APPENDIX A

IDENTIFICATION OF FUNGI IN THIS STUDY

gi|74135500|gb|DQ123646.1| *Penicillium citrinum* strain NRRL 35449 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=1110

```
Score = 880 bits (444), Expect = 0.0
Identities = 465/465 (100%), Gaps = 0/465 (0%), Strand=Plus/Plus

Query  4    AGTGCGGGCCCCTCGGGGCCCAACCTCCCACCCGTGTTGCCCGAACCTATGTTGCCTCGG  63
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  15   AGTGCGGGCCCCTCGGGGCCCAACCTCCCACCCGTGTTGCCCGAACCTATGTTGCCTCGG  74

Query  64   CGGGCCCCGCGCCCGCCGACGGCCCCCCTGAACGCTGTCTGAAGTTGCAGTCTGAGACCT  123
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  75   CGGGCCCCGCGCCCGCCGACGGCCCCCCTGAACGCTGTCTGAAGTTGCAGTCTGAGACCT  134

Query  124  ATAACGAAATTAGTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAA  183
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  135  ATAACGAAATTAGTTAAAACTTTCAACAACGGATCTCTTGGTTCCGGCATCGATGAAGAA  194

Query  184  CGCAGCGAAATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGA  243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  195  CGCAGCGAAATGCGATAACTAATGTGAATTGCAGAATTCAGTGAATCATCGAGTCTTTGA  254

Query  244  ACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTGCCC  303
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  255  ACGCACATTGCGCCCTCTGGTATTCCGGAGGGCATGCCTGTCCGAGCGTCATTGCTGCCC  314

Query  304  TCAAGCCCGGCTTGTGTGTTGGGCCCCGTcccccccGCCGGGGGGACGGGCCCGAAAGGC  363
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  315  TCAAGCCCGGCTTGTGTGTTGGGCCCCGTCCCCCCCGCCGGGGGGACGGGCCCGAAAGGC  374

Query  364  AGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTCGTCACCCGCTCTAGTAGGC  423
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  375  AGCGGCGGCACCGCGTCCGGTCCTCGAGCGTATGGGGCTTCGTCACCCGCTCTAGTAGGC  434

Query  424  CCGGCCGGCGCCAGCCGACCCCCAACCTTTAATTATCTCAGGTTG  468
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  435  CCGGCCGGCGCCAGCCGACCCCCAACCTTTAATTATCTCAGGTTG  479
```

APPENDIX B

RAW DATA OF PHAGOCYTOSIS AND KILLING ASSAY

Phagocytosis and killing of J774.1 macrophage on *Penicillium citrinum*

Table B-1 Phagocytosis of J774.1 on *P. citrinum* with MOI=10

Time (min)	**Macrophage cell count (categorize by number of internalized conidia)**											**PP**	**PI**
	0	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**		
0	100, 100, 100	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	-
30	54, 55, 54	27, 29, 26	14, 7, 15	6, 6, 3	2, 3, 2	1, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	50, 45, 46	1.72, 1.62, 1.59
60	34, 23, 34	30, 29, 35	18, 22, 22	10, 16, 10	3, 5, 6	4, 4, 1	1, 1, 1	0, 0, 2	0, 0, 0	0, 0, 0	0, 0, 0	66, 77, 77	2.03, 2.17, 2.08
120	23, 17, 20	26, 30, 40	20, 29, 21	14, 8, 7	6, 8, 8	5, 3, 2	2, 1, 1	1, 3, 3	1, 1, 0	1, 0, 0	1, 0, 0	77, 83, 80	2.64, 2.24, 2.05
240	11, 10, 15	21, 28, 36	29, 27, 18	12, 14, 14	11, 7, 8	7, 4, 4	2, 4, 2	4, 3, 3	1, 1, 0	1, 1, 0	1, 1, 0	89, 90, 85	2.93, 2.71, 2.34

Table B-2 Killing ability of J774.1 on *P. citrinum* with MOI=10

Time (min)	Control (without macrophage)		Test (co-incubate with macrophages)		% Killing
	Count	Mean CFU	Count	Mean CFU	
0	(148,144), (150,148)	(5.84×10^5), (5.96×10^5)	(146,144), (155,145)	(5.80×10^5), (6.00×10^5)	0, 0
30	(140,142), (144,151)	(5.64×10^5), (5.90×10^5)	(78,76), (87,92)	(3.08×10^5), (3.58×10^5)	45.39, 39.32
60	(139,140), (150,147)	(5.60×10^5), (5.94×10^5)	(49,45), (45,42)	(1.88×10^5), (1.74×10^5)	66.42, 70.70
120	(145,140), (146,140)	(5.72×10^5), (5.72×10^5)	(50,50), (41,49)	(2.00×10^5), (1.80×10^5)	65.03, 68.53
240	(137,146), (144,140)	(5.64×10^5), (5.68×10^5)	(50,58), (42,53)	(2.16×10^5), (1.90×10^5)	61.70, 66.54

(Test1), (Test2)

Phagocytosis and killing of J774.1 macrophage on *Penicillium marneffei*

Table B-3 Phagocytosis of J774.1 on *P. marneffei* with MOI=10

Time (min)	**Macrophage cell count (categorize by number of internalized conidia)**											**PP**	**PI**
	0	**1**	**2**	**3**	**4**	**5**	**6**	**7**	**8**	**9**	**10**		
0	100, 100, 100	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	-
30	54, 55, 54	27, 29, 26	14, 7, 15	6, 6, 3	2, 3, 2	1, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	0, 0, 0	50, 45, 46	1.72, 1.62, 1.59
60	34, 23, 34	30, 29, 35	18, 22, 22	10, 16, 10	3, 5, 6	4, 4, 1	1, 1, 1	0, 0, 2	0, 0, 0	0, 0, 0	0, 0, 0	66, 77, 77	2.03, 2.17, 2.08
120	23, 17, 20	26, 30, 40	20, 29, 21	14, 8, 7	6, 8, 8	5, 3, 2	2, 1, 1	1, 3, 3	1, 1, 0	1, 0, 0	1, 0, 0	77, 83, 80	2.64, 2.24, 2.05
240	11, 10, 15	21, 28, 36	29, 27, 18	12, 14, 14	11, 7, 8	7, 4, 4	2, 4, 2	4, 3, 3	1, 1, 0	1, 1, 0	1, 1, 0	89, 90, 85	2.93, 2.71, 2.34

Table B-4 Killing ability of J774.1 on *P. marneffei* with MOI=10

Time (min)	Control (without macrophage)		Test (co-incubate with macrophages)		% Killing
	Count	Mean CFU	Count	Mean CFU	
0	(142,146), (121,128)	(5.76 x 10^5), (4.98 x 10^5)	(144,143), (140,110)	(5.74 x 10^5), (5.00 x 10^5)	0, 0
30	(139,144), (125,110)	(5.66 x 10^5), (4.70 x 10^5)	(125,140), (112,104)	(5.30 x 10^5), (4.32 x 10^5)	6.36, 8.09
60	(136,153), (120,120)	(5.38 x 10^5), (4.80 x 10^5)	(118,ND*), (100,90)	(4.72 x 10^5), (3.80 x 10^5)	12.27, 20.83
120	(136,141), (120,120)	(5.54 x 10^5), (4.80 x 10^5)	(103,80), (72,63)	(3.66 x 10^5), (2.7 x 10^5)	33.94, 43.75
240	(116,101), (122,112)	(4.52 x 10^5), (4.68 x 10^5)	(49,40), (48,39)	(1.78 x 10^5), (1.74 x 10^5)	60.62, 62.80

APPENDIX C

PRIMERS DESIGN AND SEQUENCES ANALYSIS

C1. Cu, Zn Superoxide dismutase gene degenerate primer design

ClustalW alignment of fungal Cu, Zn SOD amino acid sequences

```
Anid-Q9HEY7         MVKAVAVLRGDSKVSGTVTFEQADENSNTTVSWNITGNDPNAERGFHIHQFGDNTNGCTS 60
Afla-AAM94904       -VKAVAVLRGDSKISGTVTFEQADANAPTTVSWNITGHDANAERAFHVHQFGDNTNGCTS 59
Afum-AAL38991       MVKAVAV-RGDSKITGTVTFEQADENSPTTVSWNIKGNDPNAKRGFHVHQFGDNTNGCTS 59
Scer-NP_012638      MVQAVAVLKGDAGVSGVVKFEQASESEPTTVSYEIAGNSPNAERGFHIHEFGDATNGCVS 60
Psin-AAR15417       MVKAVCVLRGDSKITGIVNFEQESDSSPTTISWEISNHDADAKRGFHITPFGDNTNGCTS 60
Cneo-AAK31915       MVKAVVVLKGESYVHGTVCFTQESENAPVCITGEIKDMDADAKRGMHVHEFGDNTNGCTS 60
                     *:** * :*:: : * * * * . .  . :: :* . ..:*:*.:*:  *** ****.*

Anid-Q9HEY7         AGPHFNPFGKTHGAPEDEVRHVGDLGNFKTDAEGNSKGSKTDKLIKLIGAESVLGRTLVV 120
Afla-AAM94904       AGPHFNPFGKEHGAPEDENRHVGDLGNFKTDAEGNAVGSKQDKLIKLIGAESVLGRTLVI 119
Afum-AAL38991       AGPHFNPYGKTHGAPEDSERHVGDLGNFETDAEGNAVGSKQDKLIKLIGAESVLGRTLVV 119
Scer-NP_012638      AGPHFNPFKKTHGAPTDEVRHVGDMGNVKTDENGVAKGSFKDSLIKLIGPTSVVGRSVVI 120
Psin-AAR15417       AGPHFNPHGKTHGNVTDENRHVGDMGNIETDCDGNSKGSIKDKLIKLIGPHSVIGRTVVI 120
Cneo-AAK31915       AGPHYNPFKKHHGAPTDSERHVGDLGNIQTNSCGAAQLDFSDKIISLYGPHSIIGRSLVV 120
                    ****:**. * **   *. *****:**.:*:  * :  .  *.:*.* *. *::**::*:
                    ------>

Anid-Q9HEY7         HAGTDDLGRGDSEESKKTGNAGARPACGVIGIAA 154
Afla-AAM94904       HAGTDDLGRSEHPESKKTGNAGARPACGVIGIAA 153
Afum-AAL38991       HAGTDDLGRGGNEESKKTGNAGARPACGVIGIAA 153
Scer-NP_012638      HAGQDDLGKGDTEESLKTGNAGPRPACGVIGLTN 154
Psin-AAR15417       HAGTDDLGKGGNDESLKTGNAGPRPACGVIGVAN 154
Cneo-AAK31915       HASTDDLGKGGNEESLKTGNAGARLACGVIGIST 154
                    **. ****:.   ** ******.* ******::
                                    <-------
```

Primer sequences

SOD-F: SAGPHY/FNP or 5’-WSIGCIGGICCICAITWYAAYCC-3’

