APPENDICES

APPENDIX A

STANDARD CURVE OF SUBSTRATE FOR ENZYME AZZAY

Standard Curve of Glucose

1. Stock solution of glucose was prepared by weighting 0.10 g of glucose to a 100 mL volumetric flask and diluting it to the volume with deionized water.
2. To prepare a glucose standard corresponding to a concentration of 0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9 and 1.0 mg L^{-1}, exactly pipette 0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6, 0.7, 0.8, 0.9 and 1.0 mL of the glucose solution stock to a 1 mL volumetric flasks, respectively and dilute to the volume with deionized water.
3. Add 2.0 mL of DNS-reagent into each tube and then put them in the boiling water for 15 min.
4. Add 1.0 mL of 40 % Na-K tartrate into each tube at once and then they were cooled down in room temperature.
5. The solutions were measured the absorbances at 540 nm. The results were shown in Table A1. These results were plotted as a standard curve of glucose (Figure A1).

Table A1 Concentrations of glucose and absorbance values at 540 nm

Standard no.	1	2	3	4	5	6	7	8	9	10	11
Glucose (mg L^{-1})	0.0	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	1.0
OD$_{540}$	0.000	0.189	0.460	0.745	1.021	1.249	1.510	1.765	1.969	2.160	2.348

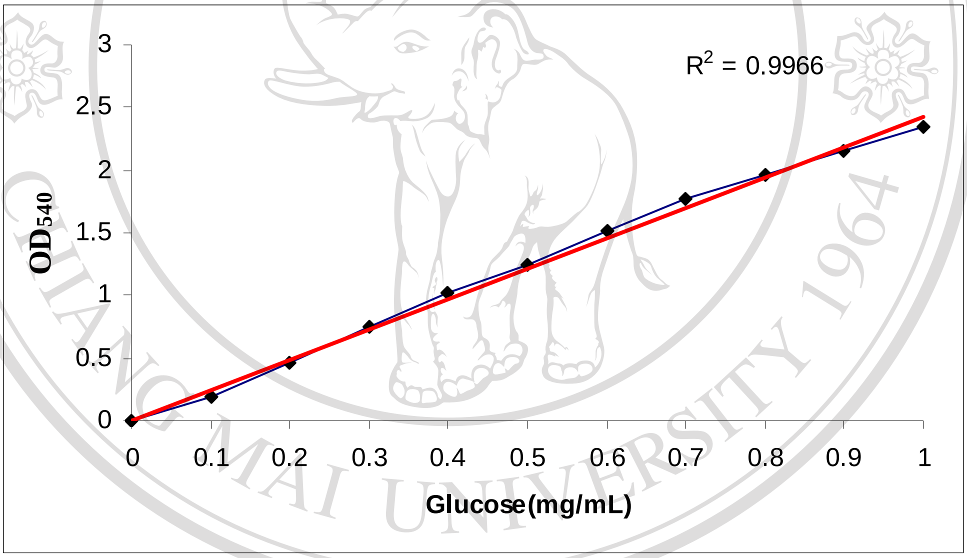

Figure A1 Glucose standard curve

Standard Curve of Protein

1. Stock solution of bovine serum albumin (BSA) was prepared by weighting 0.10 g of BSA to a 10 mL volumetric flask and diluting it to the volume with deionized water
2. To prepare a BSA standard corresponding to a concentration of 0, 50, 100, 150, 200, 250, 300 and 350 mg L^{-1}, exactly pipette 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5 and 4.0 mL of the BSA solution stock to a 10 mL volumetric flasks, respectively and dilute to the volume with deionized water.
3. The solutions were measured the absorbances at 440 nm. The results were shown in Table A2. These results were plotted as standard curve of protein (Figure A2).

Table A2 Concentrations of Bovine serum albumin and absorbance values at 440 nm

Standard no.	1	2	3	4	5	6	7	8	9
BSA (mg L^{-1})	0	50	100	150	200	250	300	350	400
OD_{440}	0	0.110	0.181	0.254	0.341	0.401	0.491	0.552	0.614

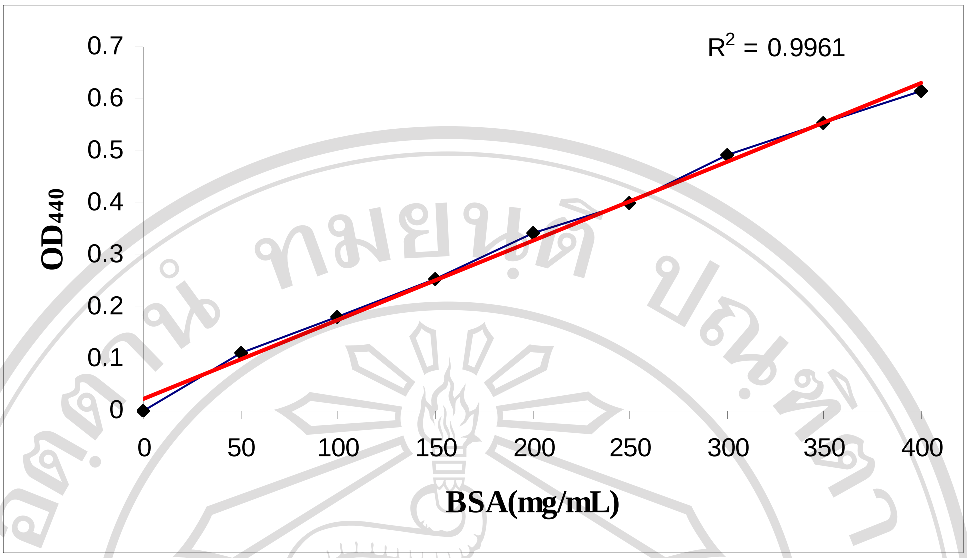

Figure A2 Protein standard curve

Standard Curve of Lipid

1. Stock solution of *p*-nitrophenol(*p*-NP) was prepared by weighting 10 mg of *p*-nitrophenol to a 100 mL volumetric flask and diluting it to the volume with 0.1 M Tris-HCl, pH 6.0.
2. To prepare a *p*-NP standard corresponding to a concentration of 0, 20, 40, 60, 80 and 100 mg L^{-1}, exactly pipette and 0.2, 0.4, 0.6, 0.8, and 1.0 mL of the *p*-NP solution stock to a 1 mL volumetric flasks, respectively and dilute to the volume with 0.1 M Tris-HCl, pH 6.0
3. Add 800 μL of 1 M Na_2CO_3 into each tube.
4. The solutions were measured the absorbances at 410 nm. The results were shown in Table A3. These results were plotted as a standard curve of lipid (Figure A3).

Table A3 Concentrations of p-nitrophenol and absorbance values at 410 nm

Standard no.	1	2	3	4	5	6
***p*-nitrophenol (mg L^{-1})**	0	20	40	60	80	100
OD_{410}	0	0.150	0.290	0.431	0.598	0.745

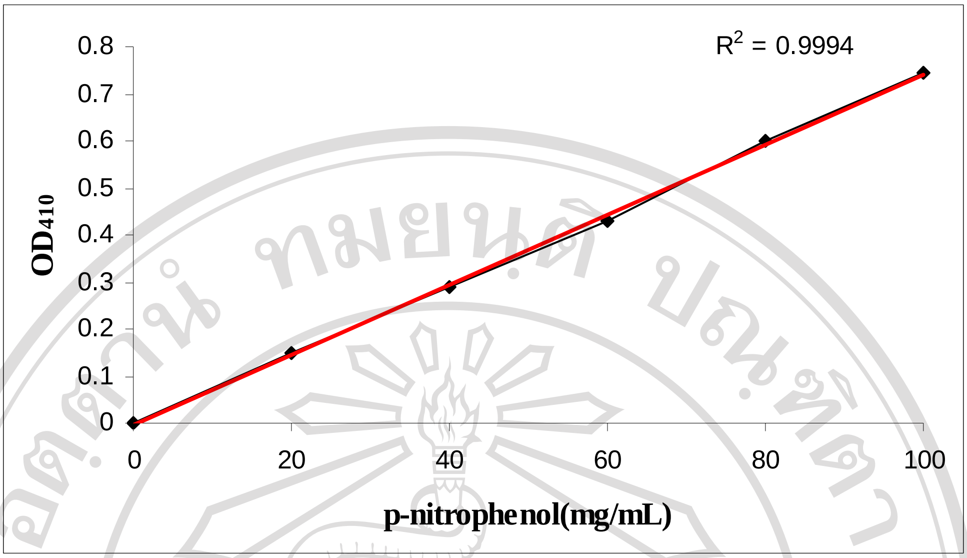

Figure A3 Lipid standard curve

APPENDIX B

DNA SEQUENCING

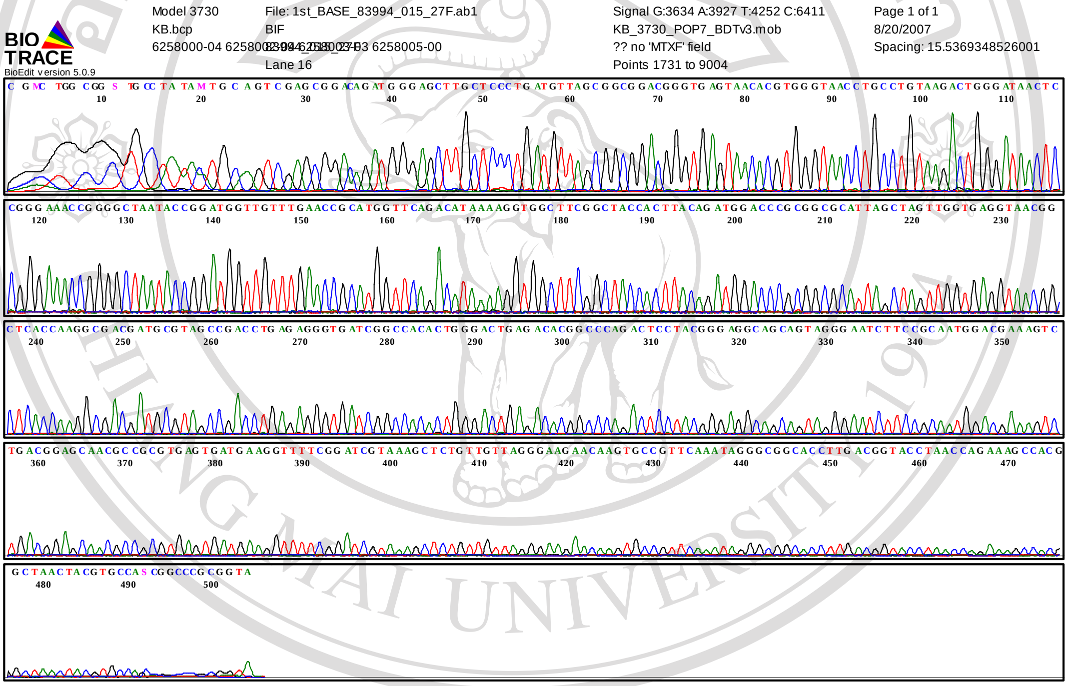

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Figure B1 The 16S rRNA sequence from primer 27F of bacterium isolate GB 12

