>X. campestris</i> pv. <i>campestris</i> str. 8004	<i>Idiomarina baltica</i> OS145
<i>X. campestris</i> pv. <i>campestris</i> str. ATCC 33913	marine <i>Gamma proteobacterium</i> HTCC2143
<i>X. campestris</i> pv. <i>campestris</i> str. B100	marine <i>Gamma proteobacterium</i> HTCC2207
<i>X. campestris</i> pv. <i>vesicatoria</i> str. 85-10	<i>Marinobacter algicola</i> DG893
<i>Xylella fastidiosa</i> 9a5c	<i>Myxococcus xanthus</i> DK 1622
<i>X. fastidiosa</i> Ann-1	<i>Nitrococcus mobilis</i> Nb-231
<i>X. fastidiosa</i> M12	<i>Oceanobacter</i> sp. RED65
	<i>Photorhabdus luminescens</i> subsp. <i>laumondii</i> TTO1
	<i>Providencia rettgeri</i>
	<i>P. stuartii</i> ATCC 25827
	<i>Pseudomonas</i> sp. 130
	<i>Pseudomonas</i> sp. GK16
	<i>Pseudomonas</i> sp. SY-77-1
	<i>Pseudomonas</i> sp. SY-77-1
	<i>Pseudomonas</i> sp. THA1
	<i>Pseudomonas</i> sp. THA2
	<i>Pseudomonas</i> sp. THA3
	<i>Pseudomonas</i> sp.
	<i>Pseudomonas aeruginosa</i> 2192
	<i>P. aeruginosa</i> C3719
	<i>P. aeruginosa</i> PA7

Table S1. Contd....

AHL-Lactonase	AHL-Acylase
Reference Organism	
<i>Bacillus</i> sp. SB4 (GenBank AAR85482.1)	<i>Ralstonia</i> sp. XJ12B (GenBank AAO41113.1)
Gamma-Proteobacteria	
	<i>P. aeruginosa</i> PACS2
	<i>P. aeruginosa</i> PAO1
	<i>P. aeruginosa</i> UCBPP-PA14
	<i>P. entomophila</i> L48
	<i>P. fluorescens</i> Pf0-1
	<i>P. fluorescens</i> Pf-5
	<i>P. putida</i> F1
	<i>P. putida</i> GB-1
	<i>P. putida</i> KT2440
	<i>P. putida</i> W619
	<i>P. syringae</i> pv. <i>phaseolicola</i> 1448A
	<i>P. syringae</i> pv. <i>syringae</i> B728a
	<i>P. syringae</i> pv. <i>tomato</i> str. DC3000
	<i>Psychrobacter cryohalolentis</i> K5
	<i>Serratia proteamaculans</i> 568
	<i>Shewanella</i> sp. ANA-3
	<i>Shewanella</i> sp. MIB015
	<i>Shewanella</i> sp. MR-4
	<i>Shewanella</i> sp. MR-7
	<i>Shewanella</i> sp. W3-18-1
	<i>Shewanella amazonensis</i> SB2B
	<i>S. baltica</i> OS155
	<i>S. baltica</i> OS185
	<i>S. frigidimarina</i> NCIMB 400
	<i>S. oneidensis</i> MR-1
	<i>S. putrefaciens</i> 200
	<i>S. putrefaciens</i> CN-32
	<i>S. woodyi</i> ATCC 51908
Delta-Proteobacteria	
<i>Desulfatibacillum alkenivorans</i> AK-01	<i>D. alkenivorans</i> AK-01
<i>Desulfovibrio desulfuricans</i> subsp. <i>desulfuricans</i> str. G20	<i>Plesiocystis pacifica</i> SIR-1
<i>D. vulgaris</i> subsp. <i>vulgaris</i> str. Hildenborough	<i>Stigmatella aurantiaca</i> DW4/3-1
<i>Desulfococcus oleovorans</i> Hxd3	
<i>Sorangium cellulosum</i> 'So ce 56'	

Table S1. Contd....

AHL-Lactonase	AHL-Acylase
Reference Organism	
<i>Bacillus</i> sp. SB4 (GenBank AAR85482.1)	<i>Ralstonia</i> sp. XJ12B (GenBank AAO41113.1)
Euryarchaeota	
<i>Archaeoglobus fulgidus</i> DSM 4304	<i>A. fulgidus</i> DSM 4304
<i>Haloarcula marismortui</i> ATCC 43049	
<i>Halobacterium salinarum</i> R1	
<i>Halorubrum lacusprofundi</i> ATCC 49239	
<i>Natronomonas pharaonis</i> DSM 2160	
<i>Thermoplasma acidophilum</i> DSM 1728	
<i>T. volcanium</i> GSS1	
Crenarchaeota	
<i>Sulfolobus solfataricus</i> P2	<i>Pyrobaculum calidifontis</i> JCM 11548
<i>Tenacibaculum</i> sp. MED152	
Sphingobacteria	
<i>Microscilla marina</i> ATCC 23134	
Spirochaetales	
<i>Leptospira interrogans</i> serovar <i>Copenhageni</i> str. Fiocruz L1-130	
<i>L. interrogans</i> serovar <i>Lai</i> str. 56601	
Nitrospirales	
<i>Thermodesulfobivrio yellowstonii</i> DSM 11347	
Planctomycetes (Ascomycota)	
<i>Aspergillus clavatus</i> NRRL 1	
<i>A. oryzae</i> RIB40	
<i>Aspergillus nidulans</i> FGSC A4	
<i>Coccidioides immitis</i> RS	
<i>Penicillium chrysogenum</i> Wisconsin 54-1255	
<i>Phaeosphaeria nodorum</i> SN15	

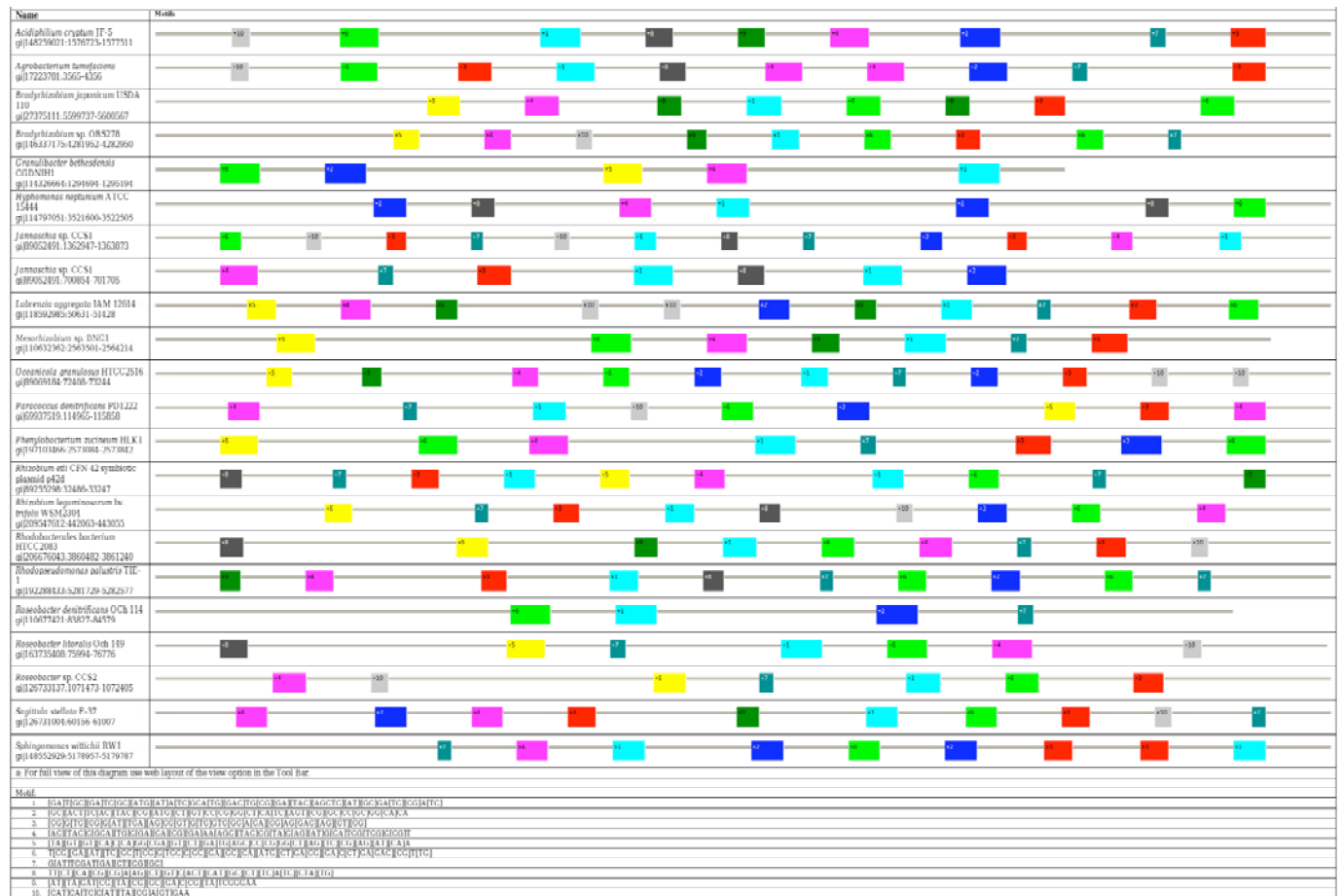


Fig. (S3). Regular expression diagram^a of signatures (nucleotides) of Alpha-Proteobacterial gene (*aiiA*) for AHL lactonase obtained with respect to *Bacillus* sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (<http://meme.edu/meme.html>)