SOD-R: KTGNAGA/PR or 5’-CKIGSICCIGCRTTICCIGTYTT-3’

Expected PCR product: ~250 bp

Homology searching of amplified PCR product fragments

S. cerevisiae 249 bp

```
  1 TGGGCGGGGC CGCAGTTTAA CCCTTTCAAG AAGACACACG GTGCTCCAAC TGACGAAGTC
 61 AGACATGTCG GTGACATGGG TAACGTAAAG ACGGACGAAA ATGGTGTGGC CAAGGGCTCC
121 TTCAAGGACT CTTTGATCAA GCTTATCGGT CCTACCTCCG TTGTAGGCAG AAGCGTCGCT
181 TATCCACGCC GGCCAAGATG ACTTAGGTAA GGGTGACACT GAAGAATCTT TGAAAACCGG
241 CAATGCCGG
```

gb|AY690619.1| *Saccharomyces cerevisiae* copper-zinc superoxide dismutase gene, complete cds, Length=496
Score = 392 bits (212), Expect = 3e-106 Identities = 223/228 (97%), Gaps = 1/228 (0%) Strand=Plus/Plus

```
Query 22   CCTTTCAAGAAGACACACGGTGCTCCAACTGACGAAGTCAGACATGTCGGTGACATGGGT  81
           ||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct 212  CCTTTCAAGAAGACACATGGTGCTCCAACTGACGAAGTCAGACATGTCGGTGACATGGGT  271

Query 82   AACGTAAAGACGGACGAAAATGGTGTGGCCAAGGGCTCCTTCAAGGACTCTTTGATCAAG  141
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 272  AACGTAAAGACGGACGAAAATGGTGTGGCCAAGGGCTCCTTCAAGGACTCTTTGATCAAG  331

Query 142  CTTATCGGTCCTACCTCCGTTGTAGGCAGAAGCGTCGCTTATCCACGCCGGCCAAGATGA  201
           ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Sbjct 332  CTTATCGGTCCTACCTCCGTTGTAGGCAGAAGCGTCG-TTATCCACGCCGGCCAAGATGA  390

Query 202  CTTAGGTAAGGGTGACACTGAAGAATCTTTGAAAACCGGCAATGCCGG  249
           ||||||||||||||||||||||||||||||||| || || ||||||||
Sbjct 391  CTTAGGTAAGGGTGACACTGAAGAATCTTTGAAGACTGGTAATGCCGG  438
```

P. marneffei **251 bp**

```
  1 GCCGGTCCTC ACTTCAACCC CTTCGGAAAG ACCCACGGTG CTCCCACCGA TGACGAACGC
 61 CATGTCGGTG ACTTGGGTAA CTTCAAGACC GATGCTCAGG GCAATGCTGT CGGCTTCGTC
121 GAGGACAAGC TCATCAAGTT GATCGGTGCT GAGAGCGTTC TCGGACGTAC TATCGTCGTC
181 CACGCCGGTA CTGACGACCT CGGCCGTGGT GGCAACGAGG AGTCCAAGAA GACTGGCAAC
241 GCTGGTCCTC G
```

ref|XM_001215721.1| *Aspergillus terreus* NIH2624 superoxide dismutase (ATEG_06543) mRNA, complete cds, Length=492
Score = 273 bits (302, Expect = 2e-70 Identities = 208/246 (84%), Gaps = 0/246 (0%) Strand=Plus/Plus

```
Query 1    GCCGGTCCTCACTTCAACCCCTTCGGAAAGACCCACGGTGCTCCCACCGATGACGAACGC  60
           ||||| ||||||||||||||||||   |||||||||||||| ||    ||||| |  |||
Sbjct 208  GCCGGCCCTCACTTCAACCCCTTCTCCAAGACCCACGGTGCCCCTGAGGATGAGGTGCGC  267

Query 61   CATGTCGGTGACTTGGGTAACTTCAAGACCGATGCTCAGGGCAATGCTGTCGGCTTCGTC  120
           || ||||||||| | ||||||||||||||||||||  ||||||| || ||||||| |
Sbjct 268  CACGTCGGTGACCTCGGTAACTTCAAGACCGATGCAGAGGGCAACGCCGTCGGCTCCAAG  327

Query 121  GAGGACAAGCTCATCAAGTTGATCGGTGCTGAGAGCGTTCTCGGACGTACTATCGTCGTC  180
            ||||||||||  ||||| |||||||||| ||||||||||| || |||||  | ||||||
Sbjct 328  CAGGACAAGCTGGTCAAGCTGATCGGTGCCGAGAGCGTTCTGGGCCGTACCCTTGTCGTC  387

Query 181  CACGCCGGTACTGACGACCTCGGCCGTGGTGGCAACGAGGAGTCCAAGAAGACTGGCAAC  240
           |||||||| ||||| || |||||||||||||||||||||||||||||||||||||| |||
Sbjct 388  CACGCCGGCACTGATGATCTCGGCCGTGGTGGCAACGAGGAGTCCAAGAAGACTGGTAAC  447

Query 241  GCTGGT  246
           || |||
Sbjct 448  GCCGGT  453
```

gb|AF401280.1| *Aspergillus flavus* Cu,Zn-superoxide dismutase mRNA, partial cds, Length=463
Score = 268 bits (296), Expect = 8e-69 Identities = 210/251 (83%), Gaps = 0/251 (0%) Strand=Plus/Plus

```
Query 1    GCCGGTCCTCACTTCAACCCCTTCGGAAAGACCCACGGTGCTCCCACCGATGACGAACGC  60
           || || |||||||||||||||||||| |||   ||||||||||||   |||||  | |||
Sbjct 179  GCTGGCCCTCACTTCAACCCCTTCGGCAAGGAGCACGGTGCTCCCGAGGATGAGAACCGC  238

Query 61   CATGTCGGTGACTTGGGTAACTTCAAGACCGATGCTCAGGGCAATGCTGTCGGCTTCGTC  120
           || |||||||||||||| |||||||||||||||||| |||| || || ||||||| |
Sbjct 239  CACGTCGGTGACTTGGGCAACTTCAAGACCGATGCTGAGGGTAACGCCGTCGGCTCCAAG  298

Query 121  GAGGACAAGCTCATCAAGTTGATCGGTGCTGAGAGCGTTCTCGGACGTACTATCGTCGTC  180
            |||||||||| || ||| |||||||||| |||||||| || || |||||| ||||| ||
Sbjct 299  CAGGACAAGCTTATTAAGCTGATCGGTGCCGAGAGCGTACTTGGCCGTACTCTCGTCATC  358

Query 181  CACGCCGGTACTGACGACCTCGGCCGTGGTGGCAACGAGGAGTCCAAGAAGACTGGCAAC  240
           |||||||||||||||||||| |||||| |||   ||  |||||||||||||||||||||
Sbjct 359  CACGCCGGTACTGACGACCTTGGCCGTAGTGAACACCCGGAGTCCAAGAAGACTGGCAAT  418

Query 241  GCTGGTCCTCG  251
           |||||| ||||
Sbjct 419  GCTGGTGCTCG  429
```

ref|XM_748622.1| ***Aspergillus fumigatus*** **Af293 Cu,Zn superoxide dismutase SOD1 (AFUA_5G09240) mRNA, complete cds, Length=477**
Score = 255 bits (282), Expect = 5e-65 Identities = 207/251 (82%), Gaps = 0/251 (0%) Strand=Plus/Plus

```
Query 1    GCCGGTCCTCACTTCAACCCCTTCGGAAAGACCCACGGTGCTCCCACCGATGACGAACGC  60
           || |||||||||||||||||||  || |||||||| || |||||    ||   ||| |||
Sbjct 193  GCTGGTCCTCACTTCAACCCCTATGGCAAGACCCATGGAGCTCCTGAGGACTCCGAGCGC  252

Query 61   CATGTCGGTGACTTGGGTAACTTCAAGACCGATGCTCAGGGCAATGCTGTCGGCTTCGTC  120
           |||||||||||| | ||||||||| ||||||||||| |||| || || ||||||| |
Sbjct 253  CATGTCGGTGACCTTGGTAACTTCGAGACCGATGCTGAGGGTAACGCCGTCGGCTCCAAG  312

Query 121  GAGGACAAGCTCATCAAGTTGATCGGTGCTGAGAGCGTTCTCGGACGTACTATCGTCGTC  180
            |||||||||| || ||| |||| ||||| ||||||||||| || || ||  | |||||
Sbjct 313  CAGGACAAGCTTATTAAGCTGATTGGTGCCGAGAGCGTTCTGGGCCGGACCTTGGTCGTT  372

Query 181  CACGCCGGTACTGACGACCTCGGCCGTGGTGGCAACGAGGAGTCCAAGAAGACTGGCAAC  240
           ||||||||||| |||||||||||  | ||||||||||||||||||||||||||||| |||
Sbjct 373  CACGCCGGTACCGACGACCTCGGAAGGGGTGGCAACGAGGAGTCCAAGAAGACTGGTAAC  432

Query 241  GCTGGTCCTCG  251
           |||||| ||||
Sbjct 433  GCTGGTGCTCG  443
```