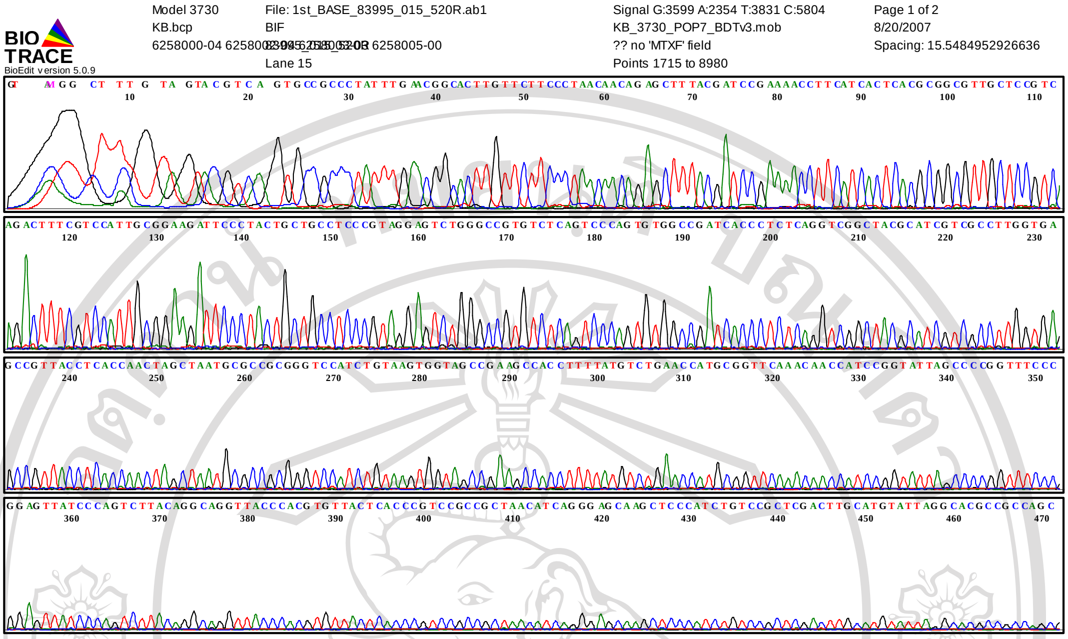

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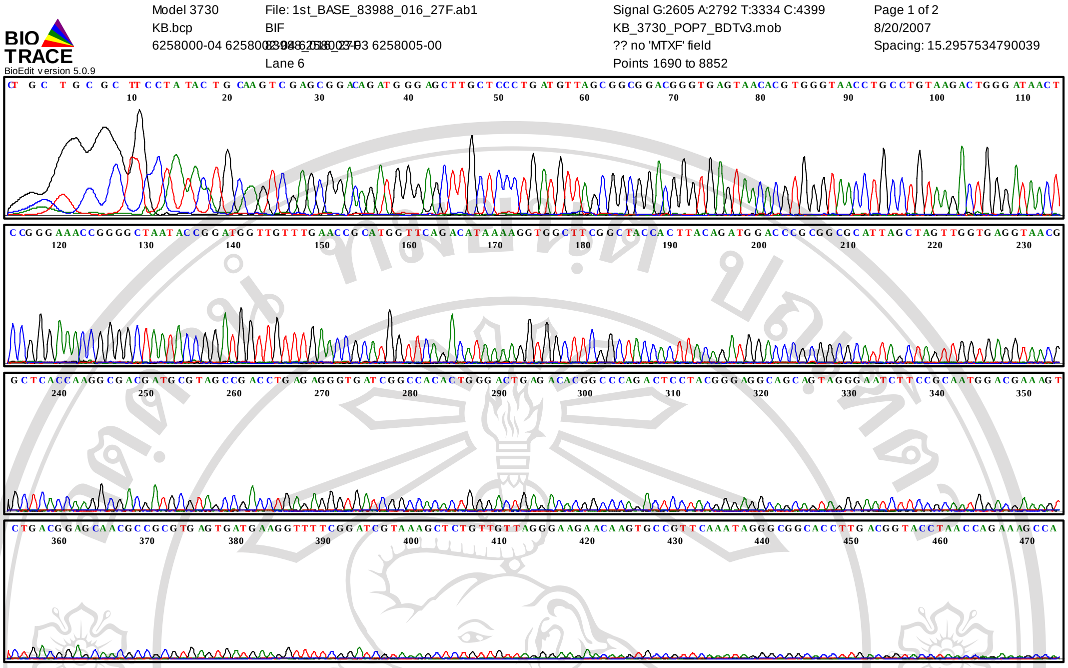
Figure B2 The 16S rRNA sequence from primer 520R of bacterium isolate GB 12



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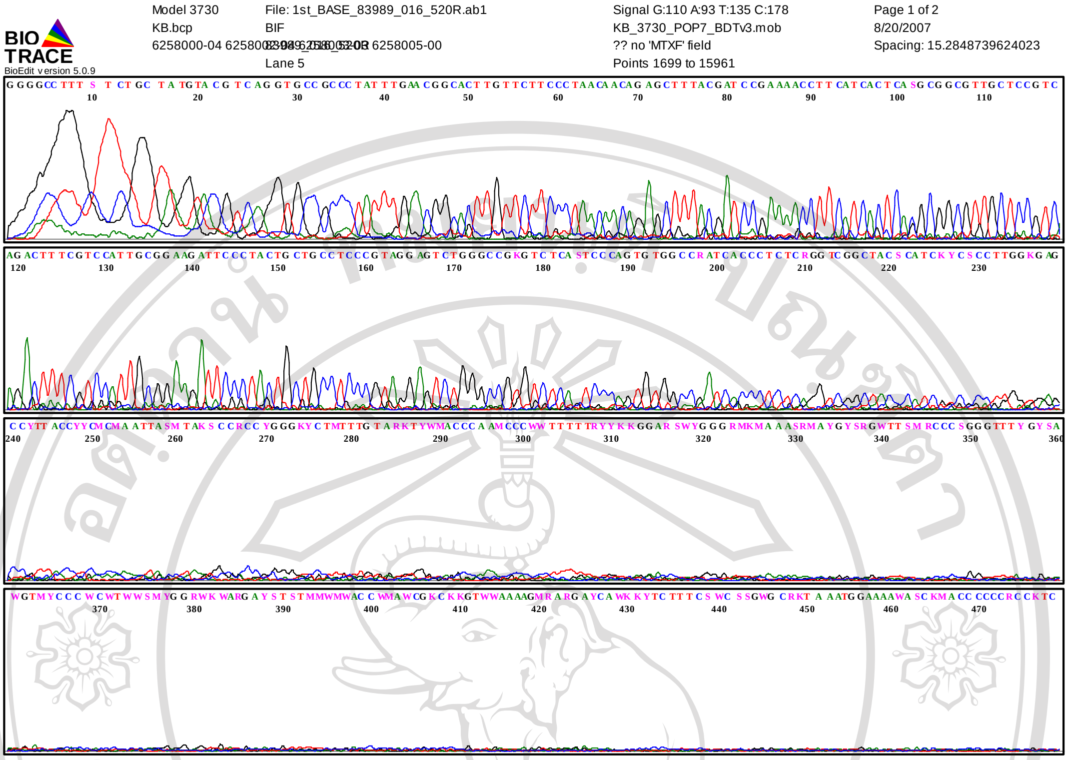
GTA3’

Figure B3 The 16S rRNA sequence from primer 27F of isolate LPC 2



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CRKTAAATGGAAAAWASCKMACCCCCCCRCCKTCWYMKCMWSTTAKW
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Figure B4 The 16S rRNA sequence from primer 520R of isolate LPC 2

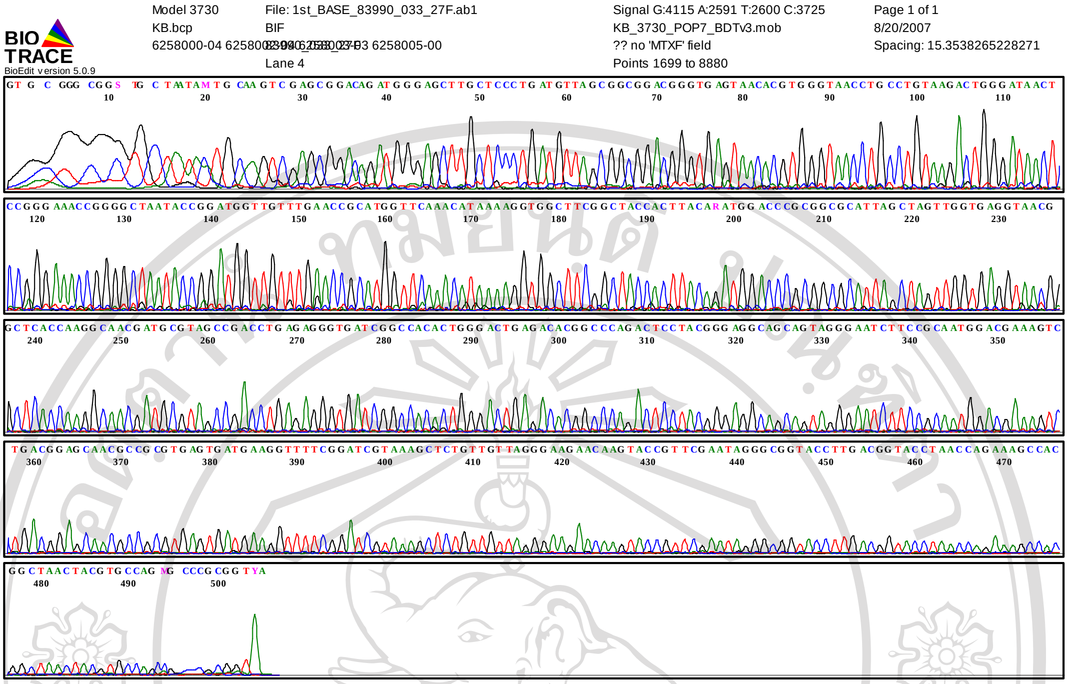

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Figure B5 The 16S rRNA sequence from primer 27F of isolate BS 1