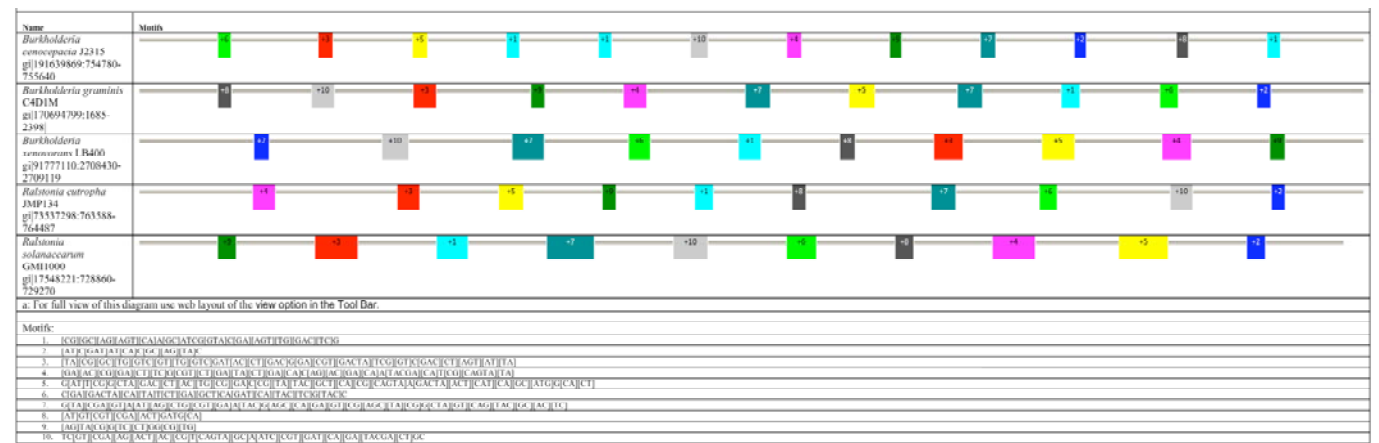


Fig. (S4). Regular expression diagram^a of signatures (nucleotides) of Beta-Proteobacterial gene (*aiiA*) for AHL lactonase obtained with respect to *Bacillus* sp. SB4 (GenBank AAR85482.1) as reference organism through MEME software (<http://meme.edu/meme.html>)

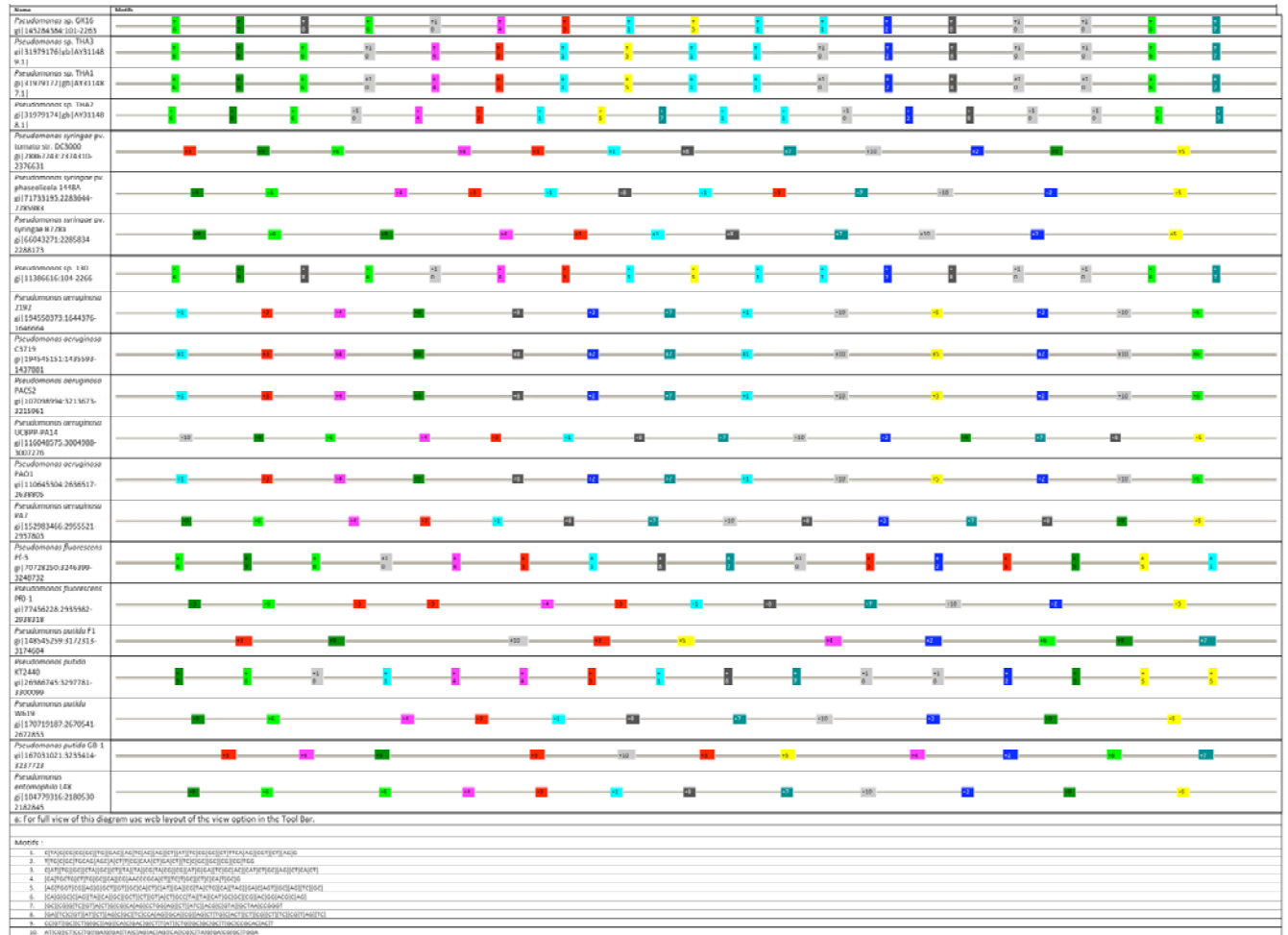


Fig. (S14). Regular expression diagram^a of signatures (nucleotides) Gamma-Proteobacterial member-*Pseudomonas* gene (*aiiA*) for AHL acylase obtained with respect to *Ralstonia* sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (<http://meme.edu/meme.html>)

