

APPENDICES

Appendix 2.1. Genetic sequence and the list of possible bacteria isolated in this study:

The software BLAST (2.2.14) was developed by Altschul *et al.*, (2006). This software gives the maximum possible matching taxonomic name of genome, indicating Bits and Value. The Bit scores subsume the statistical essence of the scoring system employed, so that to calculate significance one needs to know in addition only the size of the search space. The Expected value (E) is a parameter that describes the number of hits one can expect to see just by chance when searching a database of a particular size. It decreases exponentially the score that is assigned to a match between two sequences. Essentially, the E value describes the random background noise that exists for matches between sequences. The lower the E-value, or the closer it is to “0” the more “significant” the match is. For FA001, FA009 and FA010, reverse complement sequences are presented while for FA002, FA003, FA004 and FA005 forward sequences are presented, because these sequences were clear and consistent.

Appendix 2.1a. Genetic sequence of FA001 and the possible matching bacteria

3 Reverse complement sequence:

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GGCAGAGATGCCTTAGTGCCTTCGGGAACCGTGAGACAGGTGCTGCATGGCTGTC
GTCAGCTCGTGTTGTGAAATGTTGGGTAAAGTCCCGCAACGAGCGCAACCCCTTAT
CCTTTGTTGCCAGCGATTTCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACC
GGAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAGGGCTACA
CACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGAC
CTCATAAAGTGCGTCGTAGTCCGG
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Sequence producing significant alignment of top twenty strains:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
EF178449.1	Pantoea ananatis strain 3Pe76 16S ribosomal RNA gene, partial sequence	589	589	100%	2e-165	100%
EF094239.1	Uncultured bacterium clone Ms-R128 16S ribosomal RNA gene, partial sequence	589	589	100%	2e-165	100%
AY741162.1	Pantoea agglomerans strain S33 16S ribosomal RNA gene, partial sequence	589	589	100%	2e-165	100%
DQ517335.1	Pantoea ananatis 16S ribosomal RNA gene, partial sequence	589	589	100%	2e-165	100%

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Accession	Description	Max score	Total score	Query coverage	E value	Max ident
DQ195525.1	Pantoea ananatis strain BD 647 16S ribosomal RNA gene, partial sequence	589	589	100%	2e- 165	100%
DQ195522.1	Pantoea ananatis strain BD 602 16S ribosomal RNA gene, partial sequence	589	589	100%	2e- 165	100%
AY538694.1	Enterobacteriaceae bacterium Smarlab 3302238 16S ribosomal RNA gene, partial sequence	589	589	100%	2e- 165	100%
AY579210.1	Pantoea sp. BD 309 16S ribosomal RNA gene, partial sequence	589	589	100%	2e- 165	100%
AY530794.1	Pantoea sp. BD 336 16S ribosomal RNA gene, partial sequence	589	589	100%	2e- 165	100%
DQ133546.1	Pantoea ananatis strain BD 561 16S ribosomal RNA gene, partial sequence	589	589	100%	2e- 165	100%
DQ512490.1	Pantoea ananatis strain BD 333 16S ribosomal RNA gene, partial sequence	587	587	99%	9e- 165	100%
AY994300.1	Pantoea sp. ER 16S ribosomal RNA gene, partial sequence	587	587	99%	9e- 165	100%
AY489080.1	Soybean endophytic bacterium EN108 16S ribosomal RNA gene, partial sequence	583	583	100%	1e- 163	99%
AM489623.1	Pantoea sp. Esch5-61 partial 16S rRNA gene, strain Esch5- 61	581	581	100%	6e- 163	99%
EF094449.1	Uncultured bacterium clone Sf- A557 16S ribosomal RNA gene, partial sequence	581	581	100%	6e- 163	99%
EF050810.1	Pantoea agglomerans strain PGHL6 16S ribosomal RNA gene, partial sequence	581	581	100%	6e- 163	99%
EF050806.1	Pantoea agglomerans strain PGHLT4 16S ribosomal RNA gene, partial sequence	581	581	100%	6e- 163	99%
DQ068765.1	Pantoea sp. Co9926 16S ribosomal RNA gene, partial sequence	581	581	100%	6e- 163	99%
DQ068761.1	Pantoea sp. Co9927 16S ribosomal RNA gene, partial sequence	581	581	100%	6e- 163	99%

