APPENDICES

APPENDIX A

Media

In this study, various media were prepared with the purposes to use as isolation medium, storage medium, growth medium and medium forproduction of antifungal metabolites. All media were prepared at final volume 1,000 ml of distilled water and sterilized in an autoclave at 121°C for 15 min.

1. Inhibitory mold agar 2 (IMA-2) or broth (IMB-2) (Shimizu *et al*., 2000)

Glucose	5.0	g
Soluble starch	5.0	g
Beef extract	1.0	g
Yeast extract	1.0	g
NZ-case	2.0	g
NaCl	2.0	g
$CaCO_3$	1.0	g
Agar (for IMA-2)	15.0	g
pH 7.3		

2. ISP-2 medium: Yeast extract-malt extract agar (Shirling and Gottlieb, 1966)

Yeast extract	4.0	g
Malt extract	10.0	g
Dextrose	4.0	g
Agar	20	g
pH 7.3		

3. ISP-3 medium: Oatmeal agar (Shirling and Gottlieb, 1966)

Oatmeal	20.0	g
Agar	15.0	g
pH 7.2		

4. ISP-4 medium: Inorganic salts-starch agar (Shirling and Gottlieb, 1966)

Solution A:		
Soluble starch	10.0	g
Cool distilled water	500.0	ml
Solution B:		
K_2HPO_4	1.0	g
$MgSO_4.7H_2O$	1.0	g
NaCl	1.0	g
$(NH_4)_2.SO_4$	2.0	g
$CaCO_3$	2.0	g
Trace salts solution (A)	1.0	ml
Distilled water	500.0	ml
Agar	20.0	g
pH 7.0 to 7.4		

5. ISP-5 medium: Glycerol-asparagine agar (Shirling and Gottlieb, 1966)

L-asparagine (anhydrous basis)	1.0	g
Glycerol	10.0	g
K_2HPO_4 (anhydrous basis)	1.0	g
Trace salts solution (A)	1.0	ml
Agar	20.0	g
pH 7.0 to 7.4		

6. ISP-6 medium: Peptone-yeast extract iron agar (Shirling and Gottlieb, 1966)

Peptone Iron Agar, dehydrated	36.0	g
Yeast extract	1.0	g
Dextrose	4.0	g
pH 7.0 to 7.2		

7. ISP-7 medium: Tyrosine agar (Shirling and Gottlieb, 1966)

Glycerol	15.0	g
L-tyrosine	0.5	g
L-asparagine	1.0	g
K_2HPO_4	0.5	g
$MgSO_4.7H_2O$	0.5	g
NaCl	0.5	g
$FeSO_4.7H_2O$	0.01	g
Trace salts solution (A)	1.0	ml
Agar	20.0	g
pH 7.2 to 7.4		

8. Trace salts solution (A)

$FeSO_4.7H_2O$	0.1	g
$MnCl_2.4H_2O$	0.1	g
$ZnSo_4.7H_2O$	0.1	g
Distilled water	100.0	ml

9. Potato dextrose agar (PDA)

Potato	200.0	g
Dextrose	20.0	g
Agar	15.0	

10. Celluloseagar (CMC) (Atlas, 2010)

$(NH_4)_2SO_4$	0.5	g
KH_2PO_4	1.0	g
KCl	0.5	g
$MgSO_4$	0.2	g
$CaCl_2$	0.1	g
Yeast extract	0.5	g
Carboxymethylcellulose	10.0	g
Agar	20.0	g

pH 6.2

Dye with Congo red 0.1% and wash cell with 1N

11. Czapek solution agar(Atlas, 2010)

Sucrose	30	g
$NaNO_3$	2.0	g
K_2HPO_4	1.0	g
KCl	0.5	g
$MgSO_4.7H_2O$	0.5	g
$FeSO_4.7H_2O$	0.01	g
Congo red (add after adjust pH)	0.035	g
Agar	15	g