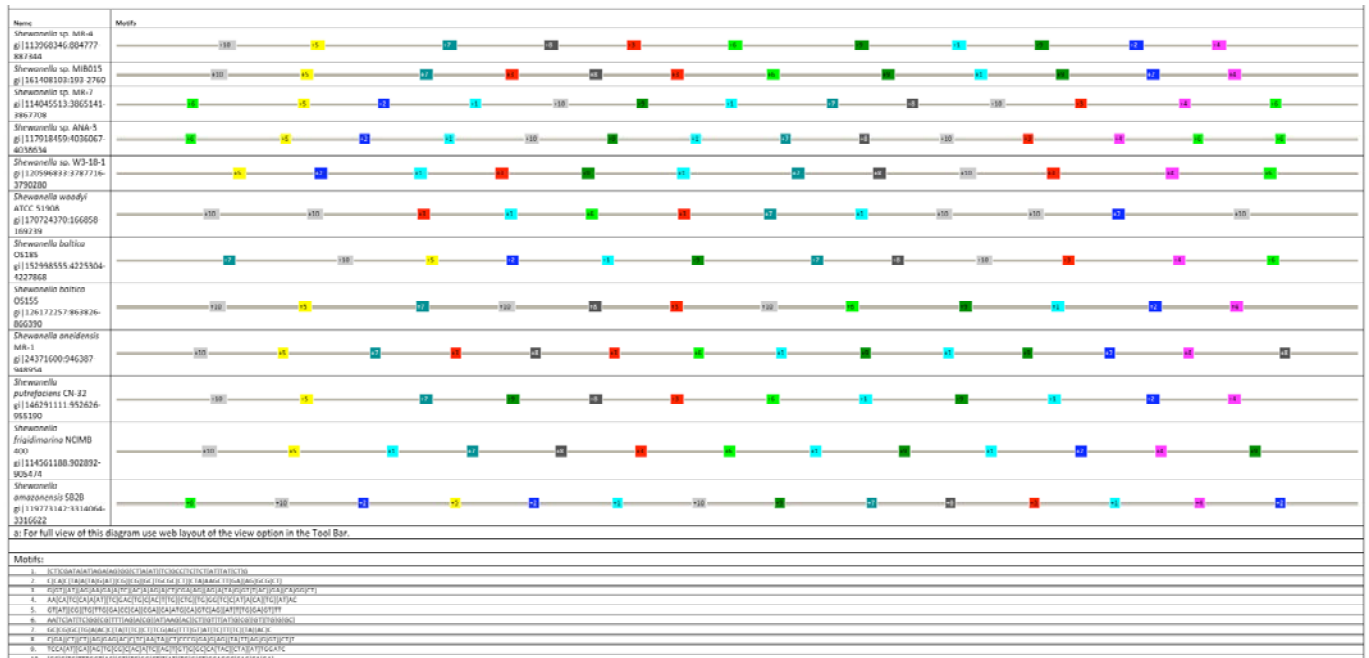


Fig. (S15). Regular expression diagram^a of signatures (nucleotides) of Gamma-Proteobacterial member - *Shewanella* sp. gene (*aiiA*) for AHL acylase obtained with respect to *Ralstonia* sp. XJ12B (GenBank AAO41113.1) as reference organism through MEME software (<http://meme.edu/meme.html>)

Table. 3S. contd....

Organism	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Firmicutes										
<i>B. cereus</i> W	-	-	+	+	-	-	-	-	-	+
<i>B. licheniformis</i> ATCC 14580	+	-	-	-	-	-	-	-	-	-
<i>B. subtilis</i> strain BSI	+	+	+	+	++	+	+	+	+	+
<i>B. thuringiensis</i> str. BCR-ZYR25	+	+	+	+	++	+	+	+	+	+
<i>B. thuringiensis</i> serovar israelensis ATCC 35646	+	+	-	+	-	-	-	-	+	-
<i>B. thuringiensis</i> str. Al Hakam	+	+	-	+	-	-	-	-	+	
<i>B. weihenstephanensis</i> KBAB4	+	-	-	-	-	-	-	-	-	+
<i>Caldicellulosiruptor saccharolyticus</i> DSM 8903	+	-	-	-	-	-	-	-	-	+
<i>Clostridium beijerinckii</i> NCIMB 8052	-	+	+	-	-	-	-	-	-	-
<i>C. bolteae</i> ATCC BAA-613	+	-	-	-	-	-	-	-	-	+
<i>C. kluyveri</i> DSM 555	+	-	-	-	-	-	+	-	-	++
<i>C. scindens</i> ATCC 35704	+	-	-	-	-	-	+	-	-	-
<i>Dorea longicatena</i> DSM 13814	-	-	+	-	-	-	-	-	+	-
<i>Geobacillus</i> sp. WCH70	+	-	-	-	-	-	-	-	-	+
<i>Lysinibacillus sphaericus</i> C3-41	+	-	-	+	-	-	+	-	-	+
<i>Moorella thermoacetica</i> ATCC 39073	+	+	-	-	-	-	-	-	-	+
<i>Pelotomaculum thermopropionicum</i> SI	+	-	-	-	-	-	+++	-	+	+
<i>Staphylococcus aureus</i> RF122	+	+	+	+	+	+	+	+	+	+
<i>S. aureus</i> subsp. <i>aureus</i> MSSA476	+	+	+	+	+	+	+	+	+	+
<i>S. aureus</i> subsp. <i>aureus</i> Mu50	+	+	+	+	+	+	+	+	+	+
<i>S. aureus</i> subsp. <i>aureus</i> MW2	+	+	+	+	+	+	+	+	+	+
<i>S. saprophyticus</i> subsp. <i>saprophyticus</i> ATCC 15305	-	+	-	-	-	-	-	-	-	-
<i>Thermosinus carboxydivorans</i> Nor1	-	-	-	-	-	-	-	+	-	-
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Deinococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Gamma-Pproteobacteria	0	0	0	0	0	0	0	0	0	0
Delta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Euryarchaeota	0	0	0	0	0	0	0	0	0	0
Crenarchaeota	0	0	0	0	0	0	0	0	0	0
Ascomycota	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Firmicutes	25/30	16/30	13/30	15/30	10/30	10/30	14/30	12/30	14/30	21/30
Total frequency of occurrence	25/110	16/110	13/110	15/110	10/110	10/110	14/110	12/110	14/110	21/110

Table S4. Representation of motifs obtained for Alpha-Proteobacteria through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (*aiiA*) of *Bacillus* sp. SB4 GenBank [AAR85482.1](#))

Organism	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Alpha-Proteobacteria										
<i>Acidiphilium cryptum</i> JF-5	+	+	+	+	-	+	+	+	+	+
<i>Agrobacterium tumefaciens</i>	+	+	++	++	-	+	+	+	-	+
<i>Bradyrhizobium japonicum</i> USDA 110	+	-	+	+	+	++	-	-	++	-
<i>Bradyrhizobium</i> sp. ORS278	+	-	+	+	+	++	+	-	+	+
<i>Granulibacter bethesdensis</i> CGDNIH1	+	+	-	+	+	+	-	-	-	-
<i>Hyphomonas neptunium</i> ATCC 15444	+	++	-	+	-	+	-	++	-	-
<i>Jannaschia</i> sp. CCS1	++	+	++	+	-	+	++	+	-	++
<i>Jannaschia</i> sp. CCS1	++	+	+	+	-	-	+	+	-	-
<i>Labrenzia aggregata</i> IAM 12614	+	+	+	+	+	+	+	-	++	++
<i>Mesorhizobium</i> sp. BNC1	+	-	+	+	+	+	+	-	+	-
<i>Oceanicola granulosus</i> HTCC2516	+	++	+	+	+	+	+	-	+	++
<i>Paracoccus denitrificans</i> PD1222	+	+	+	++	+	+	+	-	-	+
<i>Phenylobacterium zucineum</i> HLK1	+	+	+	+	+	++	+	-	-	-
<i>Rhizobium etli</i> CFN 42	++	-	+	+	+	+	++	+	+	-
<i>R. leguminosarum</i> bv. trifolii WSM2304	+	+	+	+	+	+	+	+	-	+
<i>Rhodobacterales bacterium</i> HTCC2083	+	-	+	+	+	+	+	+	+	+
<i>Rhodopseudomonas palustris</i> TIE-1	+	+	+	+	-	++	+	+	+	-
<i>Roseobacter denitrificans</i> OCh 114	+	+	-	-	-	+	+	-	-	-
<i>Roseobacter litoralis</i> Och 149	+	-	-	+	+	+	+	+	-	+
<i>Roseobacter</i> sp. CCS2	+	-	+	+	+	+	+	-	-	+
<i>Sagittula stellata</i> E-37	+	+	++	++	-	+	+	-	+	+
<i>Sphingomonas wittichii</i> RW1	++	++	++	+	-	+	+	-	-	-
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Deinococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Firmicutes	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Gamma-Proteobacteria	0	0	0	0	0	0	1	0	0	0
Delta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Euryarchaeota	0	0	0	0	0	0	1	0	0	0
Crenarchaeota	0	0	0	0	0	0	0	0	0	0
Ascomycota	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence with in Alpha-Proteobacteria	22/22	15/22	19/22	21/22	13/22	21/22	19/22	10/22	10/22	12/22
Total frequency of occurrence	22/110	15/110	19/110	21/110	13/110	21/110	21/110	10/110	10/110	12/110

Table S5. Representation of motifs obtained for Beta-Proteobacteria through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (*aiiA*) of *Bacillus* sp. SB4 GenBank [AAR85482.1](#))