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Accession	Description	Max score	Total score	Query coverage	E value	Max ident
DQ881487.1	Uncultured bacterium clone Ms-B2 16S ribosomal RNA gene, partial sequence	581	581	100%	6e-163	99%

Appendix 2.1b. Genetic sequence of FA002 and the possible matching bacteria

1 Forward sequence:

TGGGAACTGCATTCGAAACTGGCAGGCTAGAGTCTTGTAGAGGGGGGTAGAATT
 CCAGGTGTAGCGGTGAAATGCGTAGAGATCTGGAGGAATACCGGTGGCGAAGGC
 GGCCCCCTGGACAAAGACTGACGCTCAGGTGCGAAAGCGTGGGGA GCAAACAGG
 ATTAGATACCCTGGTAGTCCACGCCGTAAACGATGTCGACTTGGAGGTTGTGCC
 TTGAGGC GTGGCTTCCGGA GCTAACGCGTTAAGTCGACCGCCTGGGGAGTACGGC
 CGCAAGGTTAAA ACTCAAATGAAATTGACGGGGGCCCGCACAAGCGGTGGAGCAT
 GTGGTTTAATTCGATGCAACGCGAAGAACCTTACCTACTCTTGACATCCAGAGAA
 CTTAGCAGAGATGCTTTGGTGCCTTCGGGA ACTCTGAGACAGGTGCTGCATGGCT
 GTCGTCAGCTCGTGTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCT
 TATCCTTTGTTGCCAGCGGTCCGGCCGGGA ACTCAAAGGAGACTGCCA

Sequence producing significant alignment of top twenty strains:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
EF523432.1	Pantoea agglomerans strain IGCAR-18/07 16S ribosomal RNA gene, partial sequence	1068	1515	100%	0.0	100%
EF469213.1	Pantoea sp. KF20 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AM491469.1	Enterobacter sp. Nj-68 16S rRNA gene, strain Nj-68	1068	1068	100%	0.0	100%
EF402397.1	Uncultured bacterium clone SJTU_B_07_39 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
EF375795.1	Uncultured bacterium clone H214 16S small subunit ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
EF375792.1	Uncultured bacterium clone H179 16S small subunit ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
DQ988944.1	Bacterium CCBAU 15570 16S ribosomal RNA gene, partial	1068	1068	100%	0.0	100%

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Accession	Description	Max score	Total score	Query coverage	E value	Max ident
	sequence					
DQ865061.1	Pantoea sp. BAC-C2 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AM184264.1	Pantoea agglomerans partial 16S rRNA gene, strain WAB1925	1068	1068	100%	0.0	100%
DQ202394.1	Enterobacter cloacae strain B5 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376707.1	Uncultured bacterium clone O39 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376706.1	Uncultured bacterium clone N31 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376705.1	Uncultured bacterium clone O6 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376704.1	Uncultured bacterium clone N2 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376703.1	Uncultured bacterium clone P23 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376702.1	Uncultured bacterium clone O3 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376700.1	Uncultured bacterium clone P41 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376698.1	Uncultured bacterium clone N8 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376697.1	Uncultured bacterium clone N7 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%
AY376696.1	Uncultured bacterium clone M29 16S ribosomal RNA gene, partial sequence	1068	1068	100%	0.0	100%

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Appendix 2.1c. Genetic sequence of FA003 and the possible matching bacteria

1 Forward sequence:

GCCAATACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATTAGATACC
CTGGTAGTCCACGCCCTAAACGATGTCAACTGGTTGTCGGGCCTTCATTGGCTTG
GTAACGTANCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTC

Sequence producing significant alignment of top twenty strains:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
EF516276.1	Uncultured bacterium clone FCPU448 16S ribosomal RNA gene, complete sequence	299	299	100%	1e-78	99%
EF490654.1	Uncultured Burkholderia sp. isolate DGGE band 24-0,5DN3- 4 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF443944.1	Uncultured bacterium clone LSC_031 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF139184.1	Burkholderia sp. TNe-862 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF072735.1	Uncultured Burkholderia sp. clone GASP-WA2S3_C11 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF075912.1	Uncultured Burkholderia sp. clone GASP-WDOW3_E10 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF075866.1	Uncultured Burkholderia sp. clone GASP-WDOW3_A10 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF075836.1	Uncultured Burkholderia sp. clone GASP-WDOW2_A05 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF075488.1	Uncultured Burkholderia sp. clone GASP-WDOS1_G04 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF074046.1	Uncultured Burkholderia sp. clone GASP-WB2S3_D09 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF073647.1	Uncultured Burkholderia sp.	299	299	100%	1e-78	99%