pH 7.3

APPENDIX B

Nucleotide sequence and GenBank accession number of 16S rRNA

1) *Streptomyces rochei* ERY1

ERY1
Program BLASTN 2.2.27+
Description
All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)
Query Length 1447
Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
GQ392058.1	*Streptomyces rochei*strain A-1 16S ribosomal RNA gene, partial sequence	2658	2658	99%	0.0	99%
NR_041091.1	*Streptomyces rochei* strain NBRC 12908 16S ribosomal RNA, partial sequence >dbj|AB184237.1| *Streptomyces rochei*gene for 16S rRNA, partial sequence, strain: NBRC 12908	2612	2612	97%	0.0	99%
AF503493.1	*Streptomyces tuirus* 16S ribosomal RNA, partial sequence	2608	2608	99%	0.0	99%
AB184156.1	*Streptomyces mutabilis* gene for 16S rRNA, partial sequence, strain: NBRC 12800	2606	2606	98%	0.0	99%
JN128892.1	*Streptomyces rochei* strain SM3 16S ribosomal RNA gene, partial sequence	2604	2604	97%	0.0	99%
AF233338.1	*Streptomyces maritimus* 16S ribosomal RNA gene, partial sequence	2595	2595	97%	0.0	99%
EU570372.1	*Streptomyces rochei* strain 173315 16S ribosomal RNA gene, partial sequence	2591	2591	97%	0.0	99%

ERY1 was the most closely related to gb|GQ392058.1|*Streptomyces rochei* strain A-1 16S ribosomal RNA gene, partial sequence
Length=1518
Score = 2658 bits (1439), Expect = 0.0
Identities = 1442/1443 (99%), Gaps = 1/1443 (0%)
Strand=Plus/Plus

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Query  1     GGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCACTCTGGGACAA  60
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Sbjct  77    GGGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCACTCTGGGACAA  136

Query  61    GCCCTGGAAACGGGGTCTAATACCGGATACTGATCCTCGCAGGCATCTGCGAGGTTCGAA  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  137   GCCCTGGAAACGGGGTCTAATACCGGATACTGATCCTCGCAGGCATCTGCGAGGTTCGAA  196

Query  121   AGCTCCGGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTAGTTGGTGAGGTAACGGCTCA  180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  197   AGCTCCGGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTAGTTGGTGAGGTAACGGCTCA  256

Query  181   CCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGTACTGAGACA  240
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Sbjct  257   CCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGG-ACTGAGACA  315

Query  241   CGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGA  300
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Sbjct  316   CGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGAAAGCCTGA  375

Query  301   TGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA  360
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Sbjct  376   TGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCAGCAGGGAA  435

Query  361   GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCG  420
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Sbjct  436   GAAGCGAAAGTGACGGTACCTGCAGAAGAAGCGCCGGCTAACTACGTGCCAGCAGCCGCG  495

Query  421   GTAATACGTAGGGCGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGC  480
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Sbjct  496   GTAATACGTAGGGCGCAAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTCGTAGGCGGC  555

Query  481   TTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAG  540
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Sbjct  556   TTGTCACGTCGGTTGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCAGTCGATACGGGCAG  615

Query  541   GCTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCA  600
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Sbjct  616   GCTAGAGTTCGGTAGGGGAGATCGGAATTCCTGGTGTAGCGGTGAAATGCGCAGATATCA  675

Query  601   GGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAG  660
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Sbjct  676   GGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCCGATACTGACGCTGAGGAGCGAAAG  735

Query  661   CGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAG  720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  736   CGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGGTGGGCACTAG  795

Query  721   GTGTGGGCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCGCCTGGG  780
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Sbjct  796   GTGTGGGCAACATTCCACGTTGTCCGTGCCGCAGCTAACGCATTAAGTGCCCCGCCTGGG  855