C2. Glyceraldehyde-3-phosphate dehydrogenase gene degenerate primer design

ClustalW alignment of fungal *GAPDH* nucleotide sequences

```
Acap-AF273704       CGCGAGCATCCCCTGGGGCAAGCACGGCGTGGAATACGTCGTTGAGTCCACCGGCGTCTT 324
Aory-AB032274       CGCTGCCATCCCCTGGGGCTCCGCTGGCGCTGCCTACATCGTCGAGTCCACTGGTGTCTT 305
Afum-XM_743052      CTCTCAGATCCCCTGGTCTGAGACCGGCGCTGCCTACATCGTCGAGTCTACTGGTGTTTT 305
Cimm-AY536450       TGCCAACATCCCATGGGCCGAAACCGGTGCCGACTACGTCATTGAATCCACTGGTGTCTT 164
Pbra-AF396657       CGCCAACATCCCCTGGGGCAAGCACGGCGTCGACTATGTCGTCGAGTCCACAGGCGTCTT 539
                      *    ***** ***         ** *  *  **  ** * ** ** ** ** ** **

Acap-AF273704       CACCACCACCGAGAAGGCCAGCGCCCACTTGAAAGGCGGTGCCAAGAAGGTCATCATCTC 384
Aory-AB032274       CACCACCACCGAGAAGGCCTCCGCTCACTTGAAGGGTGGCGCCAAGAAGGTCATCATCTC 365
Afum-XM_743052      CACCACCAAGGAGAAGGCCTCCGCTCACTTGAAGGGTGGTGCCAAGAAGGTCATCATCTC 365
Cimm-AY536450       CACCACCACGGAGAAGGCCAGCGCTCACTTGAAGGGTGGCGCGAAGAAGGTCATCATCTC 224
Pbra-AF396657       CACCACCACTGAAAAGGCCAAGGCCCATTTATCTGGTGGCGCCAAAAAGGTCATCATCTC 599
                    ********  ** ******   ** ** **    ** ** ** ** **************

Acap-AF273704       CGCCCCCTCTGCAGATGCCCCCATGTTCGTCATGGGCGTCAACGAGAAAACATACGACCC 444
Aory-AB032274       TGCTCCTTCTGCTGATGCCCCCATGTTCGTTATGGGTGTCAACAACAAGGAATACAAGAC 425
Afum-XM_743052      CGCTCCTTCTGCTGATGCCCCCATGTTCGTCATGGGTGTCAACAACACCACCTACACCTC 425
Cimm-AY536450       CGCCCCATCTGCCGATGCCCCAATGTTCGTAATGGGTGTCAACAACGAGACATATAAGTC 284
Pbra-AF396657       CGCCCCATCCGCTGATGCCCCCATGTTCGTCATGGGCGTCAACGAGAAGAGTTACAGGCC 659
                     ** ** ** ** ******** ******** ***** ****** *       **     *

Acap-AF273704       GAGCGTCAACGTCCTTTCCAACGCCTCCTGCACCACCAACTGCCTCGCCCCGCTTGCAAA 504
Aory-AB032274       CGACATCAACGTCCTCTCTAACGCTTCTTGCACCACCAACTGCCTTGCTCCCCTTGCTAA 485
Afum-XM_743052      CGACATCCAGGTCCTCTCCAACGCCTCTTGCACCACCAACTGCCTTGCACCCCTGGCCAA 485
Cimm-AY536450       CGATATCAAGGTTCTCTCCAACGCCTCCTGCACAACCAACTGTCTTGCTCCTTTGGCCAA 344
Pbra-AF396657       CGACATCTCCGTCCTCTCCAACGCCTCTTGCACCACCAACTGCCTCGCTCCACTCGCCAA 719
                         **   ** ** ** ***** ** ***** ******** ** ** **  * ** **

Acap-AF273704       GGTCATCAACGACAACTTCGGCCTGACCGAGGGCCTCATGACGACCATCCACTCCTACAC 564
Aory-AB032274       GGTTATCAACGACAACTTCGGTCTCGTTGAGGGTCTCATGACCACTGTCCACTCCTACAC 545
Afum-XM_743052      GGTCATCAACGACAAGTTCGGCATTGTTGAGGGTCTCATGACCACCGTCCACTCCTACAC 545
Cimm-AY536450       GGTTGTCAATGACAACTTCGGCTTGGTTGAGGGTTTGATGACCACCGTCCACTCCTATAC 404
Pbra-AF396657       GGTCATCCACGACAACTTCGGTATTGCTGAAGGACTCATGACCACCATCCATTCCTATAC 779
                    ***  ** * ***** *****  *    ** **  * ***** **  **** ***** **

Acap-AF273704       CGCCACCCAGAAGACCGTCGACGGGCCGTCTTCCAAGGACTGGCGTGGTGGCCGCACCGC 624
Aory-AB032274       TGCTACCCAGAAGACTGTCGATGCTCCCTCCGCCAAGGACTGGCGTGGTGGACGTACCGC 605
Afum-XM_743052      CGCCACCCAGAAGGTCGTCGATGCTCCCTCCAACAAGGACTGGAGAGGTGGTCGTACTGC 605
Cimm-AY536450       CGCCACTCAGAAGACTGTCGATGGCCCATCCTCCAAGGACTGGCGTGGTGGCCGTGCCGC 464
Pbra-AF396657       TGCCACCCAGAAGACCGTCGATGGCCCTTCCCACAAGGACTGGCGTGGTGGCCGCACTGC 839
                     ** ** ******   ***** *  ** **   ********** * ***** **  * **

Acap-AF273704       TGCTCAGAACATCATCCCCAGCAGCACAGGCGCCGCCAAGGCCGTCGGCAAGGTCATCCC 684
Aory-AB032274       CGCTCAGAACATCATCCCCAGCTCCACTGGTGCTGCCAAGGCTGTCGGCAAGGTCATTCC 665
Afum-XM_743052      TGCCCAGAACATCATTCCCAGCTCGACTGGTGCTGCTAAGGCCGTCGGCAAGGTCATTCC 665
Cimm-AY536450       TGCTCAGAACATCATCCCTAGCAGCACTGGTGCCGCCAAGGCTGTTGGAAAGGTCATTCC 524
Pbra-AF396657       GGCTCAGAACATCATCCCCAGCAGCACTGGCGCCGCCAAGGCTGTAGGAAAGGTCATCCC 899
                     ** *********** ** ***   ** ** ** ** ***** ** ** ******** **
```

Primer sequences

GAP-F: 5’-ACHGGYGTYTTCACCACCA-3’

GAP-R: 5’-ATGACCTTKCCDACRGCCT-3’

Expected size ~ 400 bp

C3. Calmodulin gene

Homology searching of amplified PCR product fragments

H. capsulatum calmodulin gene fragment 570 bp

```
  1 AAGGAGGCCT TCTCTCTATT TGTAAGTTGA CTTCATTTTT GCCCCACACC TAACAGGCTT
 61 ACCAACGGCG CCTCAGGACA AGAACTAACA TCGGCATTTA TTTTTACAGG ATAAAGATGG
121 CGATGGTGAT TATTTCCACT TCCACTTGTT TCCAGAAGCT TAGGAAATGA GAGATGTAAA
181 AAATTTGTCG ACTGGGACTA GAGCTGACCA CTTGTTTAAA TGAAACAGGG CAAATCACCA
241 CCAAAGAGTT GGGAACAGTA ATGCGGTCTC TGGGACAAAA CCCTTCCGAA TCAGAACTAC
301 AGGACATGAT CAACGAGGTT GATGCAGATA ACAATGGAAC CATTGACTTC CCGGGTATGG
361 TGCCCAGTTA TTTCTCAGAT GATTTGATGC TATCTGCAAT GATGCTGTGT CTAACCGCTT
421 CTCCCTGTTT CACAGAGTTT TTGACCATGA TGGCAAGGAA AATGAAGGAT ACCGATTCTG
481 AAGAAGAAAT TCGAGAAAGC ATTCAAAGTT TTCGATCGTG ATAACAACGG TTTTATCTCC
541 TGCTGCCGAG TTACGCCCCG TGATGACTTC
```

gb|AF072882.1|AF072882 *Ajellomyces capsulatus* calmodulin (CAM1) gene, complete cds, Length=2100
Score = 941 bits (509), Expect = 0.0 Identities = 552/572 (96%), Gaps = 6/572 (1%) Strand=Plus/Plus

```
Query 1      AAGGAGGCCTTCTCTCTATTTGTAAGTTGACTTCATTTTTGCCCCACACCTAACAGGCTT  60
             |||||||||||||||||||| ||||||||||||||||||| |||||||||||||||||||
Sbjct 600    AAGGAGGCCTTCTCTCTATTCGTAAGTTGACTTCATTTTTTCCCCACACCTAACAGGCTT  659

Query 61     ACCAACGGCGCCTCAGGACAAGAACTAACATCGGCATTTATTTTTACAGGATAAAGATGG  120
             ||||||  |||||||||||||||||||||||||||||||| |||||||||||||||||||
Sbjct 660    ACCAACCACGCCTCAGGACAAGAACTAACATCGGCATTTA-TTTTACAGGATAAAGATGG  718

Query 121    CGATGGTGATTATTTCCACTTCCACTTGTTTCCAGAAGCTTAGGAAATGAGAGATGTAAA  180
             ||||||| |||||||||||||||||||||||||||||||||||| |||||||||||||||
Sbjct 719    CGATGGTAATTATTTCCACTTCCACTTGTTTCCAGAAGCTTAGGGAATGAGAGATGTAAA  778

Query 181    AAATTTGTCGACTGGGACTAGAGCTGACCACTTGTTTAAATGAAACAGGGCAAATCACCA  240
             | |||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 779    ACATTTGTTGACTGGGACTAGAGCTGACCACTTGTTTAAATGAAACAGGGCAAATCACCA  838

Query 241    CCAAAGAGTTGGGAACAGTAATGCGGTCTCTGGGACAAAACCCTTCCGAATCAGAACTAC  300
              |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Sbjct 839    CCAAAGAGTTGGGAACAGTAATGCGGTCTCTGGGGCAAAACCCTTCCGAATCAGAACTAC  898

Query 301    AGGACATGATCAACGAGGTTGATGCAGATAACAATGGAACCATTGACTTCCCGGGTATGG  360
              ||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Sbjct 899    AGGACATGATCAATGAGGTTGATGCAGATAACAATGGAACCATTGACTTCCCGGGTATGG  958

Query 361    TGCCCAGTTATTTCTCAGATG-ATTTGAT-GCTATCTGCAATGATGCTGTGTCTAACCGC  418
              ||||||||||||||||||||  ||||||| | ||||||||||||||||||||||||||||
Sbjct 959    TGCCCAGTTATTTCTCAGATTCATTTGATCG-TATCTGCAATGATGCTGTGTCTAACCGC  1017

Query 419    TTCTCCCTGTTTCACAGAGTTTTTGACCATGATGGCAAGGAAAATGAAGGATACCGATTC  478
              ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||||
Sbjct 1018   TTCTCCCTGTTTCACAGAGTTTTTGACTATGATGGCAAGGAAAATGAAGGATACCGATTC  1077

Query 479    TGAAGAAGAAATTCGAGAAAGCATTCAAAGTTTTCGATCGTGATAACAACGGTTTTATCT  538
             ||||||||||||||||||| |||||||||||||||||||||||||||||||| |||||||
Sbjct 1078   TGAAGAAGAAATTCGAGAA-GCATTCAAAGTTTTCGATCGTGATAACAACGGGTTTATCT  1136

Query 539    CCTGCTGCCGAGTTACGCCCCGTGATGACTTC  570
             | ||||||||||||||||| ||||||||||||
Sbjct 1137   C-TGCTGCCGAGTTACGCCACGTGATGACTTC  1167
```