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Accession	Description	Max score	Total score	Query coverage	E value	Max ident
	clone GASP-WB1W2_A07 16S ribosomal RNA gene, partial sequence					
DQ447833.1	Uncultured bacterium clone MSFC_4M1E 16S ribosomal RNA gene, complete sequence	299	299	100%	1e-78	99%
DQ665822.1	Burkholderia sp. NGR190 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
AM284972.1	Burkholderia nodosa 16S rRNA gene, isolate R-25486	299	299	100%	1e-78	99%
AM284970.1	Burkholderia nodosa 16S rRNA gene, isolate R-22632	299	299	100%	1e-78	99%
DQ514537.1	Burkholderia ferrariae strain FeGI01 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
AB212237.1	Burkholderia sp. M701 gene for 16S ribosomal RNA, partial sequence	299	299	100%	1e-78	99%
AY773198.1	Burkholderia sp. BR3470 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
AY773197.1	Burkholderia sp. Br3469 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
AY773196.1	Burkholderia sp. BR3467 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%

Appendix 2.1d. Genetic sequence of FA004 and the possible matching bacteria

1 Forward sequence:

TAACCTGGGAACTGCATTTGTGACTGGCGGGCTAGAGTATGGCAGAGGGGGGTA
GAATTCCACGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAATACCGATGGCG
AAGGCAGCCCCCTGGGCAATACTGACGCTCATGCACGAAAGCGTGGGGAGCAA
ACAGGATTAGATACCCTGGTAGTCCACGCCCTAAACGATGTCAACTGGTTGTCCG
GCCTTCATTGGCTTGTTAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGA GTA
CGGTCGCAAGATTA AAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGA
TGATGTGGATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGTAC
GGAAGTCCGCTGA GAGGTGGATGTGCCCCGAAAGGGAGCCGTAACACAGGTGCTG
CATGGCTGTCTCAGCTCGTGTCTGTGAGATGTTGGGTAAAGTCCCGCAACGAGCG
CAACCCTTGTCCTAGTTGCTACGCAAGAGCACTCCAGGGAGACTGCCGGTGACA
AACCGGAGGAAGGTGGGGATGACGTCAAGTCTCATGGCCCTTATGGGTAGGGC
TTCACACGTCATACA

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Sequence producing significant alignment of top twenty strains:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
EF516276.1	Uncultured bacterium clone FCPU448 16S ribosomal RNA gene, complete sequence	299	299	100%	1e-78	99%
EF490654.1	Uncultured Burkholderia sp. isolate DGGE band 24-0,5DN3- 4 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF443944.1	Uncultured bacterium clone LSC_031 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF139184.1	Burkholderia sp. TNe-862 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF072735.1	Uncultured Burkholderia sp. clone GASP-WA2S3_C11 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF075912.1	Uncultured Burkholderia sp. clone GASP-WDOW3_E10 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF075866.1	Uncultured Burkholderia sp. clone GASP-WDOW3_A10 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF075836.1	Uncultured Burkholderia sp. clone GASP-WDOW2_A05 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF075488.1	Uncultured Burkholderia sp. clone GASP-WDOS1_G04 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF074046.1	Uncultured Burkholderia sp. clone GASP-WB2S3_D09 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
EF073647.1	Uncultured Burkholderia sp. clone GASP-WB1W2_A07 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
DQ447833.1	Uncultured bacterium clone MSFC_4M1E 16S ribosomal RNA gene, complete sequence	299	299	100%	1e-78	99%

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Accession	Description	Max score	Total score	Query coverage	E value	Max ident
DQ665822.1	Burkholderia sp. NGR190 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
AM284972.1	Burkholderia nodosa 16S rRNA gene, isolate R-25486	299	299	100%	1e-78	99%
AM284970.1	Burkholderia nodosa 16S rRNA gene, isolate R-22632	299	299	100%	1e-78	99%
DQ514537.1	Burkholderia ferrariae strain FeGI01 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
AB212237.1	Burkholderia sp. M701 gene for 16S ribosomal RNA, partial sequence	299	299	100%	1e-78	99%
AY773198.1	Burkholderia sp. BR3470 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
AY773197.1	Burkholderia sp. Br3469 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%
AY773196.1	Burkholderia sp. BR3467 16S ribosomal RNA gene, partial sequence	299	299	100%	1e-78	99%