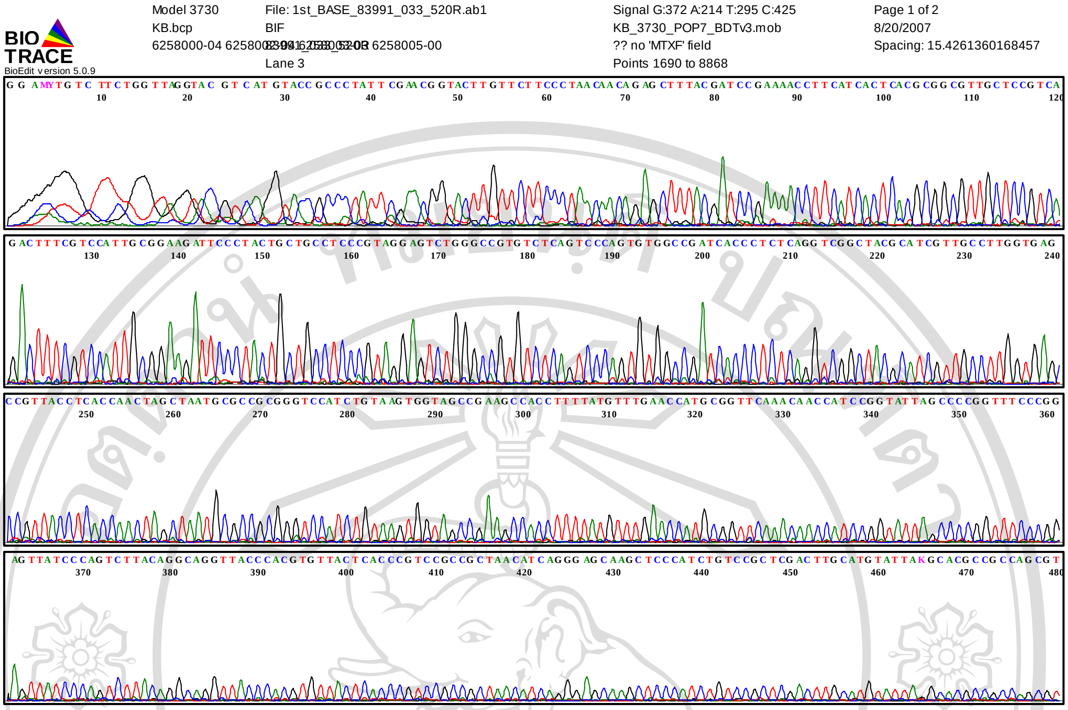

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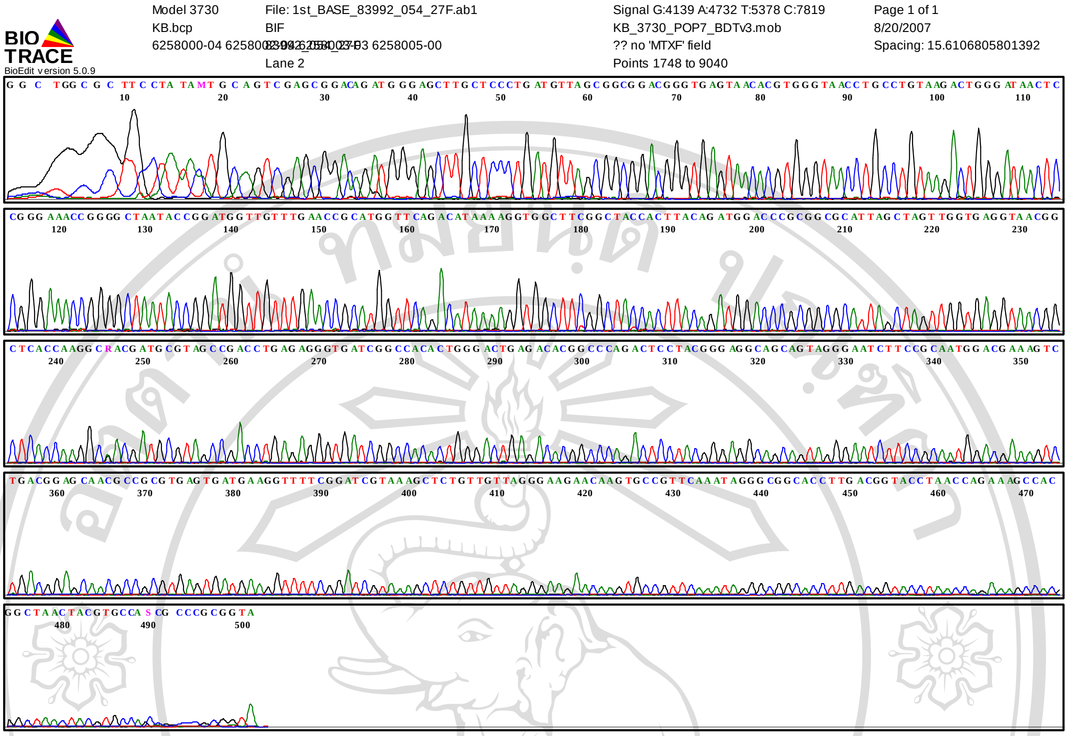
Figure B6 The 16S rRNA sequence from primer 520R of isolate BS 1



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TA3’

Figure B7 The 16S rRNA sequence from primer 27F of isolate LHE 3

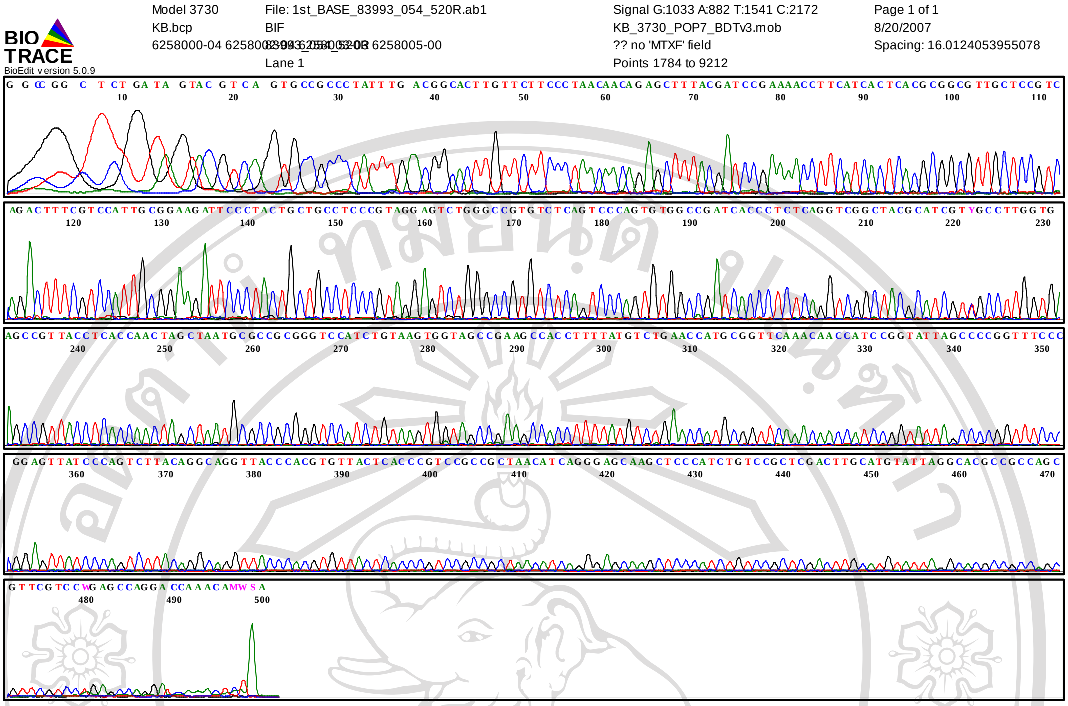

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Figure B8 The 16S rRNA sequence from primer 520R of isolate LHE 3

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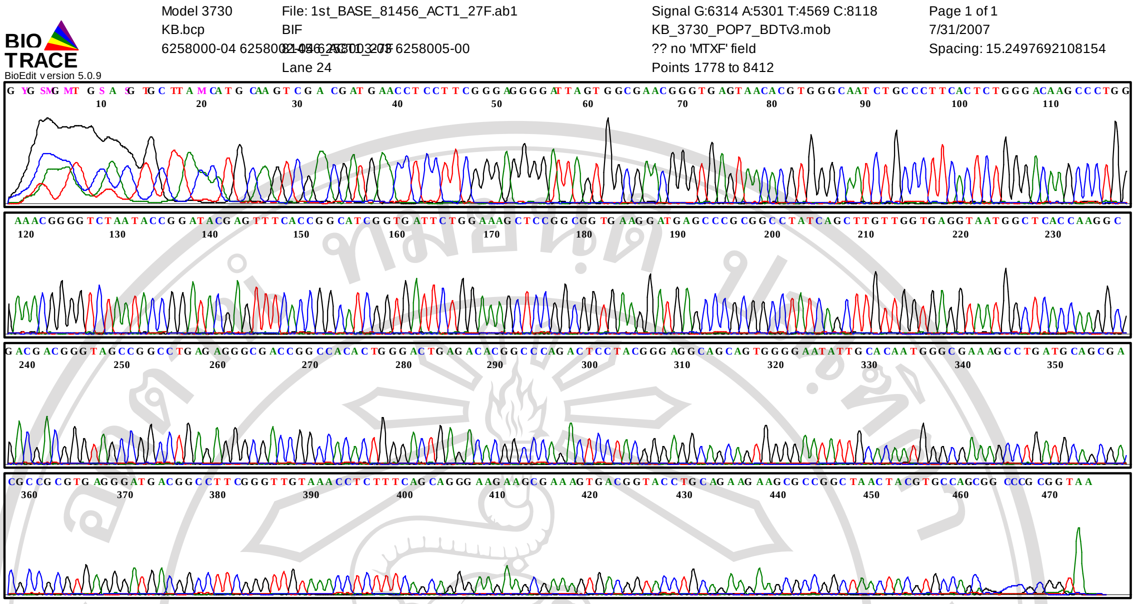

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Figure B9 The 16S rRNA sequence from primer 27F of isolate bacteria LPA 15

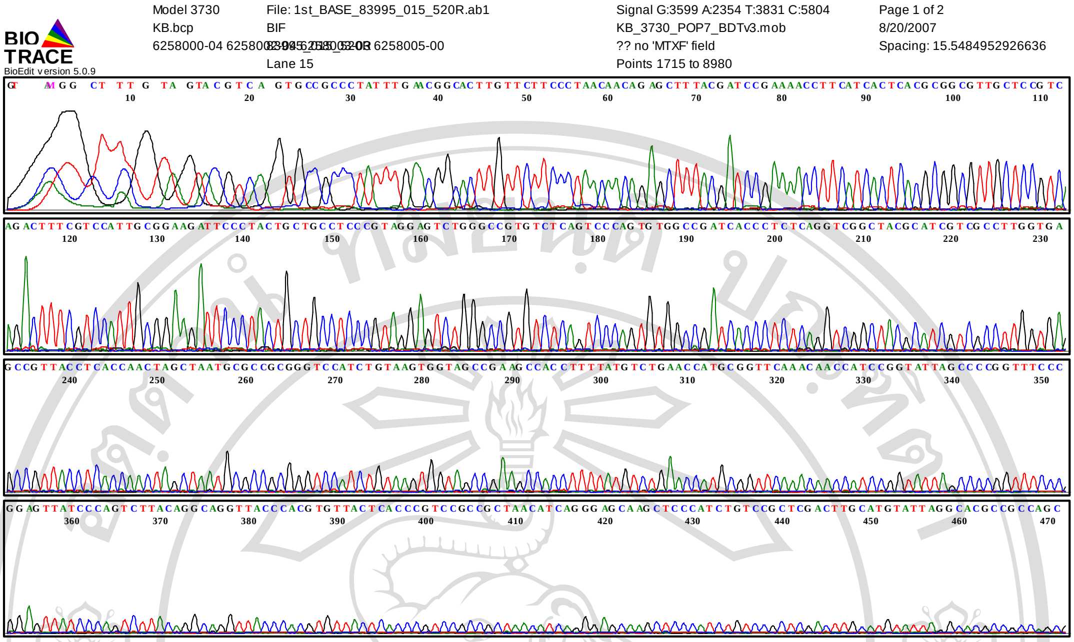

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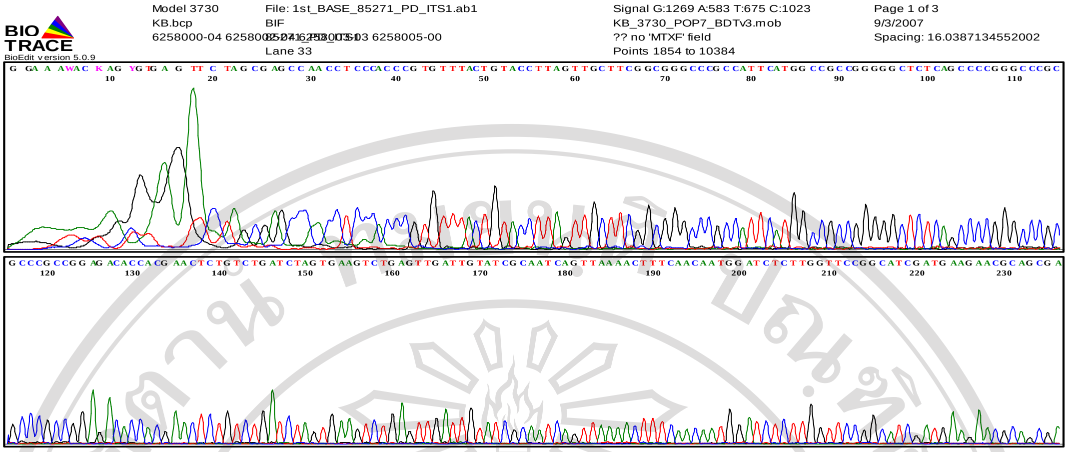
Figure B10 The 16S rRNA sequence from primer 520R of isolate bacteria LPA 15