P. marneffei calmodulin gene fragment 550 bp

```
  1 CTCTCTATTT GTAAGTTTGG ATTTCTGGTT GTCGCAATGT TGTGGTGGGT GGTTCGCTGA
 61 CTAGCCGTTT GGATGAATAG GACAAGGATG GTGATGGTGA GTGACGCCAC GAACACCAGA
121 CATATAGTCT TCGAACAAAA AGTTATTACT GCGAACAGAT ATTAATAACA TCAATAGGTC
181 AAATTACAAC CAAGGAACTG GGCACCGTCA TGCGTTCCCT CGGCCAGAAC CCTTCCGAAT
241 CCGAATTGCA GGACATGATC AACGAGGTCG ACGCTGACAA CAACGGCACA ATCGATTTCC
301 CTGGTATGAT GCAGCCTCTA TTTATCGCAG CCGTTTCCGA TCATAAGGGC AGATACTGAC
361 TGCCTTAGAA TTCTTGACAA TGATGGCCCG CAAAATGAAG GATACCGACT CCGAGGAAGA
421 GATCCGCGAG GCTTTCAAGG TGTTTGATCG TGACAACAAT GGATTCATCT CTGCTGCTGA
481 ATTGCGCCAC GTTATGACCT CGATTGGCGA AAAGTTGACC GACGACGAAG TTGACGAGAT
541 GATTCGCGAG
```

gb|AY678609.1| *Talaromyces flavus* strain AS3.6681 calmodulin (cmd) gene, partial cds, Length=540
Score = 592 bits (320), Expect = 6e-166 Identities = 469/537 (87%), Gaps = 26/537 (4%) Strand=Plus/Plus

```
Query  1    CTCTCTATTTGTAAGTTTGG-ATTTCTGGTTGTCGCAATGTTGTGGTGGGTGGTTCGCTG  59
            |||||| ||||||||||| | | || ||||||||||||||||||||||||||||| ||||
Sbjct  25   CTCTCTTTTTGTAAGTTTAGCAATT-TGGTTGTCGCAATGTTGTGGTGGGTGGTT-GCTG  82

Query  60   ACTAGCCGTTTGGATGAATAGGACAAGGATGGTGATGGTGAGTGACG-CCACGAACACCA  118
            ||||||||||| ||||| |||||||||||||| ||||||||||  || |||||||||  |
Sbjct  83   ACTAGCCGTTTTGATGAGTAGGACAAGGATGGAGATGGTGAGT--CGGCCACGAACAATA  140

Query  119  GACATATAGTC-TTCGAACAAAAAGTTATTACTGCGAACAGATATTAA-TAACATC-AAT  175
              || | || | || ||||||   |||||  | ||||||||||||| | ||  ||| |||
Sbjct  141  TCCAAA-AGGCGTT-GAACAAGG-GTTATCGCCGCGAACAGATATTGACTAT-ATCGAAT  196

Query  176  AGGTCAAATTACAACCAAGGAACTGGGCACCGTCATGCGTTCCCTCGGCCAGAACCCTTC  235
            ||||||||| |||||||||||||||||||| |||||||||||||||||||||||||| ||
Sbjct  197  AGGTCAAATCACAACCAAGGAACTGGGCACTGTCATGCGTTCCCTCGGCCAGAACCCCTC  256

Query  236  CGAATCCGAATTGCAGGACATGATCAACGAGGTCGACGCTGACAACAACGGCACAATCGA  295
            |||||||||| ||||||||||||||||||| |||||||||||||||||||||||||||||
Sbjct  257  CGAATCCGAACTGCAGGACATGATCAACGAAGTCGACGCTGACAACAACGGCACAATCGA  316

Query  296  TTTCCCTGGTATGATGCAGCCTCTATTTATCGCAGCCGTTTCCGATCATAAGGGCAGATA  355
            |||||||||||||||  |   |  |||  || |||  | |    || || | ||||| ||
Sbjct  317  TTTCCCTGGTATGAT--A---TA-ATTGCTCACAG--GAT----ATTATGATGGCAG-TA  363

Query  356  CTGACTGCCTTAGAATTCTTGACAATGATGGCCCGCAAAATGAAGGATACCGACTCCGAG  415
            || ||||||  ||||||| |||||||||||||||||||||||||||| ||||||||||||
Sbjct  364  CTAACTGCCGCAGAATTCCTGACAATGATGGCCCGCAAAATGAAGGACACCGACTCCGAG  423

Query  416  GAAGAGATCCGCGAGGCTTTCAAGGTGTTTGATCGTGACAACAATGGATTCATCTCTGCT  475
            |||||||||||||||| ||||||||||||||| |||||||||||||||||||||||||||
Sbjct  424  GAAGAGATCCGCGAGGCATTCAAGGTGTTTGACCGTGACAACAATGGATTCATCTCTGCT  483

Query  476  GCTGAATTGCGCCACGTTATGACCTCGATTGGCGAAAAGTTGACCGACGACGAAGTT  532
            || |||||||||||||||||||||||||||||||| ||||||||||||||||| |||
Sbjct  484  GCCGAATTGCGCCACGTTATGACCTCGATTGGCGAGAAGTTGACCGACGACGAGGTT  540
```

gb|AY678604.1| *Penicillium pinophilum* strain AS3.6551 calmodulin (cmd) gene, partial cds, Length=541
Score = 592 bits (320), Expect = 6e-166 Identities = 469/537 (87%), Gaps = 25/537 (4%) Strand=Plus/Plus

```
Query  1    CTCTCTATTTGTAAGTTTGGATTTCTGGTTGTCGCAATGTTGTGGTGGGTGGTTCGCTGA  60
            |||||| ||||||||||||||  ||||||||||||||||||||||||| ||||| |||||
Sbjct  25   CTCTCTTTTTGTAAGTTTGGAAATCTGGTTGTCGCAATGTTGTGGTGGATGGTTAGCTGA  84

Query  61   CTAGCCGTTTGGATGAATAGGACAAGGATGGTGATGGTGAGTGACGCCACGAACACCAGA  120
            |||||||||| ||||| |||||||||||||| ||||||||||  ||||||||||| | ||
Sbjct  85   CTAGCCGTTTTGATGAGTAGGACAAGGATGGAGATGGTGAGT-CCGCCACGAACA-C-GA  141

Query  121  C-ATA-TAGTCTTCGAACAAAAAG-TTATTACTGCGAACAGATATTAATAACATC-AATA  176
            | ||| | ||| |||||| ||| | || || |  ||| || ||||| |||| ||| ||||
Sbjct  142  CGATATTTGTC-TCGAAC-AAAGGTTTTTTTC-ACGAGCATATATTGATAAAATCTAATA  198

Query  177  GGTCAAATTACAACCAAGGAACTGGGCACCGTCATGCGTTCCCTCGGCCAGAACCCTTCC  236
            || ||||||||||| ||||||||||||||||| ||||||||||||||||||||||| |||
Sbjct  199  GGCCAAATTACAACTAAGGAACTGGGCACCGTTATGCGTTCCCTCGGCCAGAACCCCTCC  258

Query  237  GAATCCGAATTGCAGGACATGATCAACGAGGTCGACGCTGACAACAACGGCACAATCGAT  296
            ||||||||| ||||||||||||||||||| ||||||||||||||||||||||||||||||
Sbjct  259  GAATCCGAACTGCAGGACATGATCAACGAAGTCGACGCTGACAACAACGGCACAATCGAT  318

Query  297  TTCCCTGGTATGATGCAGCCTCTATT-TATCGCAGCCGTTTCCGATCATAAGGGCAGATA  355
            ||||||||||||||  |   |  ||| | || | |  ||||   || |  | ||||| ||
Sbjct  319  TTCCCTGGTATGAT--A---T-AATTGT-TCAC-G-GGTTT---AT-ACGATGGCAG-TA  364

Query  356  CTGACTGCCTTAGAATTCTTGACAATGATGGCCCGCAAAATGAAGGATACCGACTCCGAG  415
            || ||||||  |||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  365  CTAACTGCCGCAGAATTCTTGACAATGATGGCCCGCAAAATGAAGGATACCGACTCCGAG  424

Query  416  GAAGAGATCCGCGAGGCTTTCAAGGTGTTTGATCGTGACAACAATGGATTCATCTCTGCT  475
            ||||||||||| || ||||||||||||||||| |||||||||||||| || |||||||||
Sbjct  425  GAAGAGATCCGTGAAGCTTTCAAGGTGTTTGACCGTGACAACAATGGTTTTATCTCTGCT  484

Query  476  GCTGAATTGCGCCACGTTATGACCTCGATTGGCGAAAAGTTGACCGACGACGAAGTT  532
            |||||| |||||||||| ||||||||||||||||| |||||||||||||| || |||
Sbjct  485  GCTGAACTGCGCCACGTCATGACCTCGATTGGCGAGAAGTTGACCGACGATGAGGTT  541
```

gb|AY678603.1| *Penicillium aculeatum* strain AS3.6632 calmodulin (cmd) gene, partial cds, Length=540
Score = 592 bits (320), Expect = 6e-166 Identities = 468/536 (87%), Gaps = 24/536 (4%) Strand=Plus/Plus

```
Query  1    CTCTCTATTTGTAAGTTTGGATTTCTGGTTGTCGCAATGTTGTGGTGGGTGGTTCGCTGA  60
            |||||| |||||||||||||||||||  |||||||||||||||||||||||||| |||||
Sbjct  25   CTCTCTTTTTGTAAGTTTGGATTTCTACTTGTCGCAATGTTGTGGTGGGTGGTTAGCTGA  84

Query  61   CTAGCCGTT-TGGATGAATAGGACAAGGATGGTGATGGTGAGTGACGCCACGAACACCA-  118
            ||||||||| || |||| |||||||||||||| ||||||||||  |||| ||||||| | 
Sbjct  85   CTAGCCGTTCTG-ATGAGTAGGACAAGGATGGAGATGGTGAGTT-CGCCGCGAACACGAC  142

Query  119  GACATATAGTCTTCGAACAAAAAGTTATTACTGCGAACAGATATTAATA-ACATC-AATA  176
            ||||| | |||| ||||||||  | |||  || | || ||||||| ||| || || || |
Sbjct  143  GACAT-T-GTCT-CGAACAAAG-GATATCGCTACAAATAGATATTGATACAC-TCGAACA  197

Query  177  GGTCAAATTACAACCAAGGAACTGGGCACCGTCATGCGTTCCCTCGGCCAGAACCCTTCC  236
            || || || |||||||||||| |||||||||||||||||||||||||||||||||| |||
Sbjct  198  GGCCAGATCACAACCAAGGAATTGGGCACCGTCATGCGTTCCCTCGGCCAGAACCCCTCC  257

Query  237  GAATCCGAATTGCAGGACATGATCAACGAGGTCGACGCTGACAACAACGGCACAATCGAT  296
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  258  GAATCCGAATTGCAGGACATGATCAACGAGGTCGACGCTGACAACAACGGCACAATCGAT  317

Query  297  TTCCCTGGTATGATGCAGCCTCTATTTATCGCAGCCGTTTCCGATCATAAGGGCAGATAC  356
            |||||||||||| |  |  | | ||| | ||  |  |||   ||| |  | ||||| |||
Sbjct  318  TTCCCTGGTATGGTATAATC-C-ATT-A-CG--G--GTT---GAT-ACGATGGCAG-TAC  364

Query  357  TGACTGCCTTAGAATTCTTGACAATGATGGCCCGCAAAATGAAGGATACCGACTCCGAGG  416
            | | ||||  |||||||||||||||||||||||||||||||||||||||||||||||| |
Sbjct  365  TAATTGCCGCAGAATTCTTGACAATGATGGCCCGCAAAATGAAGGATACCGACTCCGAAG  424

Query  417  AAGAGATCCGCGAGGCTTTCAAGGTGTTTGATCGTGACAACAATGGATTCATCTCTGCTG  476
            |||||||||| || ||||||||||||||||| |||||||||||||||||||||||||| |
Sbjct  425  AAGAGATCCGTGAAGCTTTCAAGGTGTTTGACCGTGACAACAATGGATTCATCTCTGCCG  484

Query  477  CTGAATTGCGCCACGTTATGACCTCGATTGGCGAAAAGTTGACCGACGACGAAGTT  532
            | |||||||||||||| ||||||||||||||||| ||||||||||||||||| |||
Sbjct  485  CGGAATTGCGCCACGTCATGACCTCGATTGGCGAGAAGTTGACCGACGACGAGGTT  540
```