Appendix 2.1e. Genetic sequence of FA005 and the possible matching bacteria

1 Forward sequence:

GAACTGCATTTGTGACTGGCGGGCTAGAGTATGGCAGAGGGGGGTAGAATTCCA
 CGTGTAGCAGTGAAATGCGTAGAGATGTGGAGGAATACCGATGGCGAAGGCAGC
 CCCCTGGGCCAATACTGACGCTCATGCACGAAAGCGTGGGGAGCAAACAGGATT
 AGATACCCTGGTAGTCCACGCCCTAACGATGTCAACTGGTTGTCGGGCCTTCAT
 TGGCTTGGTAAACGTAGCTAACGCGTGAAGTTGACCGCCTGGGGAGTACGGTCGCA
 AGATTA AAACTCAAAGGAATTGACGGGGACCCGCACAAGCGGTGGATGATGTGG
 ATTAATTCGATGCAACGCGAAAAACCTTACCTACCCTTGACATGTACGGAAGTCC
 GCTGAGAGGTGGATGTGCCCCGAAAGGGAGCCGTAACACAGGTGCTGCATGGCTG
 TCGTCAGCTCGTGTGCTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTT
 GTCCTAGTTGCTACGCAAGAGCACTCCA

Sequence producing significant alignment of top twenty strains:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
EF516276.1	Uncultured bacterium clone FCPU448 16S ribosomal RNA gene, complete sequence	1029	1029	100%	0.0	100%
AF408980.1	Burkholderia sp. Ellin138 16S ribosomal RNA gene, partial	1029	1029	100%	0.0	100%

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Accession	Description	Max score	Total score	Query coverage	E value	Max ident
	sequence					
DQ156089.1	Burkholderia sp. mpa7.4 16S ribosomal RNA gene, partial sequence	1029	1029	100%	0.0	100%
AY238504.1	Burkholderia sp. 54 16S ribosomal RNA gene, partial sequence	1029	1029	100%	0.0	100%
U96941.1	Burkholderia graminis 16S ribosomal RNA gene, partial sequence	1029	1029	100%	0.0	100%
U96940.1	Burkholderia graminis 16S ribosomal RNA gene, partial sequence	1029	1029	100%	0.0	100%
U96939.1	Burkholderia graminis 16S ribosomal RNA gene, partial sequence	1029	1029	100%	0.0	100%
AF247493.1	Burkholderia sp. C4.7 16S ribosomal RNA gene, partial sequence	1021	1021	100%	0.0	99%
AF448046.1	Burkholderia sp. SOD-7 16S ribosomal RNA gene, partial sequence	1015	1015	100%	0.0	99%
U91570.1	Burkholderia caryophylli 16S ribosomal RNA gene, partial sequence	1007	1007	100%	0.0	99%
AY741358.1	Burkholderia cepacia strain ATCC 55487 16S ribosomal RNA gene, partial sequence	989	989	100%	0.0	99%
AY178062.1	Burkholderia sp. UCT 29 16S ribosomal RNA gene, partial sequence	989	989	100%	0.0	99%
DQ378168.1	Uncultured beta proteobacterium clone F02_Pitesti 16S ribosomal RNA gene, complete sequence	989	989	100%	0.0	99%
AF448045.1	Burkholderia sp. SOD-6 16S ribosomal RNA gene, partial sequence	989	989	100%	0.0	99%
EF467847.1	Burkholderia xenovorans strain B2-5 16S ribosomal RNA gene, partial sequence	981	981	100%	0.0	98%
EF149008.1	Burkholderia sp. CCBAU 11189 16S ribosomal RNA gene, partial sequence	981	981	100%	0.0	98%
EF139188.1	Burkholderia xenovorans strain TCo-26 16S ribosomal RNA	981	981	100%	0.0	98%

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Accession	Description	Max score	Total score	Query coverage	E value	Max ident
	gene, partial sequence					
CP000271.1	Burkholderia xenovorans LB400 chromosome 2, complete sequence	981	2945	100%	0.0	98%
CP000270.1	Burkholderia xenovorans LB400 chromosome 1, complete sequence	981	2945	100%	0.0	98%
AY367011.1	Burkholderia sp. Ch1-1 16S ribosomal RNA gene, partial sequence	981	981	100%	0.0	98%