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CCCTGGTATTCCGGGGGGCATGCCTGTCCGAGCGTCATTGCTGCCCATCAA
GCACGGCTTGTGTGTTGGGTCGTCGTCCCCTCTCCGGGGGGGACGGGCCCC
AAAGGCAGCGGCGGCACCGCGTCCGATCCTCGAGCGTATGGGGCTTTGTC
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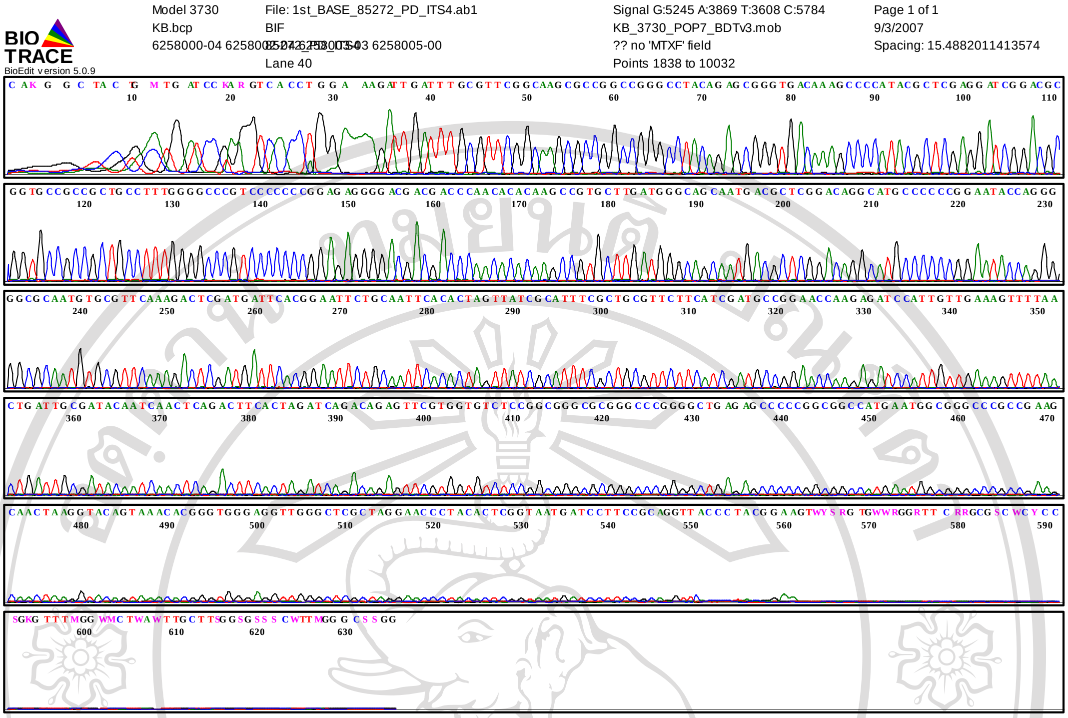
Figure B11 The ITS1-5.8S rDNA-ITS2 sequence from primer ITS 1 of isolate LHE 12



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CTCGGACAGGCATGCCCCCCGGAATACCAGGGGGCGCAATGTGCGTTCAA
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GGTGTCTCCGGCGGGCGCGGGCCCGGGGCTGAGAGCCCCCGGCGGCCATG
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CCTACGGAAGTWYSRGTGWWRGGRTTCRRGCGSCWCYCCSGKGTTTM
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Figure B12 The ITS1-5.8S rDNA-ITS2 sequence from primer ITS 4 of isolate LHE 12

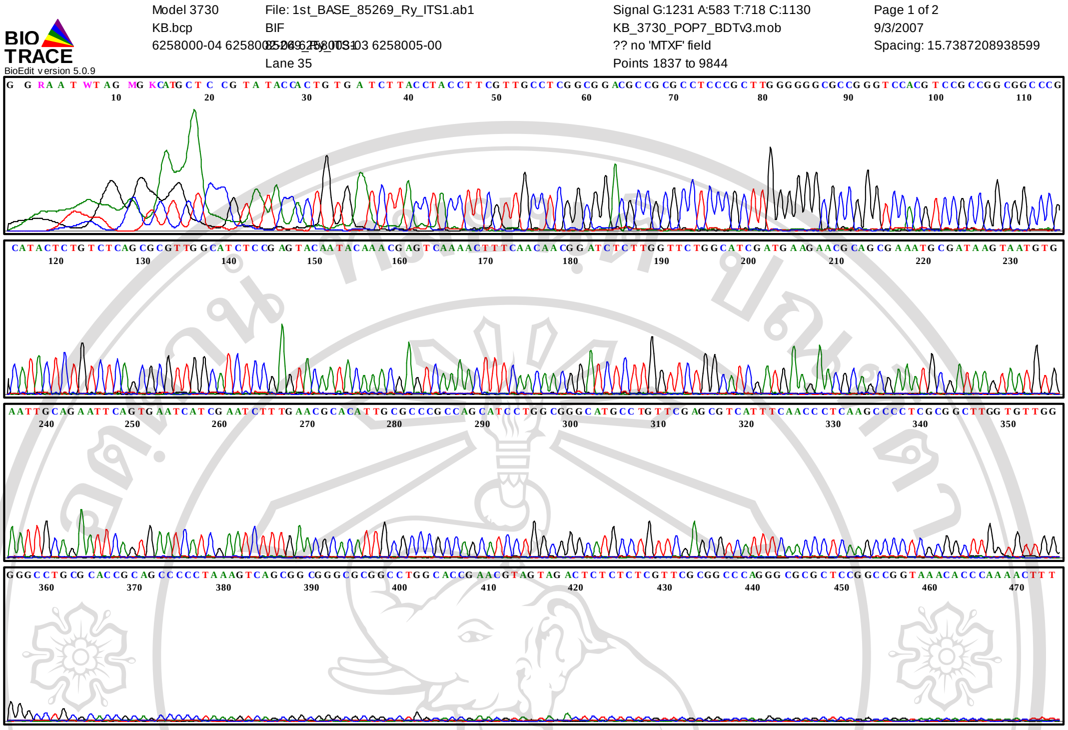

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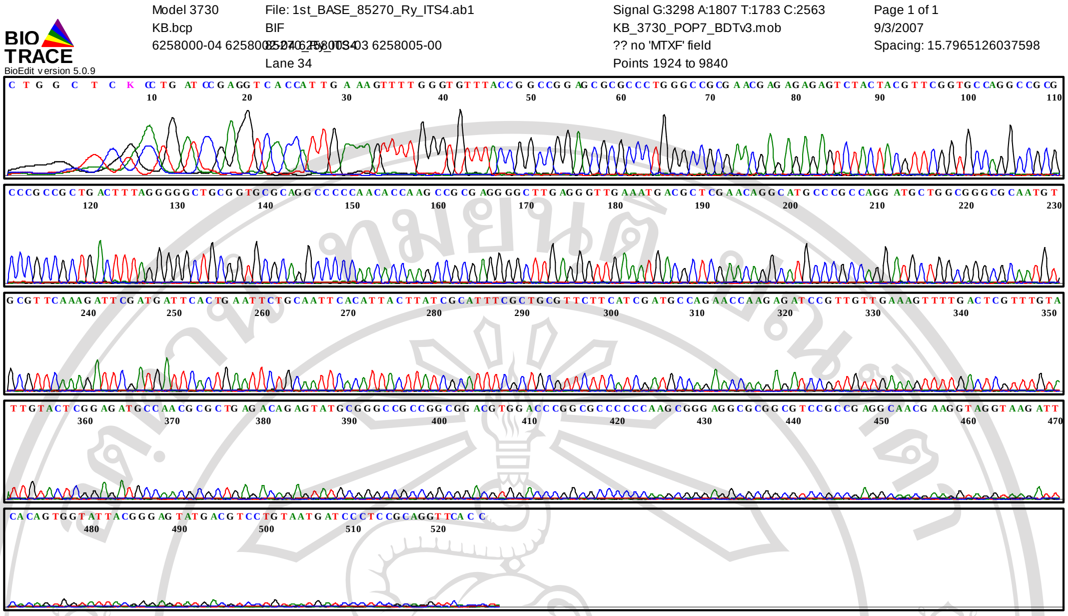
Figure B13 The ITS1-5.8S rDNA-ITS2 sequence from primer ITS 1 of isolate LHE 10



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GAAGGTAGGTAAGATTCACAGTGGTATTACGGGAGTATGACGTCCTG
TAATGATCCCTCCGCAGGTTCACC 3’

Figure B14 The ITS1-5.8S rDNA-ITS2 sequence from primer ITS 4 of isolate LHE 10

5’GCaAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGA
CGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGG
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AAAAGGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATTAGCT
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AGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGA
GGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACG
CCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAG
AACAAGTGCCGTTCAAATAGGGCGGCACCTTGACGGTACCTAACCAGAAA
GCCACGGCTAACTACGTGCCASCGGCCCG3’

Figure B15 DNA sequence of isolate GB 12

5’TGCAAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGG
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GGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACG
CCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAG
AACAAGTGCCGTTCAAATAGGGCGGCACCTTGACGGTACCTAACCAGAAA
GCCACGGCTAACTACGTGCCAGCMGCCGC3’

Figure B16 DNA sequence of isolate LPC 2

5’TAcTGCAAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGC
GGACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTC
CGGGAAACCGGGGCTAATACCGGATGGTTGTTTGAACCGCATGGTTCAAA
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AGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGG
GAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAA
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AAGCCACGGCTAACTACGTGCCAGMGCC3’

Figure B17 DNA sequence of isolate BS 1

5’AcTGCAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCG
GACGGGTGAGTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCC
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ATAAAAGGTGGCTTCGGCTACCACTTACAGATGGACCCGCGGCGCATTAG
CTAGTTGGTGAGGTAACGGCTCACCAAGGCgACGATGCGTAGCCGACCTG
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GAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAA
CGCCGCGTGAGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGA
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AAGCCACGGCTAACTACGTGCCASCGCCCG3’

Figure B18 DNA sequence of isolate LHE 3

5’TTACCGCGGGCCGCTGGCACGTAGTTAGCCGGCGCTTCTTCTGCAGGTAC
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CCCCACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTG
GCCGGTCGCCCTCTCAGGCCGGCTACCCGTCGTCGCCTTGGTGAGCCATTA
CCTCACCAACAAGCTGATAGGCCGCGGGCTCATCCTTCACCGCCGGAGCTT
TCCAGAATCACCGATGCCGGTGAAACTCGTATCCGGTATTAGACCCCGTTT
CCAGGGCTTGTCCCAGAGTGAAGGGCAGATTGCCCACGTGTTACTCACCCG
TTCGCCACTAATCCCCTCCCGAAGGAGGTTCATCGTTCGACTTGCATGTGT
TAAGCAC3’