C4. Catalase gene primer design

P. marneffei amplified PCR fragment 558 bp

```
  1 GCGGTGGATT CGTTTCTTAC CCCGAGAAGA TCCAGGCAAT CAAAAAGCGT AGCCAGGGAC
 61 CCAAGTTCCG CGAACATCAC AACCAGGCGC AGTTATTCTA CAACTCTCTT ACTGAATACG
121 AGCAACACCA CGTCGCCAAA GCGTTTAGCT TTGAGCTTGA CCATTGCGAC GACCCTGTGG
181 TCTACCAGCG CATGGCCTTG CGTATTGCAG AGATTGATCT TTCCCTCGCC CAGAAAGTCG
241 CCGTAATGGT CGGCGCCCCA ACACCTGAAA CTCCCGGAAA GCAGAACCAC GGCAAAAAGA
301 CTCGCGGTCT TTCACAAATT GACTTCAAGC CTCGTGTACC AACTGTGGCC AGCAGACGTA
361 TCGCCATAAT CATTGGCGAC GGCTTCGACT CTGTCGCTTT TAACGGAGTG TATACTGCCA
421 TCAAAGCTGC TGGCGCTCTG CCATTTGTCA TCGGCACAAA GAGACAGCCC ATCTTCGCAG
481 ATGGCGTTGA CCCCCAGACC GGAAATGGCG TAACACCCGA ACACCAATAC GAGGGTGTGC
541 GTTCTACAAT GTTCGACG
```

ClastalW alignment of *cat* gene fragments

```
Pmar-AL683912      ACTAAGGGAACAGTCAACTACTGGCCGAATCGGTTTGATGCGGTACCACCAATCAAGCCT 60
Pmar-PCR           ------------------------------------------------------------

Pmar-AL683912      GAGGACGGTGGATTCGTTTCTTACCCCGAGAAGATCCAGGCAATCAAAAAGCGTAGCCAG 120
Pmar-PCR           ----GCGGTGGATTCGTTTCTTACCCCGAGAAGATCCAGGCAATCAAAAAGCGTAGCCAG 56
                        *******************************************************

Pmar-AL683912      GGACCCAAGTTCCGCGAACATCACAACCAGGCGCAGTTATTCTACAACTCTCTTACTGAA 180
Pmar-PCR           GGACCCAAGTTCCGCGAACATCACAACCAGGCGCAGTTATTCTACAACTCTCTTACTGAA 116
                   ************************************************************

Pmar-AL683912      TACGAGCAACACCACGTCGCCAAAGCGTTTAGCTTTGAGCTTGACCATTGCGACGACCCT 240
Pmar-PCR           TACGAGCAACACCACGTCGCCAAAGCGTTTAGCTTTGAGCTTGACCATTGCGACGACCCT 176
                   ************************************************************

Pmar-AL683912      GTGGTCTACCAGCGCATGGCCTTGCGTATTGCAGAGATTGATCTTTCCCTCGCCCAGAAA 300
Pmar-PCR           GTGGTCTACCAGCGCATGGCCTTGCGTATTGCAGAGATTGATCTTTCCCTCGCCCAGAAA 236
                   ************************************************************

Pmar-AL683912      GTCGCCGTAATGGTCGGCGCCCCAACACCTGAAACTCCCGGAAAGCAGAACCACGGCAAA 360
Pmar-PCR           GTCGCCGTAATGGTCGGCGCCCCAACACCTGAAACTCCCGGAAAGCAGAACCACGGCAAA 296
                   ************************************************************

Pmar-AL683912      AAGACTCGCGGTCTTTCACAAATTGACTTCAAGCCTCGTGTACCAACTGTGGCCAGCAGA 420
Pmar-PCR           AAGACTCGCGGTCTTTCACAAATTGACTTCAAGCCTCGTGTACCAACTGTGGCCAGCAGA 356
                   ************************************************************

Pmar-AL683912      CGTATCGCCATAATCATTGGCGACGGCTTCGACTCTGTCGCTTTTAACGGAGTGTATACT 480
Pmar-PCR           CGTATCGCCATAATCATTGGCGACGGCTTCGACTCTGTCGCTTTTAACGGAGTGTATACT 416
                   ************************************************************

Pmar-AL683912      GCCATCAAAGCTGCTGGCGCTCTGCCATTTGTCATCGGCACAAAGAGACAACCCATCTTC 540
Pmar-PCR           GCCATCAAAGCTGCTGGCGCTCTGCCATTTGTCATCGGCACAAAGAGACAGCCCATCTTC 476
                   ************************************************** *********

Pmar-AL683912      GCAGATGGCGTTGACCCCCAGACCGGANATGGCGTAACACCCGAACACCAATACGAGGGT 600
Pmar-PCR           GCAGATGGCGTTGACCCCCAGACCGGAAATGGCGTAACACCCGAACACCAATACGAGGGT 536
                   *************************** ********************************

Pmar-AL683912      GTGCGTTCTACAATGTTCGACGCTACTTTCATCCCCGGTGGACCACACGTCAA 653
Pmar-PCR           GTGCGTTCTACAATGTTCGACG------------------------------- 558
                   **********************
```

Homology searching of PCR product fragments

ref|XM_742595.1| *Aspergillus fumigatus* Af293 spore-specific catalase CatA (AFUA_6G03890) mRNA, complete cds, Length=2253
Score = 178 bits (196), Expect = 3e-41 Identities = 348/506 (68%), Gaps = 15/506 (2%) Strand=Plus/Plus

```
Query  62    CAAGTTCCGCGAACATCACAACCAGGCGCAGTTATTCTACAACTCTCTTACTGAATACGA  121
             ||| || ||||| || |||||||| || ||| | |||||||||||  |  | ||  ||||
Sbjct  1389  CAAATTTCGCGAGCACCACAACCAAGCCCAGCTCTTCTACAACTCAATGTCCGAGCACGA  1448

Query  122   GCAACACCACGTCGCCAAAGCGTTTAGCTTTGAGCTTGACCATTGCGACGACCCTGTGGT  181
             | | | |||| |    || || || ||||| ||||| ||||| |||||||||||    ||
Sbjct  1449  GAAGCTCCACATGAAGAAGGCTTTCAGCTTCGAGCTCGACCACTGCGACGACCCCACCGT  1508

Query  182   CTACCAGCGCAT----GGCCTTGCGTATTGCAGAGATTGATCTTTCCCTCGCCCAGAAAG  237
             |||| | ||  |    |||| | ||  | || || || || ||    |||||||||||||
Sbjct  1509  CTACGAACGGCTCGCCGGCCAT-CGCCTCGCCGAAATCGACCTCGAGCTCGCCCAGAAAG  1567

Query  238   TCGCCGTAATGGTCGGCGCCCCAACACCTGAAACTCCCGGAAAGCAGAACCACGGCAAAA  297
             ||||||  |||||||| ||||| |  || |  |   ||   |||||||||||||||  | 
Sbjct  1568  TCGCCGAGATGGTCGGTGCCCCGATCCCAGCCAAGGCCCTCAAGCAGAACCACGGCCGAC  1627

Query  298   A-GACTCGCGGTCTTTCACAAATTGACTTCAAGCCTCGTGTACCA-ACTGTGGCCAGCAG  355
               | | |||   || || || | ||| ||||  || |  | |||  ||  | |||||| |
Sbjct  1628  GCGCCCCGCAC-CTCTCCCAGACTGAGTTCATCCC-CAAGAACCCCACCATCGCCAGCCG  1685

Query  356   ACGTATCGCCATAATCATTGGCGACGGCTTCGACTCTGTCGCTTTTAACGGAGTGTATAC  415
              || |||||||| ||||| |||||||||| |||| | ||||| || | |||  || | ||
Sbjct  1686  CCGCATCGCCATTATCATCGGCGACGGCTACGACCCCGTCGCCTTCACCGGCTTGAAGAC  1745

Query  416   TGCCATCAAAGCTGCTGGCGCTCTGCCATTTGTCATCGGCACAAAGAGACAGCCCATCTT  475
              || ||||| |||||  |||| || || ||  |||| ||||| ||| |     |||||| 
Sbjct  1746  CGCTATCAAGGCTGCCAGCGCCCTCCCCTTCATCATTGGCACCAAGCGCTCCGCCATCTA  1805

Query  476   CGCAGATGGCGTTGACCCCCAGA---CCGGAAATGGCGTAACACCCGAACACCAATACGA  532
             ||| || ||||  ||   | |||   ||   || ||| | |  || || ||||| |||||
Sbjct  1806  CGCCGACGGCGAGGA---CAAGACCTCCTCCAAGGGCATCATTCCGGACCACCACTACGA  1862

Query  533   GGGTGTGCGTTCTACAATGTTCGACG  558
              ||   ||| || || ||||||||||
Sbjct  1863  CGGCCAGCGCTCAACCATGTTCGACG  1888
```