Query  781   GAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAG  840
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Sbjct  856   GAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGCGGAG  915
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Query  841   CATGTGGCTTAATTCGACGCAACGCGAAGAACCTTACCAAGGCTTGACATACACCGGAAA  900
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Sbjct  916   CATGTGGCTTAATTCGACGCAACGCGAAGAACCTTACCAAGGCTTGACATACACCGGAAA  975

Query  901   ACCCTGGAGACAGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCAGC  960
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Sbjct  976   ACCCTGGAGACAGGGTCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTGTCGTCAGC 1035

Query  961   TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCCGTGTTGCC 1020
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1036  TCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCCGTGTTGCC 1095

Query  1021  AGCAGGCCCTTGTGGTGCTGGGGACTCACGGGAGACCGCCGGGGTCAACTCGGAGGAAGG 1080
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1096  AGCAGGCCCTTGTGGTGCTGGGGACTCACGGGAGACCGCCGGGGTCAACTCGGAGGAAGG 1155

Query  1081  TGGGGACGACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG 1140
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1156  TGGGGACGACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACGTGCTACAATGG 1215

Query  1141  CCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAAGCCGGTCTCAGTT 1200
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1216  CCGGTACAATGAGCTGCGATACCGCGAGGTGGAGCGAATCTCAAAAAGCCGGTCTCAGTT 1275

Query  1201  CGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGC 1260
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Sbjct  1276  CGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAATCGCAGATCAGC 1335

Query  1261  ATTGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTC 1320
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Sbjct  1336  ATTGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACGTCACGAAAGTC 1395

Query  1321  GGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAGGTGGGACT 1380
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Sbjct  1396  GGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGCTGTCGAAGGTGGGACT 1455

Query  1381  GGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCTGGATCACCTC 1440
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  1456  GGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGCTGGATCACCTC 1515

Query  1441  CTT  1443
             |||
Sbjct  1516  CTT  1518
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2) *Streptomyces albus*subsp. *albus* PRE5

PRE5

Program BLASTN 2.2.27+

Description

All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS,environmental samples or phase 0, 1 or 2 HTGS sequences)

Query Length 1447

Sequences producing significant alignments:

Accession	Description	Max score	Total score	Query coverage	E value	Max ident
NR_025615.1	Streptomyces albus subsp. albus strain DSM 40313 16S ribosomal RNA, partial sequence >emb|AJ621602.2| Streptomyces albus subsp. albus 16S rRNA gene, type strain DSM 40313T	2625	2625	99%	0.0	99%
DQ026669.1	Streptomyces albus subsp. albus strain NRRL B-2365 16S ribosomal RNA gene, partial sequence	2606	2606	98%	0.0	99%
AJ781753.1	Streptomyces gibsonii 16S rRNA gene, strain LMG 19912T	2591	2591	98%	0.0	99%
AJ781366.1	Streptomyces rangoonensis 16S rRNA gene, type strain LMG 20295	2591	2591	98%	0.0	99%
AB184781.1	Streptomyces albus subsp. albus gene for 16S rRNA, partial sequence, strain: NBRC 3710	2590	2590	98%	0.0	99%
NR_041208.1	Streptomyces albus subsp. albus strain NBRC 3418 16S ribosomal RNA, partial sequence >dbj|AB184771.1| Streptomyces albus subsp. albus gene for 16S rRNA, partial sequence, strain: NBRC 3418	2590	2590	98%	0.0	99%
AB184257.1	Streptomyces albus subsp. albus gene for 16S rRNA, partial sequence, strain: NBRC 13014	2584	2584	98%	0.0	99%
EF059751.1	Streptomyces albus 16S ribosomal RNA gene, partial sequence	2582	2582	98%	0.0	99%
AB184258.1	Streptomyces almquistii gene for 16S rRNA, partial sequence, strain: NBRC 13015	2582	2582	97%	0.0	99%