Appendix 2.1 f. Genetic sequence of FA009 and the possible matching bacteria

3 reverse sequence:

CGCCTGGGGAGTACGGTCGCAAGACTGAAACTCAAAGGAATTGACGGGGGCCCG
 CACAAGCGGTGGAGCATGTGGTTTAATTNGAAGCAACGCGAAGAACCTTACCAG
 GTCTTGACATCCTCTGACAATCCTAGAGATAGGACGTCCCTTCGGGGGCAGAGT
 GACAGGTGGTGCATGGTTGTCGTGACGCTCGTGTCGTGAGATGTTGGGTAAAGTCC
 CGCAACGAGCGCAACCCTTGATCTTAGTTGCCAGCATTTCAGTTGGGCACTCTAAG
 GTGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGC
 CCCTTATGACCTGGGCTACACACGTGCTACAATGGACAGAACAAAGGGCAGCGA
 AACCGCGAGGTTAAGCCAATCCCACAAATCTGTTCTCAGTTCGGATCGCAGTCTG
 CAACTCGACTGCGTGAAGCNGGAATCGCTAGTAATCGCG

Sequence producing significant alignment of top twenty strains:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
DQ378200.1	Uncultured soil bacterium clone F38_Pitesti 16S ribosomal RNA gene, complete sequence	1277	1277	100%	0.0	99%
AB232337.1	Burkholderia sp. TFA1 gene for 16S rRNA	1269	1269	100%	0.0	99%
AB232331.1	Burkholderia sp. KFA2 gene for 16S rRNA	1269	1269	100%	0.0	99%
AB118226.1	Burkholderia sp. PAMU-2.6 gene for 16S rRNA, partial sequence	1269	1269	100%	0.0	99%
AB191222.1	Uncultured Burkholderia sp. gene for 16S rRNA, partial sequence, clone:IB2	1269	1269	100%	0.0	99%
AB191214.1	Uncultured Burkholderia sp. gene for 16S rRNA, partial	1269	1269	100%	0.0	99%

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Accession	Description	Max score	Total score	Query coverage	E value	Max ident
	sequence, clone:NR					
AF247496.1	Burkholderia sp. S4.9 16S ribosomal RNA gene, partial sequence	1269	1269	100%	0.0	99%
AB191212.1	Uncultured Burkholderia sp. gene for 16S rRNA, partial sequence, clone:GN	1261	1261	100%	0.0	99%
AB191213.1	Uncultured Burkholderia sp. gene for 16S rRNA, partial sequence, clone:KY	1253	1253	100%	0.0	99%
AB232338.1	Burkholderia sp. TFA2 gene for 16S rRNA	1249	1249	100%	0.0	99%
AB266607.1	Burkholderia sp. KU-25 gene for 16S rRNA, partial sequence	1245	1245	100%	0.0	99%
DQ986324.1	Burkholderia sp. SJ98 16S ribosomal RNA gene, partial sequence	1245	1245	100%	0.0	99%
AB232336.1	Burkholderia sp. SFA4 gene for 16S rRNA	1245	1245	100%	0.0	99%
AB191229.1	Uncultured Burkholderia sp. gene for 16S rRNA, partial sequence, clone:KM(type2)	1245	1245	100%	0.0	99%
AB191228.1	Uncultured Burkholderia sp. gene for 16S rRNA, partial sequence, clone:KM(type1)	1245	1245	100%	0.0	99%
AB191226.1	Uncultured Burkholderia sp. gene for 16S rRNA, partial sequence, clone:NR	1245	1245	100%	0.0	99%
DQ139841.1	Burkholderia sp. IIPNQ1 16S ribosomal RNA gene, partial sequence	1237	1237	100%	0.0	99%
AY238505.1	Burkholderia sp. 13 16S ribosomal RNA gene, partial sequence	1237	1237	100%	0.0	99%
AB191224.1	Uncultured Burkholderia sp. gene for 16S rRNA, partial sequence, clone:CB	1237	1237	100%	0.0	99%
AB191209.1	Uncultured Burkholderia sp. gene for 16S rRNA, partial sequence, clone:IB1	1237	1237	100%	0.0	99%