Figure B19 DNA sequence of isolate LPA 15

5’GGTCAACCTGGAAAAAGATTGATTTGCGTTCGGCAAGCGCCGGCCGGGC
CTACAGAGCGGGTGACAAAGCCCCATACGCTCGAGGATCGGACGCGGTGC
CGCCGCTGCCTTTGGGGCCCGTCCCCCCCGGAGAGGGGACGACGACCCAA
CACACAAGCCGTGCTTGATGGGCAGCAATGACGCTCGGACAGGCATGCCC
CCCGGAATACCAGGGGGCGCAATGTGCGTTCAAAGACTCGATGATTCACG
GAATTCTGCAATTCACACTAGTTATCGCATTTCGCTGCGTTCTTCATCGATG
CCGGAACCAAGAGATCCATTGTTGAAAGTTTTAACTGATTGCGATACAATC
AACTCAGACTTCACTAGATCAGACAGAGTTCGTGGTGTCTCCGGCGGGCGC
GGGCCCGGGGCTGAGAGCCCCCGGCGGCCATGAATGGCGGGCCCGCCGAA
GCAACTAAGGTACAGTAAACACGGGTGGGAGGTTGGGCTCGCTAGGAACC
CTACACT3’

Figure B20 DNA sequence of isolate LHE 12

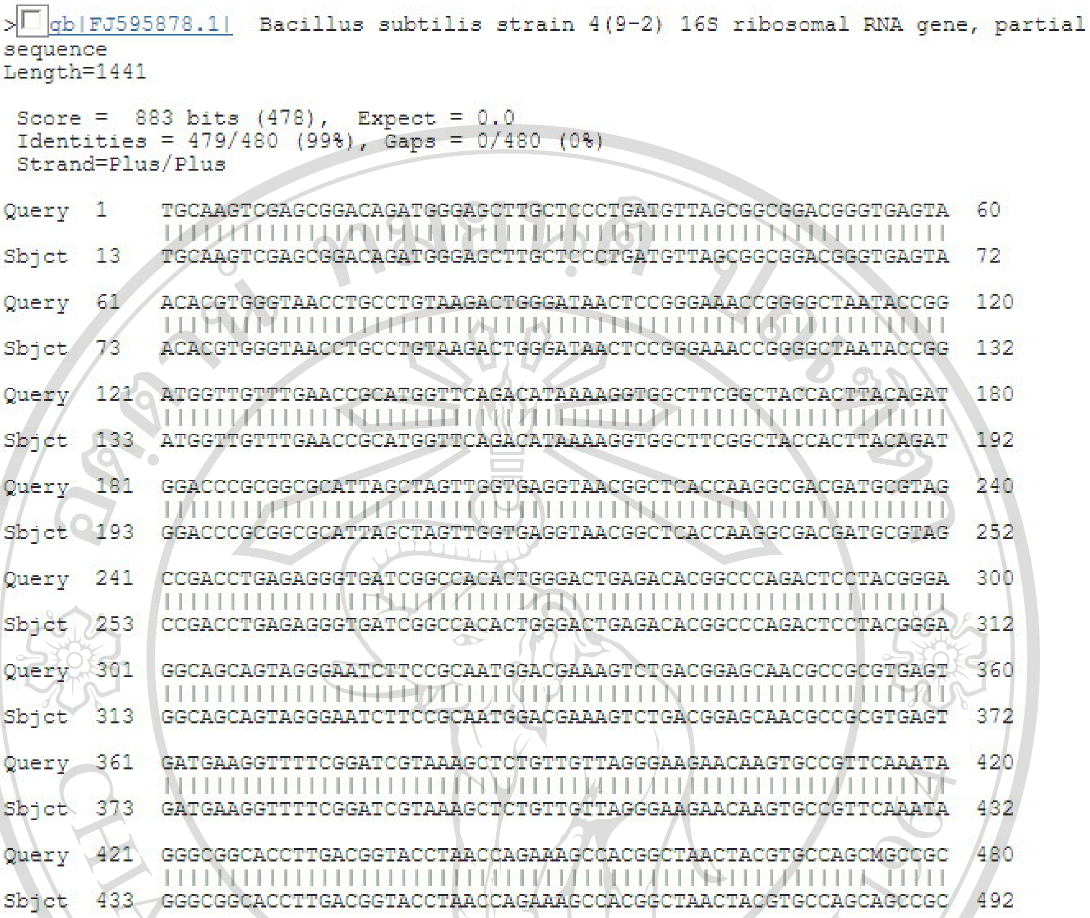
5’GATCCGAGGTCAACCATTGAAAAGTTTTGGGTGTTTACCGGCCGGAGCG
CGCCCTGGGCCGCGAACGAGAGAGAGTCTACTACGTTCGGTGCCAGGCCG
CGCCCGCCGCTGACTTTAGGGGGCTGCGGTGCGCAGGCCCCCAACACCAA
GCCGCGAGGGGCTTGAGGGTTGAAATGACGCTCGAACAGGCATGCCCGCC
AGGATGCTGGCGGGCGCAATGTGCGTTCAAAGATTCGATGATTCACTGAA
TTCTGCAATTCACATTACTTATCGCATTTCGCTGCGTTCTTCATCGATGCCA
GAACCAAGAGATCCGTTGTTGAAAGTTTTGACTCGTTTGTATTGTACTCGG
AGATGCCAACGCGCTGAGACAGAGTATGCGGGCCGCCGGCGGACGTGGAC
CCGGCGCCCCCCAAGCGGGAGGCGCGGCGTCCGCCGAGGCAACGAAGGTA

GGTAAGATTCACAGTGGTATTACGGGAGCATGACGTCCTGTA3’

Figure B21 DNA sequence of isolate LHE 10

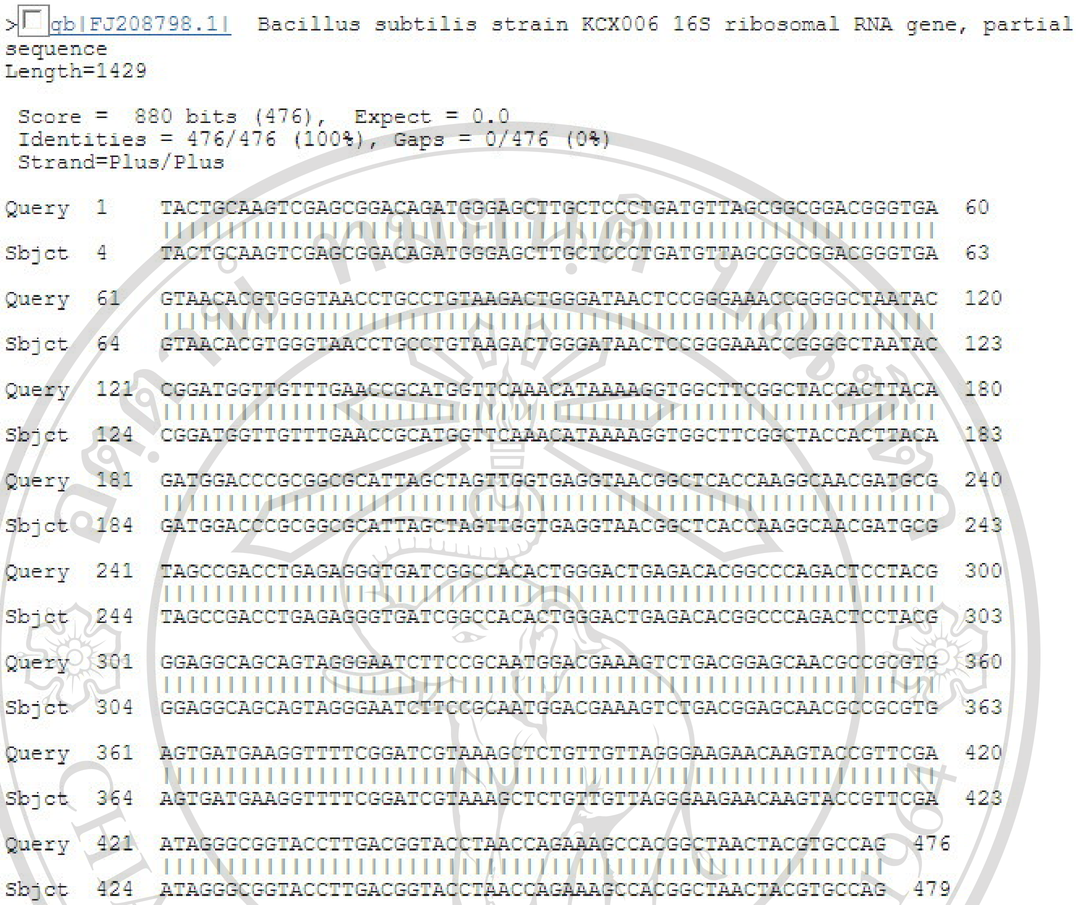
```
>gb|FJ595878.1|  Bacillus subtilis strain 4(9-2) 16S ribosomal RNA gene, partial
sequence
Length=1441

 Score =  870 bits (471),  Expect = 0.0
 Identities = 471/471 (100%), Gaps = 0/471 (0%)
 Strand=Plus/Plus

Query  1    GCAAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGACGGGTGAGTAA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  14   GCAAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGACGGGTGAGTAA  73

Query  61   CACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  74   CACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGA  133

Query  121  TGGTTGTTTGAACCGCATGGTTCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGATG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  134  TGGTTGTTTGAACCGCATGGTTCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGATG  193

Query  181  GACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  194  GACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGC  253

Query  241  CGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  254  CGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG  313

Query  301  GCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  314  GCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTG  373

Query  361  ATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTGCCGTTCAAATAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  374  ATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTGCCGTTCAAATAG  433

Query  421  GGCGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCA  471
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  434  GGCGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCA  484
```