PRE5 was the most closely related toref|NR_025615.1|*Streptomyces albus* subsp. *albus* strain DSM 40313 16S ribosomal
RNA, partial sequence emb|AJ621602.2|*Streptomyces albus* subsp. *albus*16S rRNA gene, type strain DSM 40313T
Length=1499
Score = 2625 bits (1421), Expect = 0.0
Identities = 1444/1455 (99%), Gaps = 1/1455 (0%)
Strand=Plus/Plus

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Query  1     GCTTCGGTGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCACT  60
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Sbjct  46    GCTTCGGTGGTGGATTAGTGGCGAACGGGTGAGTAACACGTGGGCAATCTGCCCTGCACT  105

Query  61    CTGGGACAAGCCCTGGAAACGGGGTCTAATACCGGATATGACACGGGATCGCATGGTCTC  120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  106   CTGGGACAAGCCCTGGAAACGGGGTCTAATACCGGATATGACACGGGATCGCATGGTCTC  165

Query  121   CGTGTGGAAAGCTCCGGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGT  180
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Sbjct  166   CGTGTGGAAAGCTCCGGCGGTGCAGGATGAGCCCGCGGCCTATCAGCTTGTTGGTGGGGT  225

Query  181   GATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGA  240
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Sbjct  226   GATGGCCTACCAAGGCGACGACGGGTAGCCGGCCTGAGAGGGCGACCGGCCACACTGGGA  285

Query  241   CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGC  300
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Sbjct  286   CTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTGGGGAATATTGCACAATGGGCGC  345

Query  301   AAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCA  360
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  346   AAGCCTGATGCAGCGACGCCGCGTGAGGGATGACGGCCTTCGGGTTGTAAACCTCTTTCA  405

Query  361   GCAGGGAAGAAGCGCGAGTGACGGTACCTGCAGAAGAAGCACCGGCTAACTACGTGCCAG  420
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Sbjct  406   GCAGGGAAGAAGCGCGAGTGACGGTACCTGCAGAAGAAGCACCGGCTAACTACGTGCCAG  465

Query  421   CAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTCG  480
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Sbjct  466   CAGCCGCGGTAATACGTAGGGTGCGAGCGTTGTCCGGAATTATTGGGCGTAAAGAGCTCG  525

Query  481   TAGGCGGCTTGTCGCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGAT  540
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Sbjct  526   TAGGCGGCTTGTCGCGTCGGATGTGAAAGCCCGGGGCTTAACCCCGGGTCTGCATTCGAT  585

Query  541   ACGGGCAGGCTAGAGTTCGGCAGGGGAGATTGGAATTCCTGGTGTAGCGGTGAAATGCGC  600
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Sbjct  586   ACGGGCAGGCTAGAGTTCGGCAGGGGAGATTGGAATTCCTGGTGTAGCGGTGAAATGCGC  645

Query  601   AGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCCGATACTGACGCTGAGG  660
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Sbjct  646   AGATATCAGGAGGAACACCGGTGGCGAAGGCGGATCTCTGGGCCGATACTGACGCTGAGG  705

Query  661   AGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGTTG  720
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Sbjct  706   AGCGAAAGCGTGGGGAGCGAACAGGATTAGATACCCTGGTAGTCCACGCCGTAAACGTTG  765

Query  721   GGCACTAGGTGTGGGCGGCATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCC  780
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Sbjct  766   GGCACTAGGTGTGGGCGGCATTCCACGTCGTCCGTGCCGCAGCTAACGCATTAAGTGCCC  825
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Query  781   CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAG  840
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Sbjct  826   CGCCTGGGGAGTACGGCCGCAAGGCTAAAACTCAAAGGAATTGACGGGGGCCCGCACAAG  885

Query  841   CGGCGGAGCATGTGGCTTAATTCGACGCAACGCGAAGAACCTTACCAAGGCTTGACATAC  900
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Sbjct  886   CGGCGGAGCATGTGGCTTAATTCGACGCAACGCGAAGAACCTTACCAAGGCTTGACATAC  945