Organism	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Beta-Proteobacteria										
<i>Burkholderia cenocepacia</i> J2315	+++	+	+	+	+	+	+	+	+	+
<i>B. graminis</i> C4D1M	+	+	+	+	+	+	++	+	+	+
<i>B. xenovorans</i> LB400	+	+	+	+	+	+	+	+	+	+
<i>Ralstonia eutropha</i> JMP134	+	+	+	+	+	+	+	+	+	+
<i>R. solanacearum</i> GMI1000	+	+	+	+	+	+	+	+	+	+
Actinobacteria	0	1	0	0	0	0	0	0	0	0
Deinococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Firmicutes	0	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	1	0	0	0	0	0	0	0	0
Gamma-Proteobacteria	0	0	0	0	0	0	0	4	0	0
Delta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Euryarchaeota	0	0	0	0	0	0	0	2	1	0
Crenarchaeota	0	0	0	0	0	0	0	0	0	0
Ascomycota	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Beta-Proteobacteria	5/5	5/5	5/5	5/5	5/5	5/5	5/5	5/5	5/5	5/5
Total frequency of occurrence	5/110	7/110	5/110	5/110	5/110	5/110	5/110	11/110	6/110	5/110

Table S6. Representation of motifs obtained for Gamma-Proteobacteria through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (*aiiA*) of *Bacillus* sp. SB4 GenBank [AAR85482.1](#))

Organism	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Gamma-Proteobacteria										
<i>Acinetobacter</i> sp. ADP1	+	+	+	+	-	+	-	+	+	+
<i>Acinetobacter baumannii</i> AB0057	-	+	+	+	+	-	+	+	+	+
<i>A. baumannii</i> ACICU	-	+	++	+	+	-	+	+	+	+
<i>A. baumannii</i> AYE	+	+	+	+	-	+	-	+	+	+
Marine gamma proteobacterium HTCC2080	-	+	-	-	-	-	-	-	-	-
<i>Marinomonas</i> sp. MWYL1	+	+	+	+	-	-	-	-	+	+
<i>Photorhabdus luminescens</i> subsp. <i>laumondii</i> TTO1	+	-	-	-	-	-	-	+	-	-
<i>Pseudomonas stutzeri</i> A1501	+	+	+	+	+	+	+	+	+	+
<i>Xanthomonas axonopodis</i> pv. <i>citri</i> str. 306	+	+	+	+	+++	+	+	+	+	+
<i>X. campestris</i> pv. <i>campestris</i> str. 8004	-	+	+	+	+	-	+	-	-	+
<i>X. campestris</i> pv. <i>campestris</i> str. ATCC 33913	+	+	+	+	++	++	+	+	+	+
<i>X. campestris</i> pv. <i>campestris</i> str. B100	-	+	+	+	+	-	+	-	-	+
<i>X. campestris</i> pv. <i>vesicatoria</i> str. 85-10	+	+	+	+	++	+	+	+	+	+
<i>Xylella fastidiosa</i> 9°5c	+	+	+	+	++	+	+	+	+	+
<i>X. fastidiosa</i> Ann-1	+	+	+	+	++	+	+	+	+	+
<i>X. fastidiosa</i> M12	+	+	+	+	++	+	+	+	+	+
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Deinococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Firmicutes	0	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Delta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Euryarchaeota	0	0	0	0	0	0	0	0	0	0
Crenarchaeota	0	0	0	0	0	0	0	0	0	0
Ascomycota	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Gamma-proteobacteria	11/16	15/16	14/16	14/16	10/16	9/16	11/16	12/16	12/16	14/16
Total frequency of occurrence	11/110	15/110	14/110	14/110	10/110	9/110	11/110	12/110	12/110	14/110

Table S7. Representation of motifs obtained for Delta-Proteobacteria through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (*aiaA*) of *Bacillus* sp. SB4 GenBank [AAR85482.1](#))

Organism	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Delta-Proteobacteria										
<i>Desulfatibacillum alkenivorans</i> AK-01	+	+	+	++	+	+	++	+	+	+
<i>Desulfococcus oleovorans</i> Hxd3	+	+	+	+	+	+	+	+	+	+
<i>Desulfovibrio desulfuricans</i> subsp. <i>desulfuricans</i> str. G20	+	+	+	+	+	+	+	+	+	+
<i>D. vulgaris</i> subsp. <i>vulgaris</i> str. Hildenborough	++	+	+	+	+	+	+	+	+	+
<i>Sorangium cellulosum</i> 'So ce 56'	+	+	+	-	+	+	++	+	+	+
Actinobacteria	0	0	0	2	0	0	0	0	0	0
Deinococcus-thermus	0	0	0	1	0	0	0	0	0	0
Firmicutes	0	0	0	3	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	1	0	0	0	0	0	0
Gamma-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Euryarchaeota	0	0	0	0	0	0	0	0	0	0
Crenarchaeota	0	0	0	0	0	0	0	0	0	0
Ascomycota	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Delta-Proteobacteria	5/5	5/5	5/5	4/5	5/5	5/5	5/5	5/5	5/5	5/5
Total frequency of occurrence	5/110	5/110	5/110	11/110	5/110	5/110	5/110	5/110	5/110	5/110

Table S8. Representation of motifs obtained for Euryarchaeota through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (*aiaA*) of *Bacillus* sp. SB4 GenBank [AAR85482.1](#))

Organism	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Euryarchaeota										
<i>Archaeoglobus fulgidus</i> DSM 4304	-	+	+	+	+	+	+	+	+	+
<i>Haloarcula marismortui</i> ATCC 43049	++	+	-	-	++	-	-	+	-	+
<i>Halorubrum lacusprofundi</i> ATCC 49239	+	+	-	+	+++	-	-	+	-	-
<i>Natronomonas pharaonis</i> DSM 2160	+	+	-	+	+	+	++	++	-	-
<i>Thermoplasma acidophilum</i> DSM 1728	+	+	+	+	+	+	+	+	+	+
<i>Thermoplasma volcanium</i> GSS1	+	+	+	+		++	+	+	+	+
<i>T. volcanium</i> GSS1	+	+	+	+	+	+	+	++	+	+
<i>T. volcanium</i> GSS1	+	+	+	+	+	+	+	++	+	+
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Deinococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Firmicutes	0	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Gamma-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Delta-Proteobacteria	0	0	0	0		0	0	0	0	0
Crenarchaeota	0	0	0	0		0	0	0	0	0
Ascomycota	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Euryarchaeota	7/8	8/8	5/8	7/8	7/8	6/8	6/8	8/8	5/8	6/8
Total frequency of occurrence	7/110	8/110	5/110	7/110	7/110	6/110	6/110	8/110	5/110	6/110

Table S9. Representation of motifs obtained for Ascomycota through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-lactonase gene (*aiiA*) of *Bacillus* sp. SB4 GenBank [AAR85482.1](#))

Organism	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Ascomycota										
<i>Aspergillus clavatus</i> NRRL 1	+	+	+	+	+	+	+	+	+	+
<i>A. oryzae</i> RIB40	+	+	+	+	+	+	+	+	+	+
<i>Coccidioides immitis</i> RS	++	+	++	+	+	+	+	+	+	+
<i>Phaeosphaeria nodorum</i> SN15	+	+	+	+	+	+	+	+	+	+
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Deinococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Firmicutes	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Gamma-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Delta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Euryarchaeota	0	0	0	0	0	0	0	0	0	0
Crenarchaeota	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Ascomycota	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4	4/4
Total frequency of occurrence	4/110	4/110	4/110	4/110	4/110	4/110	4/110	4/110	4/110	4/110

Table S10. Representation of motifs obtained for Actinobacteria through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (*aiiD*) of *Ralstonia* sp. XJ12B GenBank [AAO41113.1](#))

Organism	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Actinobacteria										
<i>Nocardioides</i> sp. JS614	+++	++	+	++	+	+++	-	+++	+	-
<i>Salinispora arenicola</i> CNS-205	+++	++	+	-	-	++	-	+++	+	++
<i>S. tropica</i> CNB-440	+	+	++	-	++	++	++	+	+	-
<i>Streptomyces</i> sp. FERM BP-5809	+	+	+	++++	+++	++	+	+	+	++
<i>Streptomyces</i> sp. M664	++	+	+	+++	++	++	+	++	+	+
<i>Streptomyces</i> sp. Mg1	++	+	+++	+	+	+	+	+	++	+++
<i>Streptomyces griseus</i> subsp. <i>griseus</i> NBRC 13350	+	+	++	+	++	+	+	++++	+	++
<i>Rhodopirellula baltica</i> SH 1	++++	+	++	+	+	-	+	++	-	+++
Cyanobacteria	0	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	1	0	0	0	0	0	0	0	0	0
Gamma-Proteobacteria	5	0	0	0	0	0	0	0	0	0
Deionococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Bacteroidetes	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Actinobacteria	9	9	9	6	7	8	7	9	9	7
Total frequency of occurrence	15/94	9/94	9/94	6/94	7/94	8/94	7/94	9/94	9/94	7/94