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Appendix 2.1g. Genetic sequence of FA010 and the possible matching bacteria

Reverse 3 sequence:

CCAGAGATGGATTGGTGCCTTCGGGAACGCTGAGACAGGTGCTGCATGGCTGTCTG
TCAGCTCGTGTGTGAAATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATC
CTTTGTTGCCAGCGATTCCGGTCGGGAACTCAAAGGAGACTGCCGGTGATAAACCG
GAGGAAGGTGGGGATGACGTCAAGTCATCATGGCCCTTACGAGTAGGGCTACAC
ACGTGCTACAATGGCGCATACAAAGAGAAGCGACCTCGCGAGAGCAAGCGGACC
TCACAAAGTGCCTCGTAGTCCGGATCGGAGTCTGCACTCGACTCCGTGAAGTCGG
AATCGCT

Sequence producing significant alignment of top twenty strains:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
EF050808.1	Pantoea agglomerans strain PGHL1 16S ribosomal RNA gene, partial sequence	1225	1225	100%	0.0	99%
EF050807.1	Pantoea agglomerans strain PGHL22 16S ribosomal RNA gene, partial sequence	1225	1225	100%	0.0	99%
EF061906.1	Pantoea sp. M60-1 16S ribosomal RNA gene, partial sequence	1225	1225	100%	0.0	99%
EF061905.1	Enterobacte sp. M208-1 16S ribosomal RNA gene, partial sequence	1225	1225	100%	0.0	99%
AY942953.1	Uncultured Pantoea sp. clone 25 16S ribosomal RNA gene, partial sequence	1225	1225	100%	0.0	99%
AF130954.1	Erwinia herbicola 16S ribosomal RNA, partial sequence	1225	1225	100%	0.0	99%
AF130948.1	Enterobacter agglomerans strain A84 16S ribosomal RNA, partial sequence	1225	1225	100%	0.0	99%
AF130947.1	Enterobacter agglomerans strain A83 16S ribosomal RNA, partial sequence	1225	1225	100%	0.0	99%
AF130928.1	Enterobacter agglomerans strain A58 16S ribosomal RNA, partial sequence	1225	1225	100%	0.0	99%
AF130913.1	Enterobacter agglomerans strain A41 16S ribosomal RNA, partial sequence	1225	1225	100%	0.0	99%
AF130896.1	Enterobacter agglomerans	1225	1225	100%	0.0	99%

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Accession	Description	Max score	Total score	Query coverage	E value	Max ident
	strain A17 16S ribosomal RNA, partial sequence					
AF130887.1	Enterobacter agglomerans strain A20 16S ribosomal RNA, partial sequence	1225	1225	100%	0.0	99%
AF130916.1	Pantoea agglomerans strain new*45con 16S ribosomal RNA gene, partial sequence	1221	1221	100%	0.0	99%
U80202.1	Erwinia herbicola 16S ribosomal RNA gene, partial sequence	1217	1217	100%	0.0	99%
AF130953.1	Pantoea agglomerans strain ATCC 27155 16S ribosomal RNA gene, partial sequence	1213	1213	100%	0.0	98%
AF130945.1	Enterobacter agglomerans strain A80 16S ribosomal RNA, partial sequence	1211	1211	100%	0.0	99%
AF130886.1	Enterobacter agglomerans strain A126 16S ribosomal RNA, partial sequence	1211	1211	100%	0.0	99%
AY173021.1	Pantoea ananatis strain BCC0105 16S ribosomal RNA gene, partial sequence	1209	1209	100%	0.0	99%
AY173020.1	Pantoea ananatis strain BCC0107 16S ribosomal RNA gene, partial sequence	1209	1209	100%	0.0	99%
AY642383.1	Pantoea stewartii subsp. stewartii strain 0028 16S ribosomal RNA gene, partial sequence	1209	1209	100%	0.0	99%

APPENDICES

Appendix 2.2.

Appendix 2.2a. 2005. API 20E: Identification system for Enterobacteriaceae and other Gram-negative rods.

Appendix 2.2b. 2005. API 20NE: Identification system for non-fastidious, non-enteric Gram-negative rods.

Appendix 3.1. Majoor, F., 2005. Capillary HPLC columns, *Phenomenex, HPLC. GC.SPE:272-273.*

Appendix 4.1. <http://www.fatcow.com.au/Companies/Becker-Underwood-Australia>.