dbj|AB079611.1| *Aspergillus oryzae* catA gene for catalase, complete cds, Length=3210
Score = 165 bits (182), Expect = 2e-37 Identities = 378/563 (67%), Gaps = 11/563 (1%) Strand=Plus/Plus

```
Query  3     GGTGGATTCGTTTCTTACCCCGAGAAGATCCAGGCAATCAAAAAGCGTAGCCAGGGACCC  62
             ||||| ||||  || ||||| | |||  |  | |  ||||| |||||  ||| | | |||
Sbjct  1982  GGTGGCTTCGCGTCCTACCCTGCGAAACTGAACGGTATCAAGAAGCGCGGCCTGAGCCCC  2041

Query  63    AAGTTCCGCGAACATCACAACCAGGCGCAGTTATTCTACAACTCTCTTACTGAATACGAG  122
             ||||||||||| || ||||||||||| ||  | ||||||||||||||  | ||  |||||
Sbjct  2042  AAGTTCCGCGAGCACCACAACCAGGCTCAACTCTTCTACAACTCTCTCTCCGAGCACGAG  2101

Query  123   CAACACCACGTCGCCAAAGCGTTTAGCTTTGAGCTTGACCATTGCGACGACCCTGTGGTC  182
              |   |||||||   || || ||  |||| || || ||||| |||||||||||  | |||
Sbjct  2102  AAGGTCCACGTCAAGAAGGCCTTCGGCTTCGAACTGGACCACTGCGACGACCCCATCGTC  2161

Query  183   TACCAGCGCATGGC---CTTGCGTATTGCAGAGATTGATCTTTCCCTCGCCCAGAAAGTC  239
             ||| ||||| | ||   |   ||| | || ||||| |||||  | ||||||||| |||||
Sbjct  2162  TACGAGCGCCTCGCCGGCCACCGTCTCGCCGAGATCGATCTCACTCTCGCCCAGGAAGTC  2221

Query  240   GCCGTAATGGTCGGCGCCCCAACACCTGAAACTCCCGGAAAGCAGAACCACGGCAAAAAG  299
             ||||   | ||||||||||| |  || || |   |       | |||||| || ||
Sbjct  2222  GCCGAGCTCGTCGGCGCCCCGATCCCAGACAAGGCACTTCGCCCGAACCATGGAAAGCGC  2281

Query  300   A-CTCGCGGTCTTTCACAAATTGACTTCAAGCCTCGT--GTA-CCAACTGTGGCCAGCAG  355
             | |  ||  |||||| || |  || |||   ||  ||  | | || ||  | |||||  |
Sbjct  2282  AGCAAGC-ATCTTTCGCAGACCGAGTTC---CCGGGTAAGCAGCCGACGATCGCCAGTCG  2337

Query  356   ACGTATCGCCATAATCATTGGCGACGGCTTCGACTCTGTCGCTTTTAACGGAGTGTATAC  415
              || |||||||| || || |||||||| | |||| | |||||||| || ||  |  |
Sbjct  2338  CCGAATCGCCATCATTATCGGCGACGGATACGACCCCGTCGCTTTCAATGGCCTCAAGGG  2397

Query  416   TGCCATCAAAGCTGCTGGCGCTCTGCCATTTGTCATCGGCACAAAGAGACAGCCCATCTT  475
              |||||||  || | ||| ||  | || || ||||| ||||| ||| |    || ||||
Sbjct  2398  CGCCATCACGGCGGTTGGAGCCTTACCGTTCGTCATTGGCACCAAGCGGTCACCTATCTA  2457

Query  476   CGCAGATGGCGTTGACCCCCAGACCGGAAATGGCGTAACACCCGAACACCAATACGAGGG  535
             ||| || || |  |||       |    || ||||| |   |||| ||||| || || ||
Sbjct  2458  CGCCGACGGTGAGGACAAATCATCTTCCAAGGGCGTGATCGCCGACCACCAGTATGACGG  2517

Query  536   TGTGCGTTCTACAATGTTCGACG  558
                ||||||| || ||||| ||||
Sbjct  2518  ACAGCGTTCGACGATGTTTGACG  2540
```

gb|AY103479.1| *Ajellomyces capsulatus* catalase A (CATA) gene, complete cds, Length=4558
Score = 107 bits (118), Expect = 4e-20 Identities = 146/204 (71%), Gaps = 0/204 (0%) Strand=Plus/Plus

```
Query  62    CAAGTTCCGCGAACATCACAACCAGGCGCAGTTATTCTACAACTCTCTTACTGAATACGA  121
             |||||||||||| |||  |||||| ||||| |||||||| ||||||||  | ||||||||
Sbjct  2455  CAAGTTCCGCGAGCATATCAACCAAGCGCAATTATTCTATAACTCTCTCTCCGAATACGA  2514

Query  122   GCAACACCACGTCGCCAAAGCGTTTAGCTTTGAGCTTGACCATTGCGACGACCCTGTGGT  181
               | | ||| |||   || || ||| |||||||| | || || ||||| |||||  | ||
Sbjct  2515  AAAGCTCCATGTCAATAATGCTTTTTGCTTTGAGTTGGATCACTGCGATGACCCCATTGT  2574

Query  182   CTACCAGCGCATGGCCTTGCGTATTGCAGAGATTGATCTTTCCCTCGCCCAGAAAGTCGC  241
             |||| |  |  | |  |  || ||| | || || || | | ||||||||||    || ||
Sbjct  2575  CTACAATAGACTTGTGTCTCGGATTTCTGAAATCGACCATGCCCTCGCCCAAGCCGTTGC  2634

Query  242   CGTAATGGTCGGCGCCCCAACACC  265
              || |  |||||||| || || ||
Sbjct  2635  AGTGAAAGTCGGCGCACCGACCCC  2658
```

C5. Primer for *sodA* expression

```
cDNA             ATGGTCAAGGCTGTCGCTGTCCTCCGTGGAGACTCCAACATCAAGGGTACCGTCACCTTT 60
gDNA             ---GTCAAGGCTGTCGCTGTCCTCCGTGGAGACTCCAACATCAAGGGTACCGTCACCTTT 57
                    *********************************************************

cDNA             GAACAGGCTGACGAGAACTCCCCTACCACCATCTCATGGAACATCACCGGCCACGACGCC 120
gDNA             GAACAGGCTGACGAGAACTCCCCTACCACCATCTCATGGAACATCACCGGCCACGACGCC 117
                 ************************************************************

cDNA             AACGCTGAGCGTGGCATCCACGTTCACCAGTTCGGTGACAACACCAACGGCTGCACATCT 180
gDNA             AACGCTGAGCGTGGCATCCACGTTCACCAGTTCGGTGACAACACCAACGGCTGCACATCT 177
                 ************************************************************

cDNA             GCCGGTCCTCACT----------------------------------------------- 193
gDNA             GCCGGTCCTCACTGTATGCTTCCGACCTCCTCACTCCTCACTTCTCACTAAAGTGTTGGC 237
                 *************

cDNA             --------------------------TCAACCCCTTCGGAAAGACCCACGGTGCTCCCAC 227
gDNA             ATCACCGTACTAATAGAAATTCATAGTCAACCCCTTCGGAAAGACCCACGGTGCTCCCAC 297
                                           **********************************

cDNA             CGATGACGAACGCCATGTCGGTGACTTGGGTAACTTCAAGACCGATGCTCAGGGCAATGC 287
gDNA             CGATGACGAACGCCATGTCGGTGACTTGGGTAACTTCAAGACCGATGCTCAGGGCAATGC 357
                 ************************************************************

cDNA             TGTCGGCTTCGTCGAGGACAAGCTCATCAAGTTGATCGGTGCTGAGAGCGTTCTCGGA-- 345
gDNA             TGTCGGCTTCGTCGAGGACAAGCTCATCAAGTTGATCGGTGCTGAGAGCGTTCTCGGAGT 417
                 **********************************************************

cDNA             ---------------------------------------------------------CGT 348
gDNA             ATGTCCCAATTTTCTATGAGCATCTAGATGTTGTGTATATGTACTAACCGTTAATAGCGT 477
                                                                          ***

cDNA             ACTATCGTCGTCCACGCCGGTACTGACGACCTCGGCCGTGGTGGCAACGAGGAGTCCAAG 408
gDNA             ACTATCGTCGTCCACGCCGGTACTGACGACCTCGGCCGTGGTGGCAACGAGGAGTCCAAG 537
                 ************************************************************

cDNA             AAGACTGGCAACGCTGGTCCTCGTCCTGCTTGCG-------------------------- 444
gDNA             AAGACTGGCAACGCTGGTCCTCGTCCTGCTTGCGGTAAGCTGTCTATTCTCAAACAAAGG 597
                 **********************************
```

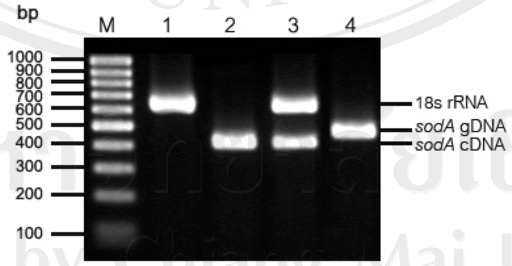

Figure C5. The amplified product of duplex RT-PCR with RRF1/RRH1 (18S rRNA) and specific primers for *sodA*. The product of 18S rRNA is 630 bp (lane 1), 448 bp of *sodA* is shown in lane 2 and mixed primers in lane 3. Lane 4 shows 521 bp amplified product form gDNA of *P. marneffei*.

C6. Primer for *gapdh* expression

```
cDNA            GTCCGAGACTGGTGCCGCTTACATTGTCGAGTCCACCGGTGTCTTCACCACCACCGAGAA
gDNA            GTCCGAGACTGGTGCCGCTTACATTGTCGAGTCCACCGGTGTCTTCACCACCACCGAGAA
                ************************************************************

cDNA            GGCCTCTGCTCACTTGAAGGGTGGCGCCAAGAAGGTCGTCATCTCTGCTCCTTCCGCAGA
gDNA            GGCCTCTGCTCACTTGAAGGGTGGCGCCAAGAAGGTCGTCATCTCTGCTCCTTCCGCAGA
                ************************************************************

cDNA            TGCTCCT--------------------------------------------------ATG
gDNA            TGCTCCTGTCAGTCCTCTCCCCTTCGTGGCCCTGTGGCCTGTTGCTAACCTATGTAGATG
                *******                                                  ***

cDNA            TTCGTCATGGGTGTCAACCACACAACCTACAAGAGCTCAGACACCATCATCTCCAACGCT
gDNA            TTCGTCATGGGTGTCAACCACACAACCTACAAGAGCTCAGACACCATCATCTCCAACGCT
                ************************************************************

cDNA            TCTTGCACCACCAACTGCTTGGCTCCCCTCGCCAAGATTGTCAACGACAACTGGGGTCTT
gDNA            TCTTGCACCACCAACTGCTTGGCTCCCCTCGCCAAGATTGTCAACGACAACTGGGGTCTT
                ************************************************************

cDNA            GTTGAGGGTCTCATGACCACCATTCACTCCTACACTGCTACCCAGAAGACCGTTGATGGT
gDNA            GTTGAGGGTCTCATGACCACCATTCACTCCTACACTGCTACCCAGAAGACCGTTGATGGT
                ************************************************************

cDNA            CCCTCCGCCAAGGACTGGCGTGGTGGTCGTACCGCTGCTCAGAACATCATTCCCAGCAGC
gDNA            CCCTCCGCCAAGGACTGGCGTGGTGGTCGTACCGCTGCTCAGAACATCATTCCCAGCAGC
                ************************************************************

cDNA            ACTGGTGCCGCCAAGGCTGTCGGAAAGGTCATTCCTGCCCTTAACGGAAAGCTCACTGGA
gDNA            ACTGGTGCCGCCAAGGCTGTCGGAAAGGTCATTCCTGCCCTTAACGGAAAGCTCACTGGA
                ************************************************************

cDNA            ATGTCCATGCGTGTTCCTACCTCCAACGTCTCCGTTGTTGACTTGACCTGCCGCACTGAG
gDNA            ATGTCCATGCGTGTTCCTACCTCCAACGTCTCCGTTGTTGACTTGACCTGCCGCACTGAG
                ************************************************************
```

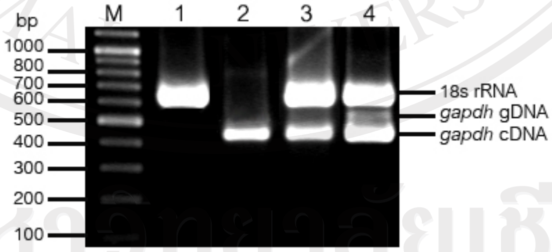

Figure C6. The amplified product of duplex RT-PCR with RRF1/RRH1 (18S rRNA) and specific primers for *gapdh*. The product of 18S rRNA is 630 bp (lane 1), 420 bp of *gapdh* is shown in lane 2 and mixed primers in lane 3. Lane 4 shows 470 bp amplified product of contaminated gDNA of *P. marneffei*.