Table S11: Representation of motifs obtained for Bacteroidetes through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (*aiiD*) of *Ralstonia* sp. XJ12B GenBank [AAO41113.1](#))

Organisms	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Bacteroidetes										
<i>Algoriphagus</i> sp. PR1	++	+	+	+	+++	+	+	+	+	+
<i>Microscilla marina</i> ATCC 23134	+	+	+	+	-	+	+	+	+	++
<i>Pedobacter</i> sp. BAL39	+	-	++	+	+	+	++	+	+	+
<i>Polaribacter irgensii</i> 23-P	+	+	+	+	++		++	+	+	+
<i>Robiginitalea biformata</i> HTCC2501	++	++	+	+	+	+	++	+	+	+
<i>R. biformata</i> HTCC2501	-	+	+	-	+	+	+	+	-	+
<i>Salinibacter ruber</i> DSM 13855	-	-	+	-	-	-	+	+	-	-
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Cyanobacteria	1	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Gamma-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Deionococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Bacteroidetes	5	5	7	5	5	5	7	7	5	6
Total Frequency of occurrence	6/94	5/94	7/94	5/94	5/94	5/94	7/94	7/94	5/94	6/94

Table S12. Representation of motifs obtained for Cyanobacteria through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (*aiiD*) of *Ralstonia* sp. XJ12B GenBank [AAO41113.1](#))

Organisms	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Cyanobacteria										
<i>Cyanothece</i> sp. CCY 0110	+	+	+	+	+	++	+	+	+	++
<i>Cyanothece</i> sp. ATCC 51142	+	+	+	+	+	+	+	+	+	++
<i>Cyanothece</i> sp. PCC 8802	+	+	+	+	+	++	+	++	+	+
<i>Cyanothece</i> sp. PCC 7424	+	+	+	+	+	+	+	+	+	+
<i>Cyanothece</i> sp. PCC 7822	+	+	+	+	+	+++	+	+	+	+
<i>Synechocystis</i> sp. PCC 6803	+	++	+	+	+	+	++	-	++	+
<i>Cyanothece</i> sp. PCC 8801	+	+	+	++	+	+	+	-	-	-
<i>Nostoc punctiforme</i> PCC 73102 (<i>Nostoc punctiforme</i> ATCC 29133)	-	+	+	++	+	+	+	-	-	-
<i>Microcoleus chthonoplastes</i> PCC 7420	-	+	+	+	+	++	+	-	-	-
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Bacteroides	0	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Gamma-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Deionococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Cyanobacteria	7	9	9	9	9	9	9	5	6	6
Total Frequency of occurrence	7/94	9/94	9/94	9/94	9/94	9/94	9/94	5/94	6/94	6/94

Table S13. Representation of motifs obtained for Alpha-Proteobacteria through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (*aiiD*) of *Ralstonia* sp. XJ12B GenBank [AAO41113.1](#))

Organisms	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Alphaproteobacteria										
<i>Bermanella marisrubri</i> strain RED65	+	+	-	-	-	-	++	-	++	+
<i>Caulobacter</i> sp. K31	+	++	++	+	++	+	+++	++	+	+
<i>Erythrobacter litoralis</i> HTCC2594	+	+	++	+	++	++	++	+	+	++++
<i>Erythrobacter</i> sp. NAP1	+	+	++	++	+	++	++	++	++	++
<i>Erythrobacter</i> sp. SD-21	+	-	-	+	+	-	-	++	+++	+
<i>Hyphomonas neptunium</i> ATCC 15444	-	-	-	-	-	+	+	-	++	++
<i>Parvibaculum lavamentivorans</i> DS-1	+++	++	+	++	++	++	+	+	+	++
<i>Sphingopyxis alaskensis</i> RB2256	++	+	+	+	+	+	+	+	+	+
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Cyanobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Gamma-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Deionococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Bacteroidetes	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Alpha-Proteobacteria	7	6	5	6	6	6	7	6	8	8
Total frequency of occurrence	7/94	6/94	5/94	6/94	6/94	6/94	7/94	6/94	8/94	8/94

Table S14. Representation of motifs obtained for Beta-Proteobacteria through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (*aiiD*) of *Ralstonia* sp. XJ12B GenBank [AAO41113.1](#))

Organism	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Beta-Proteobacteria										
<i>Acidovorax avenae</i> subsp. <i>citrulli</i> AAC00-1	+	++	+	+	+	+++	+++	++	++	+
<i>Delfia acidovorans</i>	++	+	++	+	+	+++	++	++	+	++
<i>Limnobacter</i> sp. MED105	+	++	++	++	+	+	+	+	+	+
<i>Ralstonia</i> sp. XJ12B	+++	-	+	++	+++	++	-	-	++	-
<i>Ralstonia eutropha</i> H16	+	++	++	-	++	++	+++	-	+	++
<i>R. metallidurans</i> CH34	-	++	-	-	+	-	++	++	+	+
<i>R. pickettii</i> 12J	+++	+	+	+	++	++++	+	+	+	+
<i>R. solanacearum</i> GMI1000	++	+	+	++++	+++	+	++	+	+	+
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Cyanobacteria	0	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Gamma-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Deionococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Bacteroidetes	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Beta-Proteobacteria	7	7	7	6	7	7	7	6	8	7
Total frequency of occurrence	7/94	7/94	7/94	6/94	8/94	7/94	7/94	6/94	8/94	7/94

Table S16. contd....

Organisms	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Gamma-Proteobacteria - Shewanella spp.										
<i>P. fluorescens</i> Pf0-1	-	-	-	-	-	-	-	-	-	-
<i>P. putida</i> F1	-	-	-	-	-	-	-	-	-	-
<i>P. putida</i> KT2440	-	-	-	-	-	-	-	-	-	-
<i>P. putida</i> W619	-	-	-	-	-	-	-	-	-	-
<i>P. putida</i> GB-1	-	-	-	-	-	-	-	-	-	-
<i>P. entomophila</i> L48	-	-	-	-	-	-	-	-	-	-
<i>Shewanella</i> sp. MR-4	+	+	+	+	+	+	+	+	++	+
<i>Shewanella</i> sp. MIB015	+	+	++	+	+	+	+	+	++	+
<i>Shewanella</i> sp. MR-7	++	+	+	+	+	++	++	+	+	++
<i>Shewanella</i> sp. ANA-3	++	+	+	+	+	+++	+	+	+	++
<i>Shewanella</i> sp. W3-18-1	++	+	++	+	+	+	+	+	+	+
<i>Shewanella woodyi</i> ATCC 51908	++	+	++	-	-	+	+	-	-	++++
<i>S. baltica</i> OS185	+	+	+	+	+	+	++	+	+	++
<i>S. baltica</i> OS155	+	+	+	+	+	+	+	+	+	+++
<i>S. oneidensis</i> MR-1	++	+	++	+	+	+	+	+	++	+
<i>S. putrefaciens</i> CN-32	++	+	+	+	+	+	+	+	+	+
<i>S. frigidimarina</i> NCIMB 400	++	+	+	+	+	+	+	+	+	+
<i>S. amazonensis</i> SB2B	++	+++	+	+	+	+	+	+	+	++
<i>S. putrefaciens</i> 200	-	-	-	-	-	-	-	-	-	-
<i>Alteromonas macleodii</i> 'Deep ecotype'	-	-	-	-	-	-	-	-	-	-
<i>Azotobacter vinelandii</i> AvOP	-	-	-	-	-	-	-	-	-	-
<i>Cellvibrio japonicus</i> Ueda107	-	-	-	-	-	-	-	-	-	-
<i>Gamma proteobacterium</i> KT 71	-	-	-	-	-	-	-	-	-	-
<i>Hahella chejuensis</i> KCTC 2396	-	-	-	-	-	-	-	-	-	-
<i>Idiomarina baltica</i> OS145	-	-	-	-	-	-	-	-	-	-
Marine Gamma proteobacterium HTCC2143	-	-	-	-	-	-	-	-	-	-
Marine Gamma proteobacterium HTCC2207	-	-	-	-	-	-	-	-	-	-
<i>Marinobacter algicola</i> DG893	-	-	-	-	-	-	-	-	-	-
<i>Myxococcus xanthus</i> DK 1622	-	-	-	-	-	-	-	-	-	-
<i>Photorhabdus luminescens</i> subsp. <i>Laumondii</i> TTO1	-	-	-	-	-	-	-	-	-	-
<i>Plesiocystis pacifica</i> SIR-1	-	-	-	-	-	-	-	-	-	-
<i>Psychrobacter cryohalolentis</i> K5	-	-	-	-	-	-	-	-	-	-
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Bacteroidetes	0	0	0	0	0	0	0	0	0	0
Cyanobacteria	0	0	0	0	0	0	0	0	0	0
Deionococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Frequency of occurrence within Gamma-Proteobacteria	12	12	12	11	11	12	12	11	11	12
Total frequency of occurrence	12/94	12/94	12/94	11/94	11/94	12/94	12/94	11/94	11/94	12/94