Query  901   ACCGGAAAGCCGTAGAGATACGGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTG  960
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Sbjct  946   ACCGGAAAGCCGTAGAGATACGGCCCCCCTTGTGGTCGGTGTACAGGTGGTGCATGGCTG 1005

Query  961   TCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCT 1020
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Sbjct  1006  TCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTGTCCT 1065

Query  1021  GTGTTGCCAGCAACTCCTTTCGGGGAGGTTGGGGACTCACGGGAGACTGCCGGGGTCAAC 1080
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Sbjct  1066  GTGTTGCCAGCAACTCCTTTCGGGGAGGTTGGG-ACTCACGGGAGACTGCCGGGGTCAAC 1124

Query  1081  TCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACG 1140
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Sbjct  1125  TCGGAGGAAGGTGGGGACGACGTCAAGTCATCATGCCCCTTATGTCTTGGGCTGCACACG 1184

Query  1141  TGCTACAATGGCCGGTACAATGACCTGCAATGCCGTGAGGTGAAGCGAATCTCAAAAAGC 1200
             |||||||||||||||||||||| |||| |||||||||||||| ||||||||||||||||
Sbjct  1185  TGCTACAATGGCCGGTACAATGAGCTGCGATGCCGTGAGGTGGAGCGAATCTCAAAAAGC 1244

Query  1201  CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT 1260
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Sbjct  1245  CGGTCTCAGTTCGGATTGGGGTCTGCAACTCGACCCCATGAAGTCGGAGTCGCTAGTAAT 1304

Query  1261  CGCAAATCACCATTGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACG 1320
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Sbjct  1305  CGCAGATCAGCATTGCTGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACG 1364

Query  1321  TCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAATCGTCA 1380
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Sbjct  1365  TCACGAAAGTCGGTAACACCCGAAGCCGGTGGCCCAACCCCTTGTGGGAGGGAGTCGTCG 1424

Query  1381  AAGGTGGGACTGGCGATTGGGACAAATTCGTAACAAGGTACCCGTACCGGAAGGTGCGGC 1440
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Sbjct  1425  AAGGTGGGACTGGCGATTGGGACGAAGTCGTAACAAGGTAGCCGTACCGGAAGGTGCGGC 1484

Query  1441  TGGATCACCTCCTTT  1455
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Sbjct  1485  TGGATCACCTCCTTT  1499
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CURRICULUM VITAE

Author's Name	Miss Prapaipit Suwitchayanon
Date/Year of Birth	July 3th, 1986
Place of Birth	Chiang Mai, Thailand
Education	2003 High School from NawamintrachutitPayap, Mae Rim District, Chiang Mai, Thailand 2007 Bachelor's degree from Department of Plant Pathology, Faculty of Agriculture, Chiang Mai University, Thailand 2009 Master's degree from Department of Plant Pathology, Faculty of Agriculture, Chiang Mai University, Thailand 2017 Doctoral degree from Department of Entomology and Plant Pathology, Faculty of Agriculture, Chiang Mai University, Thailand
Scholarship	2013 The Graduate School, Chiang Mai University, Thailand
Publications	Kunasakdakul, K., Suwitchayanon, P. and Phuakjaiphaeo, C. 2012. Antifungal Pathogen Activities and Growth Promotion of EndophyticActinomycetes on *Brassica* Seedling. Chiang Mai University Journal 11(1): 7-12. Suwitchayanon, P., Phuakjaiphaeo C. and Kunasakdakul, K. 2012. Identification and Evaluations of EndophyticActinomycetes Strain GAR1 on Biocontrol Effect of *Pythiumaphanidermatum* and Plant Growth Promoting Properties. Proceedings: 1st ASEAN Plus Three Graduate Research Congress, Chiang Mai, Thailand. ST: 173-720.

Experiences	Researcher in Project of Research and Development of Agricultural Bio-products in order to Reduce Agro-Chemical on Highland Plantations funding supported by Highland Research and Development Institute (Public organization) during November 2009 to September 2012