C7. Primers for *acuD* expression

```
cDNA                GGCTGATATCATGGGTA--------------------------------- 712
gDNA                GGCTGATATCATGGGTATGACTGTTTGCCATCTCCCAATGGAAAGAATGA 2250
                    *****************


cDNA                -----------------------CCGACCTCCTTGCCATTGCACGTACCG 739
gDNA                ATCTAACATTGACTATATAGGTACCGACCTCCTTGCCATTGCACGTACCG 2300
                                           ***************************

cDNA                ACTCCGAAGCTGCTACTCTCATCACTTCTACCATCGACTACCGCGACCAC 789
gDNA                ACTCCGAAGCTGCTACTCTCATCACTTCTACCATCGACTACCGCGACCAC 2350
                    **************************************************

cDNA                GCCTACTTACTCGGATCTACCAACCCCAGCCTCCAACCTCTTAATGACCT 839
gDNA                GCCTACTTACTCGGATCTACCAACCCCAGCCTCCAACCTCTTAATGACCT 2400
                    **************************************************

cDNA                GATGGTTGCTGCCGAACAGTCCGGCAAATCCGGTGAACAACTCCAAGCCA 889
gDNA                GATGGTTGCTGCCGAACAGTCCGGCAAATCCGGTGAACAACTCCAAGCCA 2450
                    **************************************************

cDNA                TCGAAGACTCATGGATCGCTCAAGCCGGCATCAAGAAATTTGACGACGCC 939
gDNA                TCGAAGACTCATGGATCGCTCAAGCCGGCATCAAGAAATTTGACGACGCC 2500
                    **************************************************

cDNA                GTGATCGACACCATCAACCAAGGCAGCTTTGCCAATAAGAAAGAACTCAT 989
gDNA                GTGATCGACACCATCAACCAAGGCAGCTTTGCCAATAAGAAAGAACTCAT 2550
                    **************************************************

cDNA                CAACAGGTACCTCACAGCTGCCAAGGGCAAGAGCAACTCTGAAGCCCGTG 1039
gDNA                CAACAGGTACCTCACAGCTGCCAAGGGCAAGAGCAACTCTGAAGCCCGTG 2600
                    **************************************************

cDNA                CAATTGCCAAGGGAATCACCGGCATGGATATTTACTGGAACTGGGATGCG 1089
gDNA                CAATTGCCAAGGGAATCACCGGCATGGATATTTACTGGAACTGGGATGCG 2650
                    **************************************************

cDNA                CCCCGAACCCGAGGGGGTTTCTATAGGTACCAGGGTGGTACGCAATGCGC 1139
gDNA                CCCCGAACCCGAGGGGGTTTCTATAGGTACCAGGGTGGTACGCAATGCGC 2700
                    **************************************************

cDNA                CGTCAACCGTGCCGTCGCTTATGCACCATTCGCCGATCTGATTTGGATGG 1189
gDNA                CGTCAACCGTGCCGTCGCTTATGCACCATTCGCCGATCTGATTTGGATGG 2750
                    **************************************************

cDNA                AGAGCAAGCTTCCTGATTACAAGCAAGCCAAGGAGTTTGCTGATGGTGTG 1239
gDNA                AGAGCAAGCTTCCTGATTACAAGCAAGCCAAGGAGTTTGCTGATGGTGTG 2800
                    **************************************************
```

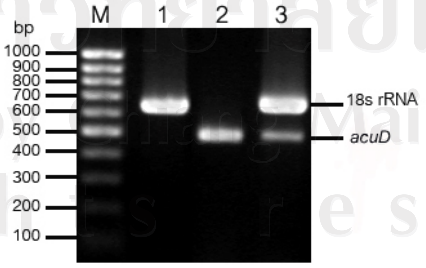

Figure C7. The amplified product of duplex RT-PCR with RRF1/RRH1 (18S rRNA) and specific primers for *acuD*. The product of 18S rRNA is 630 bp (lane 1), 450 bp of *acuD* is shown in lane 2 and mixed primers in lane 3.

C8. Primer for *hsp70* expression

```
gDNA            ACTTCGACTCTCGCCTTGTCAACCACTTTGCCTCCGAGTTCAAGAGGAAATATAAGAGTA 840
cDNA            ACTTCGACTCTCGCCTTGTCAACCACTTTGCCTCCGAGTTCAAGAGGAAATATAAGA--- 838
                *********************************************************

gDNA            TGTGATATACCCCCATCTGTTTTACAAGAATTGATAAGCTAACAACTTTCACAGAGGGTA 900
cDNA            ------------------------------------------------------AGG---

gDNA            CGTCAAAAATCCGAAATGAATTCTCATTCCCTCCCGTCTCTTGCATTCTTATTTGATATT 960
cDNA            ------------------------------------------------------------

gDNA            TGGAGCTTGGCTCTGGAGACTTCCTCAGAACCATCTGAAGAATGCATATGAAGACTCCCA 1020
cDNA            ------------------------------------------------------------

gDNA            ATATGAATCCATCTCCTTCCCTTTCATCCGCACTTGACTCTTGAAGAACTCCTCAGATGC 1080
cDNA            ------------------------------------------------------------

gDNA            TAACATGTGAAATAGATTTGACCACCAATGCTCGTGCTCTCCGCCGTCTCCGCACTGCCT 1140
cDNA            ---------------ATTTGACCACCAATGCTCGTGCTCTCCGCCGTCTCCGCACTGCCT 885
                               *********************************************

gDNA            GTGAGCGTGCTAAGCGTACCCTCTCTTCTTCCGCCCAGACCTCCATTGAGATCGACTCTC 1200
cDNA            GTGAGCGTGCTAAGCGTACCCTCTCTTCTTCCGCCCAGACCTCCATTGAGATCGACTCTC 945
                ************************************************************

gDNA            TCTTCGAGGGTATTGACTTCTACACCTCCATCACCCGTGCTCGTTTCGAGGAGCTCTGCC 1260
cDNA            TCTTCGAGGGTATTGACTTCTACACCTCCATCACCCGTGCTCGTTTCGAGGAGCTCTGCC 1005
                ************************************************************

gDNA            AGGATCTCTTCCGTTCCACCATGGAGCCCGTCGAGCGTGTCCTCCGTGATGCCAAGACCG 1320
cDNA            AGGATCTCTTCCGTTCCACCATGGAGCCCGTCGAGCGTGTCCTCCGTGATGCCAAGACCG 1065
                ************************************************************

gDNA            ACAAGTCTTCTGTCCACGAAATCGTCTTGGTCGGTGGTTCCACCCGTATCCCCAAGATCC 1380
cDNA            ACAAGTCTTCTGTCCACGAAATCGTCTTGGTCGGTGGTTCCACCCGTATCCCCAAGATCC 1125
                ************************************************************

gDNA            AGAAGCTCGTCACCGACTTCTTCAACAAGGAGCCCAACAAGTCCATCAACCCCGATGAGG 1440
cDNA            AGAAGCTCGTCACCGACTTCTTCAACAAGGAGCCCAACAAGTCCATCAACCCCGATGAGG 1185
                ************************************************************

gDNA            CTGTTGCCTACGGTGCTGCCGTCCAGGCTGCTATCCTTTCTGGTGACACTTCTTCCAAGT 1500
cDNA            CTGTTGCCTACGGTGCTGCCGTCCAGGCTGCTATCCTTTCTGGTGACACTTCTTCCAAGT 1245
                ************************************************************

gDNA            CCACCAACGAAATCTTGCTTCTCGACGTTGCTCCTCTCTCCGTCGGTATTGAGACTGCTG 1560
cDNA            CCACCAACGAAATCTTGCTTCTCGACGTTGCTCCTCTCTCCGTCGGTATTGAGACTGCTG 1305
                ************************************************************
```

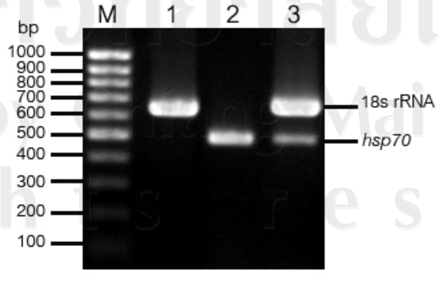

Figure C8. The amplified product of duplex RT-PCR with RRF1/RRH1 (18S rRNA) and specific primers for *hsp70*. The product of 18S rRNA is 630 bp (lane 1), 440 bp of *hsp70* is shown in lane 2 and mixed primers in lane 3.