Table S17. Representation of motifs obtained for Gamma-Proteobacterial members other than *Pseudomonas* spp. and *Shewanella* spp. through MEME (<http://meme.edu/meme.html>) software and the frequency of their occurrence across other taxonomical group using SMS (Sequence Manipulation Suite: http://www.bioinformatics.org/sms2/dna_pattern.html). (Reference: AHL-acylase gene (*aiiD*) of *Ralstonia* sp. XJ12B GenBank [AAO41113.1](#))

Organisms	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Gamma-Proteobacteria										
<i>Pseudomonas</i> sp. GK16	-	-	-	-	-	-	-	-	-	-
<i>Pseudomonas</i> sp. THA3	-	-	-	-	-	-	-	-	-	-
<i>Pseudomonas</i> sp. THA1	-	-	-	-	-	-	-	-	-	-
<i>Pseudomonas</i> sp. THA2	-	-	-	-	-	-	-	-	-	-
<i>Pseudomonas syringae</i> pv. <i>tomato</i> str. DC3000	-	-	+	-	-	-	-	-	-	-
<i>P. syringae</i> pv. <i>phaseolicola</i> 1448°	-	-	+	-	-	-	-	-	-	-
<i>P. syringae</i> pv. <i>syringae</i> B728a	-	-	+	-	-	-	-	-	-	-
<i>P. syringae</i>	-	-	-	-	-	-	-	-	-	-
<i>P. aeruginosa</i> 2192	-	-	-	-	-	-	-	+	-	-
<i>P. aeruginosa</i> C3719	-	-	-	-	-	-	-	+	-	-
<i>P. aeruginosa</i> PACS2	-	-	-	-	-	-	-	+	-	-
<i>P. aeruginosa</i> UCBPP-PA14	-	-	-	-	-	-	-	+	-	-
<i>P. aeruginosa</i> PAO1	-	-	-	-	-	-	-	+	-	-
<i>P. aeruginosa</i> PA7	-	-	-	-	-	-	-	-	-	-
<i>P. fluorescens</i> Pf-5	-	+	-	-	-	-	-	-	-	-
<i>P. fluorescens</i> Pf0-1	-	+	+	-	-	-	-	-	-	-
<i>P. putida</i> F1	-	-	-	-	-	-	-	-	-	-
<i>P. putida</i> KT2440	-	-	-	-	-	-	-	-	-	-
<i>P. putida</i> W619	-	-	-	-	-	-	-	-	-	-
<i>P. putida</i> GB-1	-	-	-	+	-	-	-	-	-	-
<i>P. entomophila</i> L48	-	-	-	-	-	-	-	-	-	-
<i>Shewanella</i> sp. ANA-3	-	-	-	-	-	-	-	-	-	-
<i>Shewanella</i> sp. MR-4	-	-	-	-	-	-	-	-	-	-
<i>Shewanella</i> sp. MIB015	-	-	-	-	-	-	-	-	-	-
<i>Shewanella</i> sp. MR-7	-	-	-	-	-	-	-	-	-	-
<i>Shewanella</i> sp. W3-18-1	-	-	-	-	-	-	-	-	-	-
<i>Shewanella woodyi</i> ATCC 51908	-	-	-	-	-	-	-	-	-	-
<i>S. baltica</i> OS185	-	-	-	-	-	-	-	-	-	-
<i>S. baltica</i> OS155	-	-	-	-	-	-	-	-	-	-
<i>S. oneidensis</i> MR-1	-	-	-	-	-	-	-	-	-	-
<i>S. putrefaciens</i> CN-32	-	-	-	-	-	-	-	-	-	-
<i>S. frigidimarina</i> NCIMB 400	-	-	-	-	-	-	-	-	-	-
<i>S. putrefaciens</i> 200	-	-	-	-	-	-	-	-	-	-
<i>S. amazonensis</i> SB2B	-	-	-	-	-	-	-	-	-	-
<i>Alteromonas macleodii</i> 'Deep ecotype'	-	-	-	-	-	-	-	+	+	+
<i>Azotobacter vinelandii</i> AvOP	+	+	+	++	+	+	+	+	++	+
<i>Cellvibrio japonicus</i> Ueda107	+++	++	++	++	+	+	+	+	+	+

Table S17. contd....

Organisms	Signatures (Nucleotides)									
	M1	M2	M3	M4	M5	M6	M7	M8	M9	M10
Gamma-Proteobacteria										
<i>Congregibacter litoralis</i> KT71	-	+	-	-	+	-	+	-	+	+
<i>Hahella chejuensis</i> KCTC 2396	+	++	+	+	+	++	+	+	+++	+
<i>Idiomarina baltica</i> OS145	+	+	+	+	+	+	++	+	+	+
Marine Gamma proteobacterium HTCC2143	+	+	++	-	-	+	-	-	+	-
Marine Gamma proteobacterium HTCC2207	-	+	-	+	++	+	+++	++	+	++
<i>Marinobacter algicola</i> DG893	++	+	+	++++	+	+	++	+	+	+
<i>Photorhabdus luminescens</i> subsp. <i>laumondii</i> TTO1	+	+++	+	+	+	++	+	+	+	+
<i>Psychrobacter cryohalolentis</i> K5	+	-	-	-	+	-	+	+	+++	+
Actinobacteria	0	0	0	0	0	0	0	0	0	0
Bacteroidetes	0	0	0	0	0	0	0	0	0	0
Cyanobacteria										
Deionococcus-Thermus	0	0	0	0	0	0	0	0	0	0
Alpha-Proteobacteria	0	0	0	0	0	0	0	0	0	0
Beta-Proteobacteria	0	0	0	0	2	0	0	0	0	0
Frequency of occurrence within Gamma-Proteobacteria	8	11	12	8	9	8	9	14	11	10
Total frequency of occurrence	8/94	11/94	12/94	8/94	11/94	8/94	9/94	14/94	11/94	10/94

ADDITIONAL FILE 4

SIGNATURE ANALYSIS – FREQUENCY AND DISTRIBUTION PATTERN

AHL-lactonase and -acylase specific signature: The sequences of 4 to 30 data sets submitted groupwise to MEME program (<http://meme.nbcr.net/meme/meme.html>) revealed ten signatures (25-30 nucleotides, nts in length) for each species. Regular expression diagram of signatures (nucleotides) (Additional files) and the frequency of occurrence of motifs obtained through MEME for different taxonomic groups (Additional files) have been presented with reference to:

i) AHL-lactonase gene (*aiiA*) of *Bacillus* sp. SB4 GenBank [AAR85482.1](#) (Additional files 2-3):

a) Actinobacteria: Data (Figure S1 and Table S2) reveal that seven out of 10 signatures designated as M1, M3 to M6, M9 and M10 were observed to be present at high frequency among actinobacterial members. These can be considered as unique as they were absent from all other taxonomic groups. Incidentally, the order of occurrence of these signatures within the gene *aiiA* didn't follow any unique pattern.