Figure B22 Species of bacteria which it has DNA sequence closet isolate GB 12



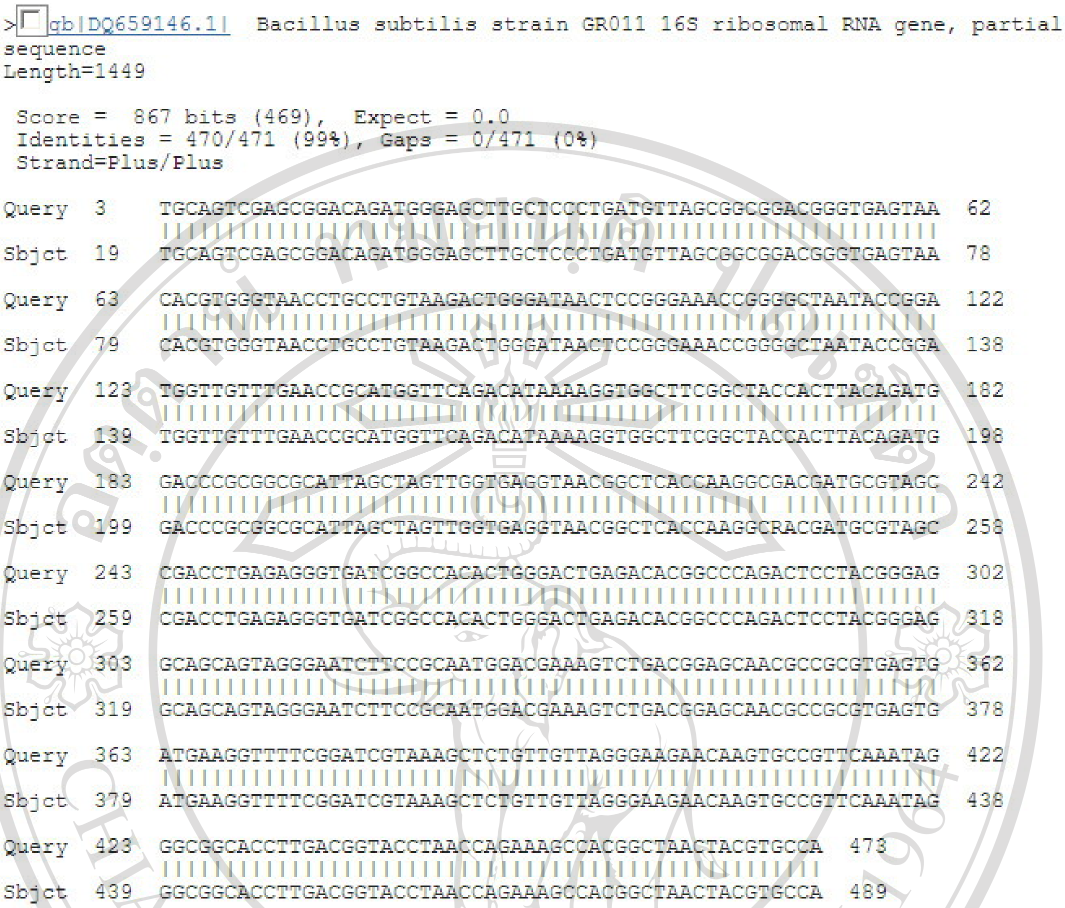
```
>gb|FJ595878.1|  Bacillus subtilis strain 4(9-2) 16S ribosomal RNA gene, partial
sequence
Length=1441

 Score =  883 bits (478),  Expect = 0.0
 Identities = 479/480 (99%), Gaps = 0/480 (0%)
 Strand=Plus/Plus

Query  1    TGCAAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGACGGGTGAGTA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  13   TGCAAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGACGGGTGAGTA  72

Query  61   ACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  73   ACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGG  132

Query  121  ATGGTTGTTTGAACCGCATGGTTCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  133  ATGGTTGTTTGAACCGCATGGTTCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGAT  192

Query  181  GGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  193  GGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAG  252

Query  241  CCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  253  CCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGA  312

Query  301  GGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGT  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  313  GGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGT  372

Query  361  GATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTGCCGTTCAAATA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  373  GATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTGCCGTTCAAATA  432

Query  421  GGGCGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCMGCCGC  480
            |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Sbjct  433  GGGCGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGC  492
```

Figure B23 Species of bacteria which it has DNA sequence closet isolate LPC 2



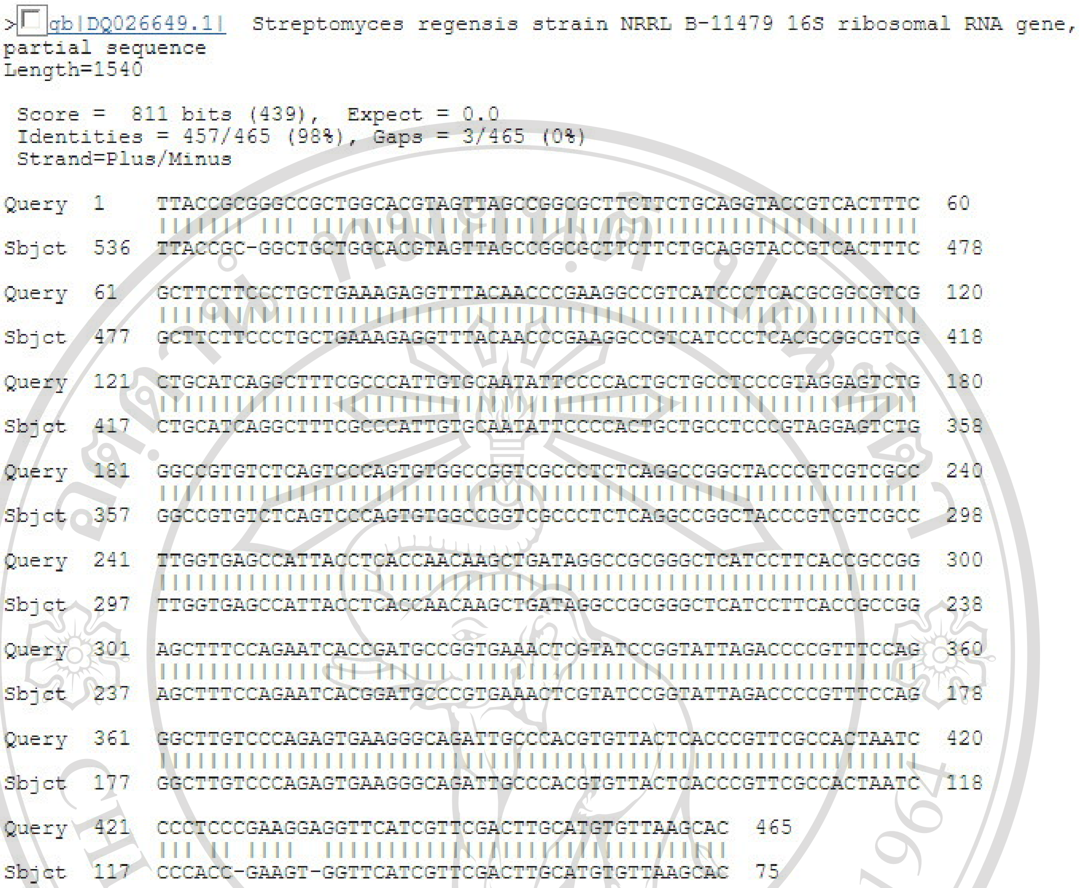
```
>☐gb|FJ208798.1|  Bacillus subtilis strain KCX006 16S ribosomal RNA gene, partial
sequence
Length=1429

 Score =  880 bits (476),  Expect = 0.0
 Identities = 476/476 (100%), Gaps = 0/476 (0%)
 Strand=Plus/Plus

Query  1    TACTGCAAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGACGGGTGA  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  4    TACTGCAAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGACGGGTGA  63

Query  61   GTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATAC  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  64   GTAACACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATAC  123

Query  121  CGGATGGTTGTTTGAACCGCATGGTTCAAACATAAAAGGTGGCTTCGGCTACCACTTACA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  124  CGGATGGTTGTTTGAACCGCATGGTTCAAACATAAAAGGTGGCTTCGGCTACCACTTACA  183

Query  181  GATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACGATGCG  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  184  GATGGACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCAACGATGCG  243

Query  241  TAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  244  TAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACG  303

Query  301  GGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTG  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  304  GGAGGCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTG  363

Query  361  AGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTACCGTTCGA  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  364  AGTGATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTACCGTTCGA  423

Query  421  ATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAG  476
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  424  ATAGGGCGGTACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCAG  479
```

Figure B24 Species of bacteria which it has DNA sequence closet isolate BS 1



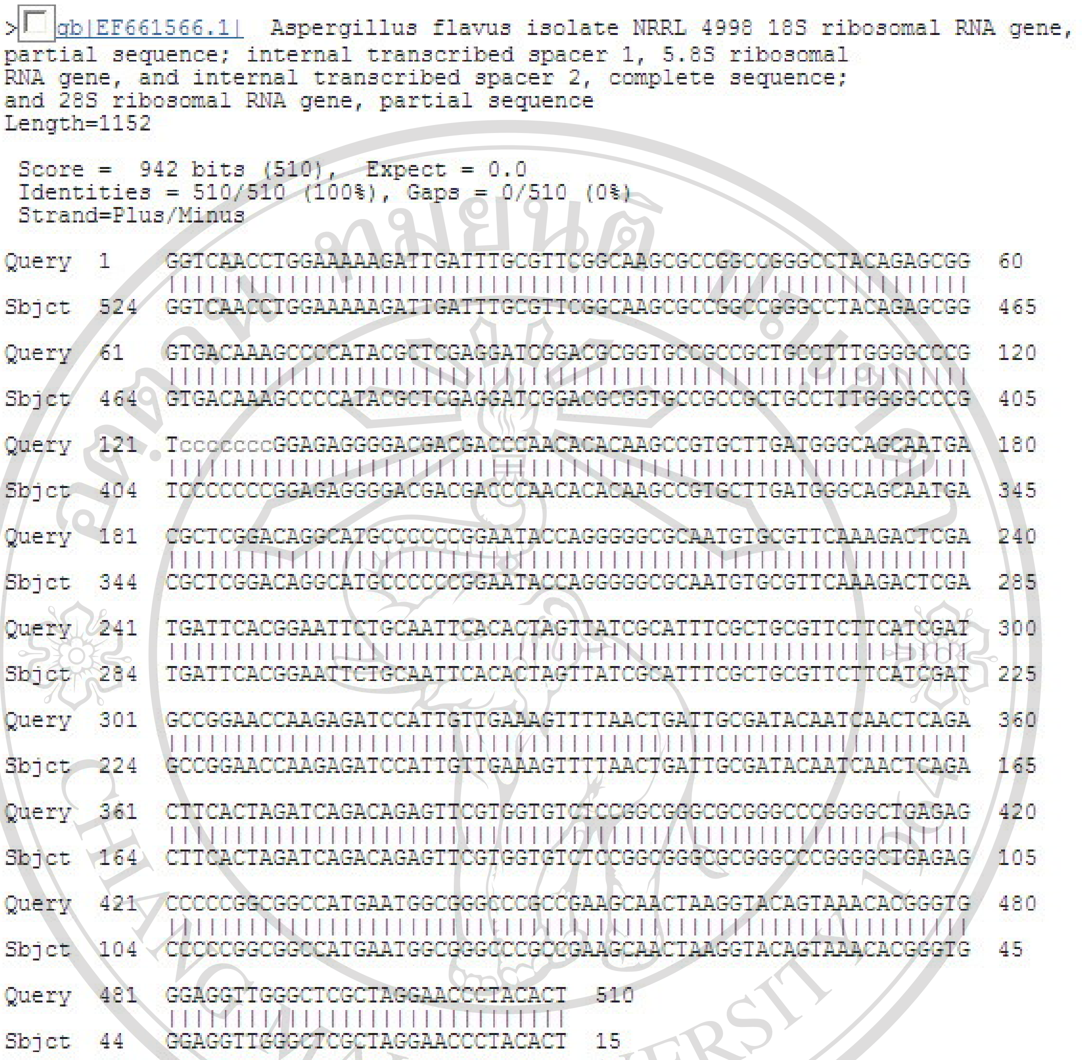
```
>☐gb|DQ659146.1|  Bacillus subtilis strain GR011 16S ribosomal RNA gene, partial
sequence
Length=1449

 Score =  867 bits (469),  Expect = 0.0
 Identities = 470/471 (99%), Gaps = 0/471 (0%)
 Strand=Plus/Plus

Query  3    TGCAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGACGGGTGAGTAA  62
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  19   TGCAGTCGAGCGGACAGATGGGAGCTTGCTCCCTGATGTTAGCGGCGGACGGGTGAGTAA  78

Query  63   CACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGA  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  79   CACGTGGGTAACCTGCCTGTAAGACTGGGATAACTCCGGGAAACCGGGGCTAATACCGGA  138

Query  123  TGGTTGTTTGAACCGCATGGTTCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGATG  182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  139  TGGTTGTTTGAACCGCATGGTTCAGACATAAAAGGTGGCTTCGGCTACCACTTACAGATG  198

Query  183  GACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCGACGATGCGTAGC  242
            ||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Sbjct  199  GACCCGCGGCGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCRACGATGCGTAGC  258

Query  243  CGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG  302
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  259  CGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG  318

Query  303  GCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTG  362
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  319  GCAGCAGTAGGGAATCTTCCGCAATGGACGAAAGTCTGACGGAGCAACGCCGCGTGAGTG  378

Query  363  ATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTGCCGTTCAAATAG  422
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  379  ATGAAGGTTTTCGGATCGTAAAGCTCTGTTGTTAGGGAAGAACAAGTGCCGTTCAAATAG  438

Query  423  GGCGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCA  473
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  439  GGCGGCACCTTGACGGTACCTAACCAGAAAGCCACGGCTAACTACGTGCCA  489
```