b) Firmicutes: Data (Figure S2 and Table S3) reveal two signatures – M1 and M10 among Firmicutes to occur with highest frequencies of 25/30 and 21/30. These signatures can be considered as unique on the basis of their absence from all other taxonomic groups. The order of distribution of all the 10 signatures was almost similar (M5)-M4-M7-M1-M2-M3-M10-M4-M8-M9-M5 in the cases of *Bacillus* sp. SB4, *Bacillus* sp. 91, *Bacillus* sp. A24, *B. cereus*, *B. subtilis* strain BS1 and *B. thuringiensis* strain BCR-ZYR25. Two other *B. thuringiensis* str. Al Hakam and *B. thuringiensis* serovar israelensis ATCC 35646 have only 4/10 signatures ordered as M9-M4-M1-M2. Another distinct group possessing primarily two signatures oriented as M10-M1 was constituted of *Bacillus anthracis* str. Ames, *Bacillus weihenstephanensis* KBAB4, *Clostridium boltea* ATCC BAA-613, *Clostridium kluyveri* DSM 555, *Geobacillus* sp. WCH70 *M. thermoacetica* ATCC 39073. Signatures in similar orientation: M9-M3-M4-M7-M10-M6-M1-M8-M2-M5 were observed in all the strains of *S. aureus*: RF122, MW2, MSSA476 and Mu50.

c) γ -Proteobacteria: Data (Figure S3 and Table S4) reveals that five signatures – M1, M3, M4, M6 and M7 in genes (*aiiA*) from organisms belonging to γ -Proteobacteria occurred with a high frequency of 19/22 to 22/22. These signatures can be considered as unique on the basis of their absence from all other taxonomic groups. A screening of the regular expression diagram (Additional file 6) however, didn't reveal any pattern of occurrence of the signatures within the gene to be unique to any genera. *A. tumefaciens* and *Sagittula stellata* E-37 showed repetitiveness for M3 and M4, and *Jannaschia* sp. CCS1 had many signatures in duplicate – M1, M3, M7 and M10.

d) *_*-Proteobacteria: Data (Figure S4 and Table S5) reveals that all the 10 signatures were present in *Burkholderia* spp. and *Ralstonia* spp. Except the signatures – M2, M8 and M10, all other signatures were present exclusively among these 5 organisms of *_*-Proteobacterial group. Incidentally no correlation between the genera and the order of distribution of the signatures - M1, M3, M4, M5, M6, M7 and M9 could be established.

e) *_*-Proteobacteria: Data (Figure S5 and Table S6) reveals that signatures M2, M3, M4 and M10 were found to occur with higher frequency of 14/16 to 15/16. All the signatures were exclusive to this *_*-Proteobacterial group, since these were absent from all other taxonomic groups. High similarity in the order of occurrence of the signatures was observed largely within the genera such as *Acinetobacter*, *Xanthomonas* and *Xylella*.

f) *_*-Proteobacteria: Data (Figure S6 and Table S7) reveals that all the signatures except M4 were present in all the members of this taxonomic group and were unique, since they were not observed in any other taxonomic group. The order of occurrence of these signatures was different in all the organisms of this group.

g) Euryarchaeota: Data (Figure S7 and Table S8) reveals that all the signatures except M3 and M9 were present with a high frequency among the different members of Euryarchaeota. These can be considered as unique to this group as these could not be observed among other taxonomic groups.

h) Ascomycota: Data (Figure S8 and Table S9) reveals that all the 10 signatures were present with equal frequency and were unique to this taxonomic group. The order of occurrence of these signatures within the gene for AHL-lactonase of these organisms was almost identical except *Aspergillus oryzae* RIB40, which had signatures M1 and M3 in duplicate.

ii) AHL-acylase gene (*aiiD*) of *Ralstonia* sp. XJ12B GenBank [AAO41113.1](#) (Additional files 2-3):

a) Actinobacteria: Data (Figure S9 and Table S10) show that signatures M1 to M3, M8 and M9 were present with a high frequency of 9/9. All signatures except M1 can be considered as unique to Actinobacteria on the basis of their absence from all other taxonomic groups where as M1 was also present in organisms belonging to *_*-Proteobacteria and *_*-Proteobacteria. Visual observation of Figure (Additional file 18) reveals that there is a lot of variation in the order of occurrence of the 10 signatures. However, it can be recorded that all the signatures showed multiplicity of occurrence in the range of 2 to 4.

b) Bacteroidetes: Data (Figure S10 and Table S11) revealed that signatures – M3, M7 and M8 were present in all the organisms under consideration. Duplication of signatures was observed in 5 out of 7 organisms. No characteristic order of occurrence of signatures or their location at a give position within the gene sequence was evident. However, all the signatures can be considered as unique except M1, which was found to occur among cyanobacterial members as well.

c) Cyanobacteria: Data (Figure S11 and Table S12) revealed that signatures – M2 to M7 were present in all the organisms under consideration with a frequency of 9/9. Duplication of signatures was observed in 7 out of 9 organisms. Characteristic order of occurrence of signatures or their location at a give position within the gene sequence was evident among *Cyanothece* spp. as M4-M7-M2-(M10)-M5-M8-M1-M6-M3-M9-M10. On the other hand, similarities in order of signatures were also evident among *Nostoc*, *Microcoleus* and some *Cyanothece* strains as M6-M5-M2-M7-(M4)-M3-(M1)-M4. However, signatures can be considered as unique as these were found to occur exclusively among cyanobacteria.

d) *_*-Proteobacteria: Data (Figure S12 and Table S13) show that signatures – M1, M7, M9 and M10 occurred with high frequency of 7/8 to 8/8. All the signatures were found to be present only with the members of *_*-Proteobacteria, hence may be considered as unique. There was no unique order of occurrence of signatures which could be correlated to any genera or species. All the signatures were present as repeats in at least one of the organisms and each organism had at least one of the signatures as duplicated.

e) *_*-Proteobacteria: Data (Figure S13 and Table S14) show that almost all the signatures were present at high frequency of 6/8 to 7/8. Due their absence from other taxonomic groups, we may consider them as unique to *_*-Proteobacterial members. Out of the 10 signatures, at least one of them was found to be present as multiple repeats and each of the organisms had at least one of the signatures in repeat form. We could not draw any co-relation between the order of occurrence of the signatures and the organisms possessing them, primarily because of their high repetition with the gene.

f) *_*-Proteobacteria: As this group of organisms was quite large we have presented the organisms in three categories (to suit to the criteria of MEME procedures - See Methods for justifications): i) *Pseudomonas* spp. (Figure S14 and Table S15) show, ii) *Shewanella* spp. (Additional files 30,31) show and iii) others members of *_*-Proteobacterial group (Figure S15 and Table S16).

i) For *Pseudomonas* spp. (Figure S14 and Table S15) signatures M1 to M10 occurred with a high frequency of 19/21 to 20/21. Except signature M4, none of the signatures were found in any other member of *_*-Proteobacteria or any other taxonomical group, which may thus be called as unique to *Pseudomonas* spp. Signatures M1 and M8 were found to be absent only from the two strains of *Pseudomonas putida* - F1 and GB-1.

ii) For *Shewanella* spp. (Figure S15 and Table S16), signatures M1 to M10 occurred with a high frequency of 11/12 to 12/12. *Shewanella woodyi* ATCC 51908 was the only organism which lacked signatures M4, M5, M8 and M9. The signatures observed here were absent among all other members of *_*-Proteobacteria or any other taxonomical group, which may thus be called as unique to *Shewanella* spp. No clear cut co-relation could be drawn between the order of occurrence of the signatures and the organisms possessing them.

iii) For *_*-Proteobacterial members other than *Pseudomonas* spp. and *Shewanella* spp. The information on the occurrence of signature (Figure S16 and Table S17) shows that the overall frequency of signatures was low which may be because of high diversity of organisms in this “category”. Signatures M3 and M8 occurred with a relatively high frequency of 12/16 to 14/16. Signatures M1, M6, M7, M9 and M10 were found to be present only among the organisms under consideration. We could not draw any clear cut co-relation between the order of occurrence of the signatures and the organisms possessing them. *Alteromonas macleodii* 'Deep ecotype' was unique as it possessed only three signatures – M8, M9 and M10.

ADDITIONAL FILE 5

Organism	Gi. Number	Signature (Nucleotide) No.							
		M1	M2	M3	M4	M6	M7	M9	M10
<i>Pseudomonas</i> sp. THA1	gi 31979172 gb AY311487.1	■		■			■	■	■
<i>Pseudomonas</i> sp. THA2	gi 31979174 gb AY311488.1	■	■	■	■		■		■
<i>Pseudomonas</i> sp. THA3	gi 31979176 gb AY311489.1	■	■	■	■		■	■	■
<i>Pseudomonas</i> sp. 130	gi 11386616:104-2266	■	■	■	■		■	■	■
<i>Pseudomonas</i> sp. GK16	gi 145284384:101-2263	■	■		■			■	■
<i>Pseudomonas aeruginosa</i> PA01	gi 110645304:2636517-2638805	■	■		■	■	■	■	■
<i>Pseudomonas aeruginosa</i> C3719	gi 194545151:1435593-1437881	■	■	■	■	■	■	■	■
<i>Pseudomonas aeruginosa</i> PACS2	gi 107098994:3213673-3215961	■	■	■	■	■	■	■	■
<i>Pseudomonas aeruginosa</i> 2192	gi 194550373:1644376-1646664	■	■		■	■	■	■	■
<i>Pseudomonas aeruginosa</i> UCBCPP-PA14	gi 116048575:3004988-3007276	■		■				■	■
<i>Pseudomonas aeruginosa</i> PA7	gi 152983466:2955521-2957803	■		■				■	■

Fig. (S17). Signatures of AHL-acylase gene in *Pseudomonas* spp. Figure showing Similarity of signatures of gene (aaiD) for AHL-acylase of *Pseudomonas* spp.

ADDITIONAL FILE 6

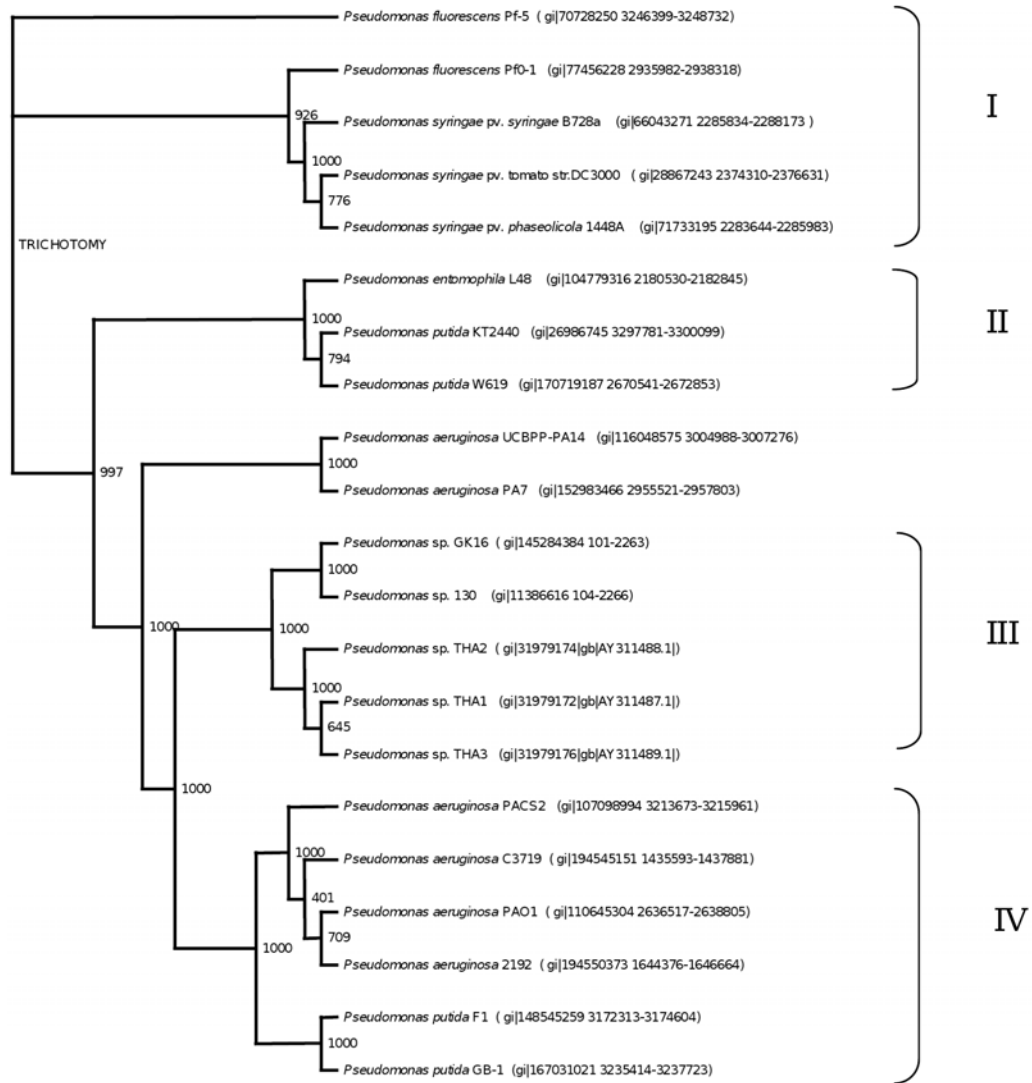


Fig. (S18a). Phylogenetic tree based on AHL-acylase gene. Figure showing Phylogenetic trees based on full length sequences of gene (aiiD) for AHL-acylase of *Pseudomonas* spp.

ADDITIONAL FILE 7

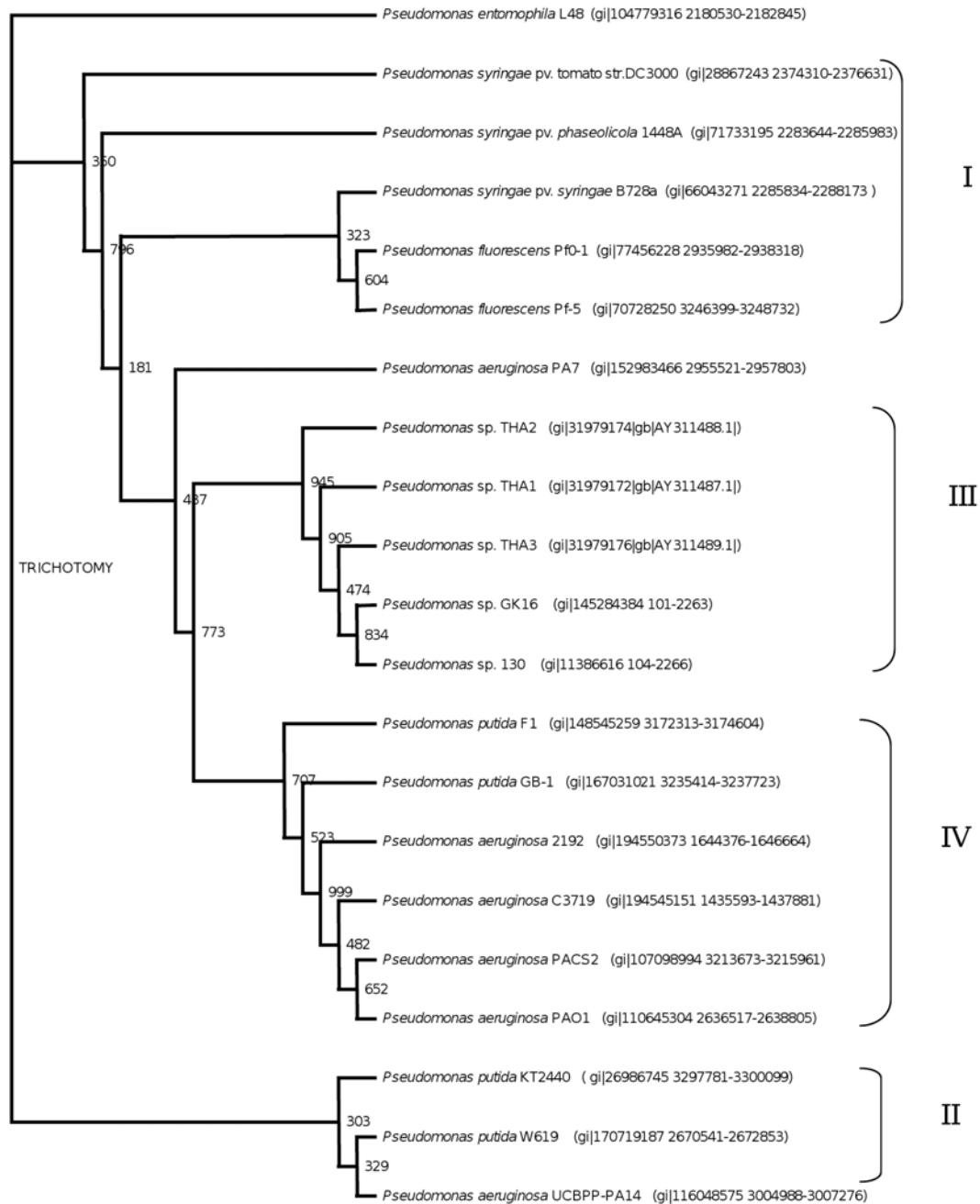


Fig. (S18b). Phylogenetic tree based on regular expressions of AHL-acylase gene: Figure showing Phylogenetic trees based on regular expressions of signatures of gene (aiiD) for AHL-acylase of *Pseudomonas* spp.