Figure B25 Species of bacteria which it has DNA sequence closet isolate LHE 3



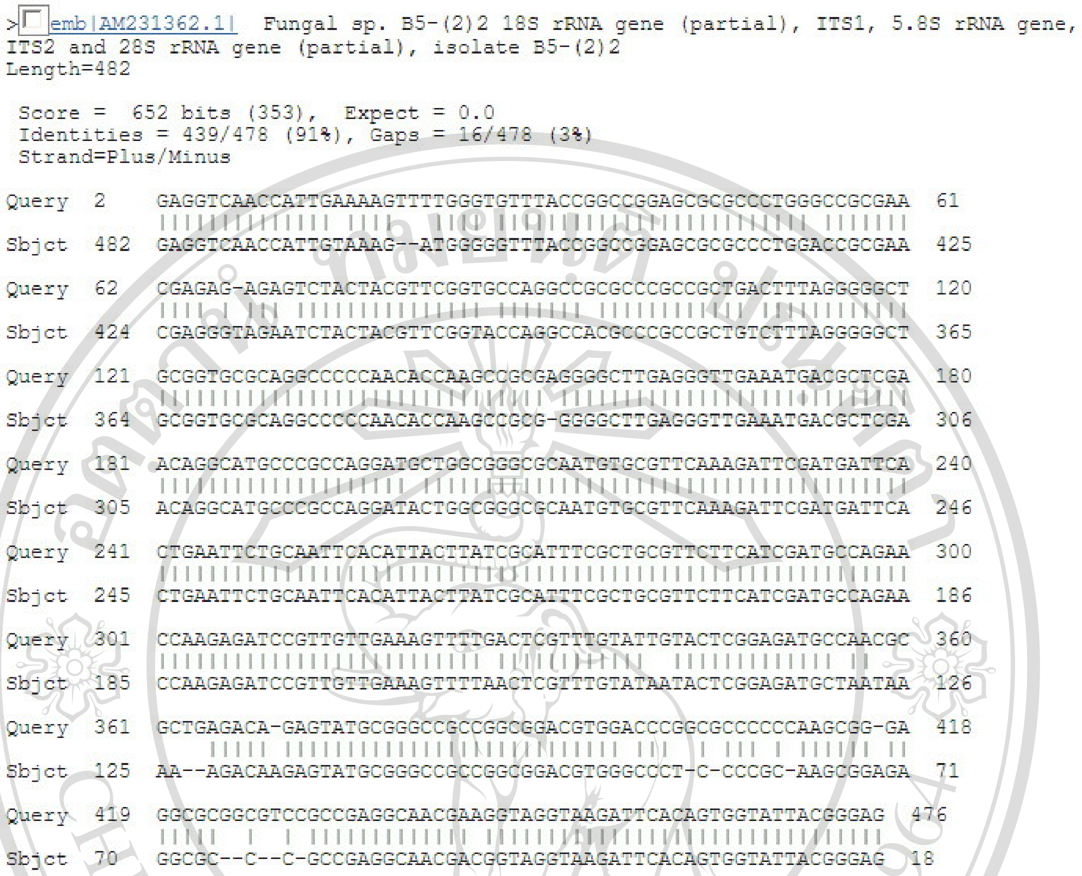
```
>☐gb|DQ026649.1|  Streptomyces regensis strain NRRL B-11479 16S ribosomal RNA gene,
partial sequence
Length=1540

 Score =  811 bits (439),  Expect = 0.0
 Identities = 457/465 (98%), Gaps = 3/465 (0%)
 Strand=Plus/Minus

Query  1    TTACCGCGGGCCGCTGGCACGTAGTTAGCCGGCGCTTCTTCTGCAGGTACCGTCACTTTC  60
            ||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  536  TTACCGC-GGCTGCTGGCACGTAGTTAGCCGGCGCTTCTTCTGCAGGTACCGTCACTTTC  478

Query  61   GCTTCTTCCCTGCTGAAAGAGGTTTACAACCCGAAGGCCGTCATCCCTCACGCGGCGTCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  477  GCTTCTTCCCTGCTGAAAGAGGTTTACAACCCGAAGGCCGTCATCCCTCACGCGGCGTCG  418

Query  121  CTGCATCAGGCTTTCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTG  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  417  CTGCATCAGGCTTTCGCCCATTGTGCAATATTCCCCACTGCTGCCTCCCGTAGGAGTCTG  358

Query  181  GGCCGTGTCTCAGTCCCAGTGTGGCCGGTCGCCCTCTCAGGCCGGCTACCCGTCGTCGCC  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  357  GGCCGTGTCTCAGTCCCAGTGTGGCCGGTCGCCCTCTCAGGCCGGCTACCCGTCGTCGCC  298

Query  241  TTGGTGAGCCATTACCTCACCAACAAGCTGATAGGCCGCGGGCTCATCCTTCACCGCCGG  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  297  TTGGTGAGCCATTACCTCACCAACAAGCTGATAGGCCGCGGGCTCATCCTTCACCGCCGG  238

Query  301  AGCTTTCCAGAATCACCGATGCCGGTGAAACTCGTATCCGGTATTAGACCCCGTTTCCAG  360
            |||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||||
Sbjct  237  AGCTTTCCAGAATCACGGATGCCCGTGAAACTCGTATCCGGTATTAGACCCCGTTTCCAG  178

Query  361  GGCTTGTCCCAGAGTGAAGGGCAGATTGCCCACGTGTTACTCACCCGTTCGCCACTAATC  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  177  GGCTTGTCCCAGAGTGAAGGGCAGATTGCCCACGTGTTACTCACCCGTTCGCCACTAATC  118

Query  421  CCCTCCCGAAGGAGGTTCATCGTTCGACTTGCATGTGTTAAGCAC  465
            ||| || ||||  ||||||||||||||||||||||||||||||||
Sbjct  117  CCCACC-GAAGT-GGTTCATCGTTCGACTTGCATGTGTTAAGCAC  75
```

Figure B26 Species of bacteria which it has DNA sequence closet isolate LPA15



```
>☐gb|EF661566.1|  Aspergillus flavus isolate NRRL 4998 18S ribosomal RNA gene,
partial sequence; internal transcribed spacer 1, 5.8S ribosomal
RNA gene, and internal transcribed spacer 2, complete sequence;
and 28S ribosomal RNA gene, partial sequence
Length=1152

 Score =  942 bits (510),  Expect = 0.0
 Identities = 510/510 (100%), Gaps = 0/510 (0%)
 Strand=Plus/Minus

Query  1    GGTCAACCTGGAAAAAGATTGATTTGCGTTCGGCAAGCGCCGGCCGGGCCTACAGAGCGG  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  524  GGTCAACCTGGAAAAAGATTGATTTGCGTTCGGCAAGCGCCGGCCGGGCCTACAGAGCGG  465

Query  61   GTGACAAAGCCCCATACGCTCGAGGATCGGACGCGGTGCCGCCGCTGCCTTTGGGGCCCG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  464  GTGACAAAGCCCCATACGCTCGAGGATCGGACGCGGTGCCGCCGCTGCCTTTGGGGCCCG  405

Query  121  TccccccccGGAGAGGGGACGACGACCCAACACACAAGCCGTGCTTGATGGCAGCAATGA  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  404  TCCCCCCCGGAGAGGGGACGACGACCCAACACACAAGCCGTGCTTGATGGCAGCAATGA  345

Query  181  CGCTCGGACAGGCATGCCCCCCGGAATACCAGGGGGCGCAATGTGCGTTCAAAGACTCGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  344  CGCTCGGACAGGCATGCCCCCCGGAATACCAGGGGGCGCAATGTGCGTTCAAAGACTCGA  285

Query  241  TGATTCACGGAATTCTGCAATTCACACTAGTTATCGCATTTCGCTGCGTTCTTCATCGAT  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  284  TGATTCACGGAATTCTGCAATTCACACTAGTTATCGCATTTCGCTGCGTTCTTCATCGAT  225

Query  301  GCCGGAACCAAGAGATCCATTGTTGAAAGTTTTAACTGATTGCGATACAATCAACTCAGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  224  GCCGGAACCAAGAGATCCATTGTTGAAAGTTTTAACTGATTGCGATACAATCAACTCAGA  165

Query  361  CTTCACTAGATCAGACAGAGTTCGTGGTGTCTCCGGCGGGCGCGGGCCCGGGGCTGAGAG  420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  164  CTTCACTAGATCAGACAGAGTTCGTGGTGTCTCCGGCGGGCGCGGGCCCGGGGCTGAGAG  105

Query  421  CCCCCGGCGGCCATGAATGGCGGGCCCGCCGAAGCAACTAAGGTACAGTAAACACGGGTG  480
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  104  CCCCCGGCGGCCATGAATGGCGGGCCCGCCGAAGCAACTAAGGTACAGTAAACACGGGTG  45

Query  481  GGAGGTTGGGCTCGCTAGGAACCCTACACT  510
            ||||||||||||||||||||||||||||||
Sbjct  44   GGAGGTTGGGCTCGCTAGGAACCCTACACT  15
```

Figure B27 Species of fungi which it has DNA sequence closet isolate LHE 12



```
>☐emb|AM231362.1|  Fungal sp. B5-(2)2 18S rRNA gene (partial), ITS1, 5.8S rRNA gene,
ITS2 and 28S rRNA gene (partial), isolate B5-(2)2
Length=482

 Score =  652 bits (353),  Expect = 0.0
 Identities = 439/478 (91%), Gaps = 16/478 (3%)
 Strand=Plus/Minus

Query  2    GAGGTCAACCATTGAAAAGTTTTGGGTGTTTACCGGCCGGAGCGCGCCCTGGGCCGCGAA  61
            |||||||||||||| ||||   |||| ||||||||||||||||||||||||| |||||||
Sbjct  482  GAGGTCAACCATTGTAAAG--ATGGGGGTTTACCGGCCGGAGCGCGCCCTGGACCGCGAA  425

Query  62   CGAGAG-AGAGTCTACTACGTTCGGTGCCAGGCCGCGCCCGCCGCTGACTTTAGGGGGCT  120
            |||| | ||| ||||||||||||||| ||||||| |||||||||||| ||||||||||||
Sbjct  424  CGAGGGTAGAATCTACTACGTTCGGTACCAGGCCACGCCCGCCGCTGTCTTTAGGGGGCT  365

Query  121  GCGGTGCGCAGGCCCCCAACACCAAGCCGCGAGGGGCTTGAGGGTTGAAATGACGCTCGA  180
            ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  364  GCGGTGCGCAGGCCCCCAACACCAAGCCGCG-GGGGCTTGAGGGTTGAAATGACGCTCGA  306

Query  181  ACAGGCATGCCCGCCAGGATGCTGGCGGGCGCAATGTGCGTTCAAAGATTCGATGATTCA  240
            |||||||||||||||||||| |||||||||||||||||||||||||||||||||||||||
Sbjct  305  ACAGGCATGCCCGCCAGGATACTGGCGGGCGCAATGTGCGTTCAAAGATTCGATGATTCA  246

Query  241  CTGAATTCTGCAATTCACATTACTTATCGCATTTCGCTGCGTTCTTCATCGATGCCAGAA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  245  CTGAATTCTGCAATTCACATTACTTATCGCATTTCGCTGCGTTCTTCATCGATGCCAGAA  186

Query  301  CCAAGAGATCCGTTGTTGAAAGTTTTGACTCGTTTGTATTGTACTCGGAGATGCCAACGC  360
            |||||||||||||||||||||||||| ||||||||||||  ||||||||||||| ||
Sbjct  185  CCAAGAGATCCGTTGTTGAAAGTTTTAACTCGTTTGTATAATACTCGGAGATGCTAATAA  126

Query  361  GCTGAGACA-GAGTATGCGGGCCGCCGGCGGACGTGGACCCGGCGCCCCCCAAGCGG-GA  418
                ||||| ||||||||||||||||||||||||||| |||  | ||| | |||||| ||
Sbjct  125  AA--AGACAAGAGTATGCGGGCCGCCGGCGGACGTGGGCCCT-C-CCCGC-AAGCGGAGA  71

Query  419  GGCGCGGCGTCCGCCGAGGCAACGAAGGTAGGTAAGATTCACAGTGGTATTACGGGAG  476
            |||||  |  | ||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct  70   GGCGC--C--C-GCCGAGGCAACGACGGTAGGTAAGATTCACAGTGGTATTACGGGAG  18
```

Figure B28 Species of fungi which it has DNA sequence closet with isolate LHE 10

APPENDIX C

PICTURES

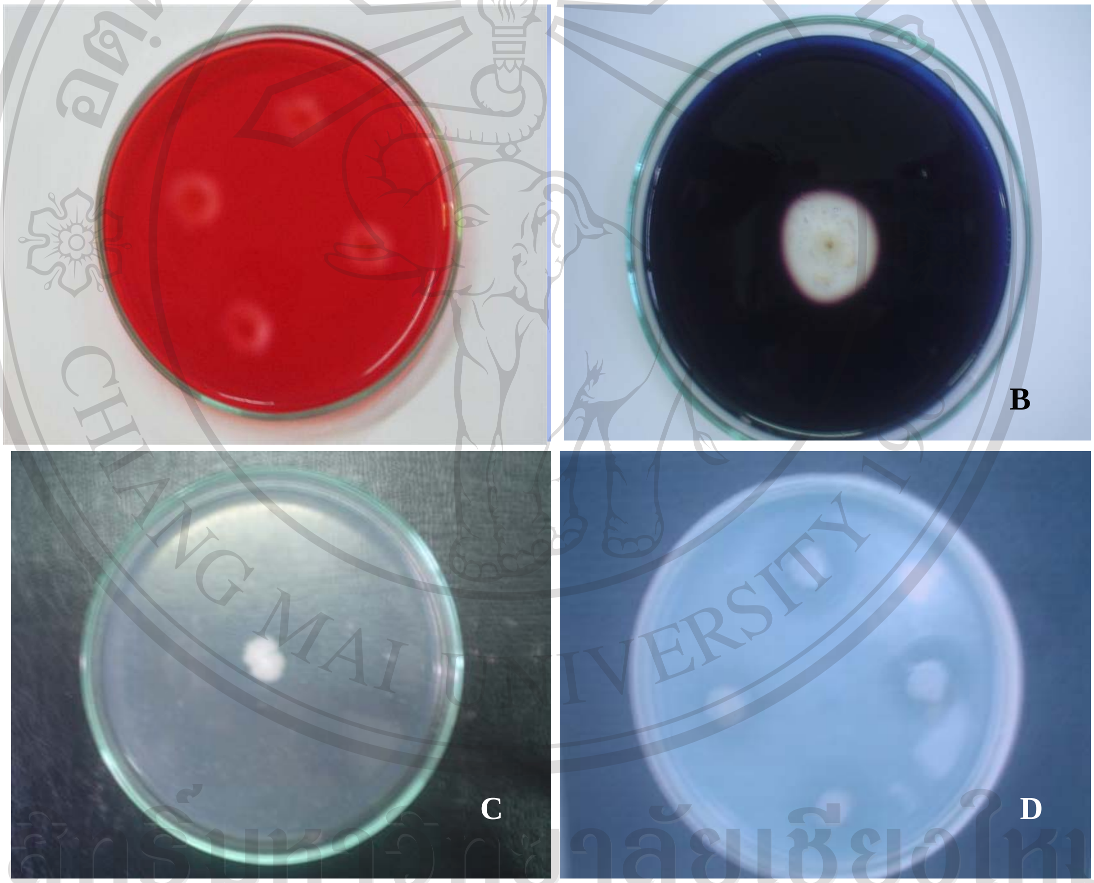


Figure C1 The clearing zone around the colonies on medium

A. CMC agar

B. Starch agar

C. Skim milk agar

D. Tributyrin agar

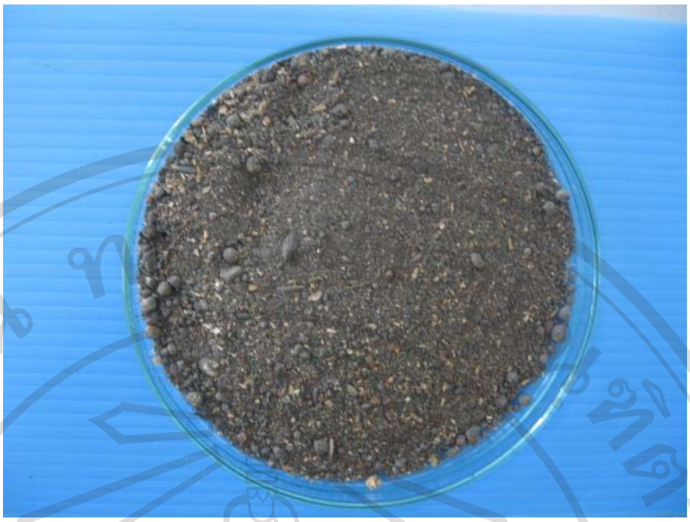


Figure C2 Compost inoculum powder (CMU)

Figure C3 Packaging of CMU inoculum

Figure C4 The composting process

Figure C5 Turning the pile

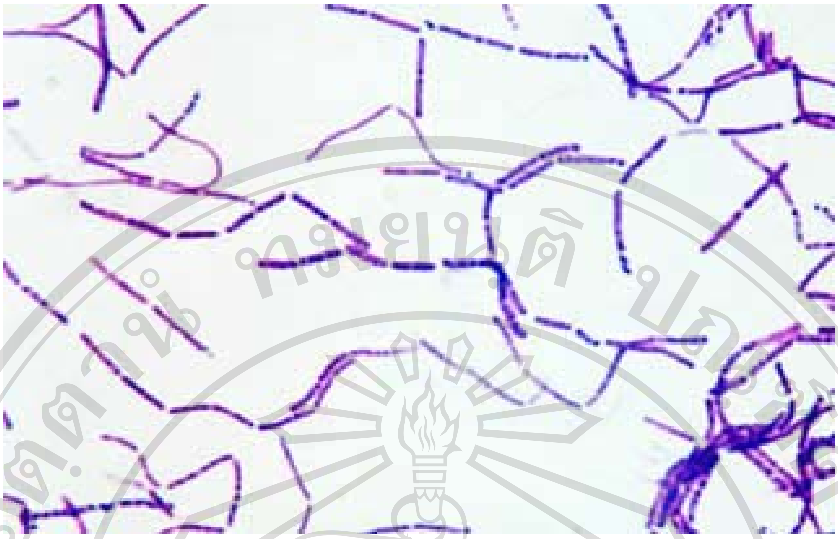


Figure C6 The microscopic photo (100×) of *Bacillus subtilis* GB12

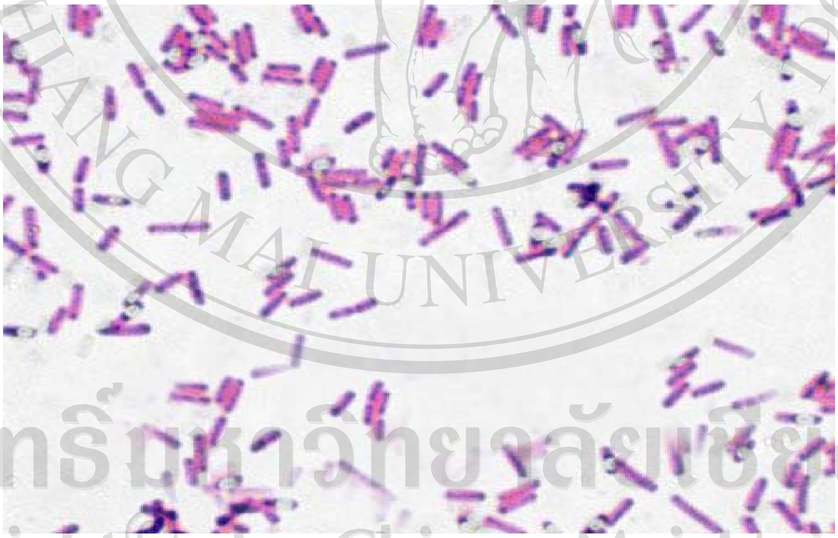


Figure C7 The microscopic photo (100×) of *Bacillus subtilis* LPC 2

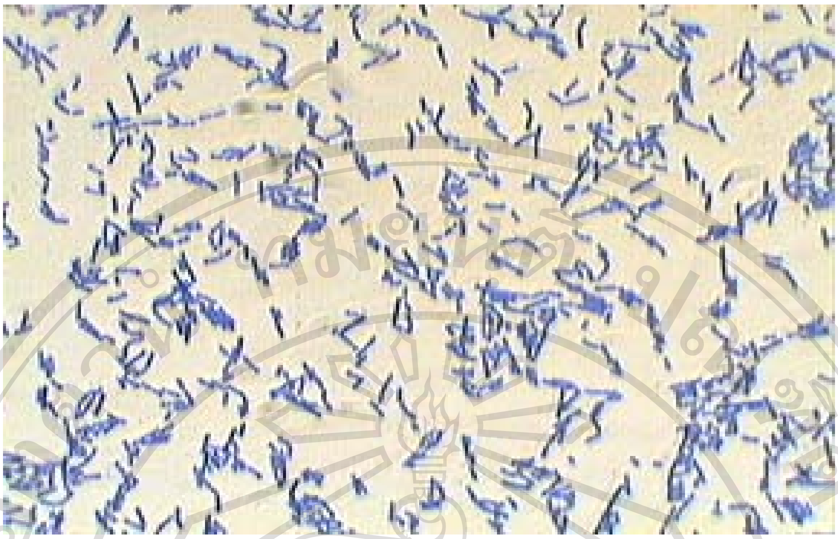


Figure C8 The microscopic photo (100×) of *Bacillus subtilis* LHE 3

Figure C9 The microscopic photo (100×) of *Bacillus subtilis* BS1

Figure C10 The microscopic photo (100×) of *Aspergillus flavus* LHE12

Figure C11 The colony characterization of isolate LHE 10

Figure C12 The colony characterization of *Streptomyces regensis* LPA 15

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