C9. Primer for *P. marneffei cam* expression

```
PM-CAM          CTCTCTATTTGTAAGTTTGGATTTCTGGTTGTCGCAATGTTGTGGTGGGTGGTTCGCTGA 60
PrimerF         ------------------------CTGGTTGTCGCAATGTTGTG---------------- 20
                                        ********************

PM-CAM          CTAGCCGTTTGGATGAATAGGACAAGGATGGTGATGGTGAGTGACGCCACGAACACCAGA 120

PM-CAM          CATATAGTCTTCGAACAAAAAGTTATTACTGCGAACAGATATTAATAACATCAATAGGTC 180

PM-CAM          AAATTACAACCAAGGAACTGGGCACCGTCATGCGTTCCCTCGGCCAGAACCCTTCCGAAT 240

PM-CAM          CCGAATTGCAGGACATGATCAACGAGGTCGACGCTGACAACAACGGCACAATCGATTTCC 300

PM-CAM          CTGGTATGATGCAGCCTCTATTTATCGCAGCCGTTTCCGATCATAAGGGCAGATACTGAC 360

PM-CAM          TGCCTTAGAATTCTTGACAATGATGGCCCGCAAAATGAAGGATACCGACTCCGAGGAAGA 420

PM-CAM          GATCCGCGAGGCTTTCAAGGTGTTTGATCGTGACAACAATGGATTCATCTCTGCTGCTGA 480
                ------------------------------------------------------TGCTGA
                                                                      ******
PM-CAM          ATTGCGCCACGTTATGACCTCGATTGGCGAAAAGTTGACCGACGACGAAGTTGACGAGAT 540
                ATTGCGCCACGTTATG--------------------------------------------
                ****************
```

C10. Primers for *P. marneffei cat* expression

```
PM-CAT          CAAAAAGACTCGCGGTCTTTCACAAATTGACTTCAAGCCTCGTGTACCAACTGTGGCCAG 420
PrimerF         ------------------------------------------TGTACCAACTGTGGCCAG 18
                                                          ******************

PM-CAT          CAGACGTATCGCCATAATCATTGGCGACGGCTTCGACTCTGTCGCTTTTAACGGAGTGTA 480
PrimerF         CAGA-------------------------------------------------------- 22
                ****

PM-CAT          TACTGCCATCAAAGCTGCTGGCGCTCTGCCATTTGTCATCGGCACAAAGAGACAACCCAT 540

PM-CAT          CTTCGCAGATGGCGTTGACCCCCAGACCGGAAATGGCGTAACACCCGAACACCAATACGA 600

PM-CAT          GGGTGTGCGTTCTACAATGTTCGACGCTACTTTCATCCCCGGTGGACCACACGTCAAGAC 660

PM-CAT          CCTTGCCAGGATCGGACGGATTCGCCACTGGATAACAGAAACATTCGGTCACCTCAAAGC 720

PM-CAT          GCTCGGCGCGACAGGTGAGGCCGTCGATTTTGTCAAGCAGGCGCTTCTAGGTGTGGAGGC 780

PM-CAT          TGTACAATTTGCTAGTCAGAGTAGCACTGGTGTCGTTGAGTCGTATGGCGTGGTTACTGC 840
PrimerR         ----------------------AGCACTGGTGTCGTTGAGTCGT---------------- 22
                                      **********************
```

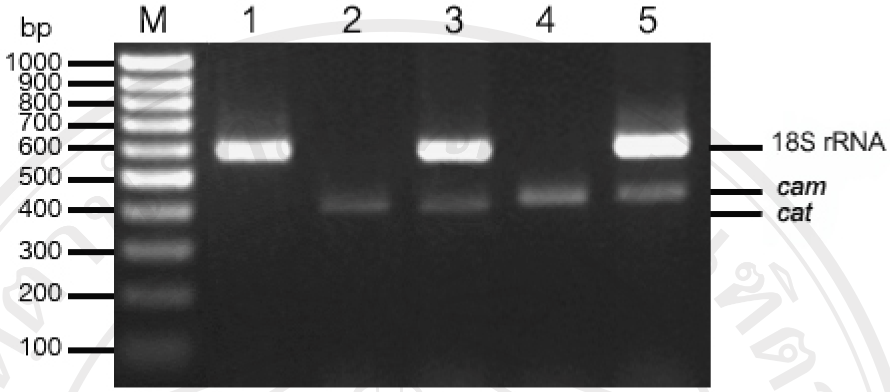

Figure C9-10. The amplified product of duplex RT-PCR with RRF1/RRH1 (18S rRNA) and specific primers for *cat* and *cam*. The product of 18S rRNA is 630 bp (lane 1), 420 bp of *cat* and 450 bp of *cam* are shown in lane 2 and 4, respectively. Duplex reactions of *cat* and *cam* are shown in lane 3 and 5, respectively.

C11. Primers for *cpeA* expression

```
cDNA            GATACGCCGTCACAGTACCCTTCACTCCCGGTCGCACAGATGCTTCCCAAGAGCAGACTG 1800
PrimerF         -----------------------------------------------CAAGAGCAGACTG 13
                                                               *************

cDNA            ACGTCCAATCCTTCAGCGACATGGAGCCCATTGCTGATGGTTTCCGTAACTACGGCTCAT 1860
PrimerF         ACGTCCA----------------------------------------------------- 20
                *******

cDNA            CCACCTCTCGCGTTCGTGCTGAGGAGTGGCTCATCGATAAGGCACAGCTTTTGACCCTCA 1920

cDNA            GTGCACCCGAGTTGGCCGTTCTCATCGGCGGTCTCCGTGTCCTCAACACAAACTACGACG 1980

cDNA            GCTCTGCTCACGGTGTCTTCACCCAGCGCCCAGGCAAGTTGACCAACGACTTCTTCGTCA 2040

cDNA            ACCTCTTGGACATGAACACCGCATGGAAATCAATTGGTGGTGTCGACCTCTACGAGGGCA 2100

cDNA            CAGATCGCAAGACTGGCGCCAAGAAGTGGACTGCTACTCGTAACGATCTCGTCTTTGGCT 2160

cDNA            CCAACGCTGAGTTGCGTGCTATTGCTGAGGTGTACGGTAGCTCTGATGGCCAGGAGAAGT 2220
PrimerR         ---------------------------AGGTGTACGGTAGCTCTGATGG----------- 22
                                           **********************
```

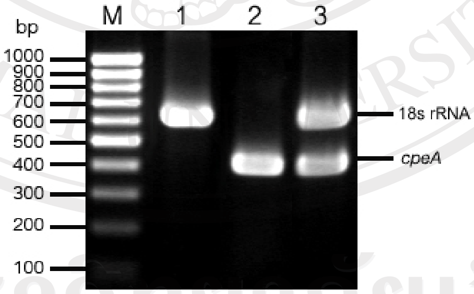

Figure C11. The amplified product of duplex RT-PCR with RRF1/RRH1 (18S rRNA) and specific primers for *cpeA*. The product of 18S rRNA is 630 bp (lane 1), 400 bp of *cpeA* is shown in lane 2 and mixed primers in lane 3.

APPENDIX D

STATISTIC ANALYSIS

Phagocytosis and killing assay

1. Percentage of phagocytosis

Table D-1 Paired Samples statistics of percentage of phagocytosis

	Mean	N	Std. Deviation	Std. Error Mean
Pair 1 PP30-PC	47.000	3	2.646	1.528
PP30-PM	49.667	3	4.726	2.728
Pair 2 PP60-PC	73.000	3	6.083	3.512
PP60-PM	72.333	3	3.512	2.028
Pair 3 PP120-PC	80.000	3	3.000	1.732
PP120-PM	90.667	3	9.292	5.364
Pair 4 PP240-PC	88.000	3	2.646	1.528
PP240-PM	93.667	3	7.506	4.333

Table D-2 Statistic significance of percentage of phagocytosis by Paired Samples Test

	Paired Differences					t	df	Sig. (2-tailed)
	Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference				
				Lower	Upper			
Pair 1 PP30PC-PM	-2.667	6.506	3.756	-18.83	13.496	-0.710	2	0.551
Pair 2 PP60PC-PM	0.667	9.452	5.457	-22.81	24.146	0.122	2	0.914
Pair 3 PP120PC-PM	-10.667	7.095	4.096	-28.29	6.957	-2.604	2	0.121
Pair 4 PP240PC-PM	-5.667	8.737	5.044	-27.37	16.037	-1.123	2	0.378

PP = Percentage of phagocytosis, PM = *P. marneffei*, PC = *P. citrinum*

2. Phagocytic index

Table D-3 Paired Samples statistics of phagocytic index

	Mean	N	Std. Deviation	Std. Error Mean
Pair 1 PI30 PC	1.643	3	0.068	0.039
PM	1.600	3	0.208	0.120
Pair 2 PI60 PC	2.093	3	0.071	0.041
PM	2.503	3	0.046	0.027
Pair 3 PI120 PC	2.310	3	0.301	0.174
PM	3.980	3	0.676	0.390
Pair 4 PI240 PC	2.660	3	0.298	0.172
PM	4.570	3	0.439	0.253

Table D-4 Statistic significance of phagocytic index by Paired Samples Test

	Paired Differences					t	df	Sig. (2-tailed)
	Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference Lower	Upper			
Pair 1 PI30PC-PM	0.043	0.167	0.096	-0.370	0.457	0.451	2	0.696
Pair 2 PI60PC-PM	-0.410	0.046	0.026	-0.524	-0.296	-15.497	2	0.004*
Pair 3 PI120PC-PM	-1.670	0.390	0.225	-2.638	-0.701	-7.422	2	0.018*
Pair 4 PI240PC-PM	-1.910	0.450	0.260	-3.028	-0.792	-7.352	2	0.018*

PI = Phagocytic index, PM = *P. marneffei*, PC = *P. citrinum*, *$P < 0.05$

3. Percentage of killing

Table D-5 Paired Samples statistics of percentage of killing

	Mean	N	Std. Deviation	Std. Error Mean
Pair 1 PK30 PC	42.400	2	4.229	2.990
PM	7.225	2	1.223	0.865
Pair 2 PK60 PC	68.560	2	3.026	2.140
PM	16.550	2	6.053	4.280
Pair 3 PK120 PC	66.780	2	2.475	1.750
PM	38.845	2	6.937	4.905
Pair 4 PK240 PC	64.120	2	3.422	2.420
PM	61.710	2	1.541	1.090

Table D-6 Statistic significance of percentage of killing by Paired Samples Test

	Paired Differences					t	df	Sig. (2-tailed)
	Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference				
				Lower	Upper			
Pair 1 PK30PC-PM	35.175	3.005	2.125	8.174	62.176	16.553	1	0.038*
Pair 2 PK60PC-PM	52.010	3.026	2.140	24.82	79.201	24.304	1	0.026*
Pair 3 PK120PC-PM	27.935	4.462	3.155	-12.153	68.023	8.854	1	0.072
Pair 4 PK240PC-PM	2.410	1.881	1.330	-14.489	19.309	1.812	1	0.321

PK = Percentage of killing, PM = *P. marneffei*, PC = *P. citrinum*, $^{*}P < 0.05$

Relative genes expression by RT-PCR analysis

4. Relative genes expression levels of *P. marneffei* in different phases

Table D-7 Paired Samples statistics of relative genes expression in different phases

		Mean	N	Std. Deviation	Std. Error Mean
sodA	Mycelium	0.190	2	0.085	0.060
	Conidia	0.420	2	0.085	0.060
	Yeast	0.635	2	0.120	0.085
cpeA	Mycelium	0.215	2	0.007	0.005
	Conidia	0.535	2	0.035	0.025
	Yeast	0.915	2	0.021	0.015
hsp70	Mycelium	0.675	2	0.007	0.005
	Conidia	0.695	2	0.021	0.015
	Yeast	0.755	2	0.007	0.005
acuD	Mycelium	0.435	2	0.092	0.065
	Conidia	0.450	2	0.042	0.030
	Yeast	0.490	2	0.057	0.040
gapdh	Mycelium	0.615	2	0.021	0.015
	Conidia	0.755	2	0.007	0.005
	Yeast	0.525	2	0.078	0.055

Table D-8 Statistic significance of relative genes expression in different phases by Paired Samples Test

	Paired Differences					t	df	Sig. (2-tailed)
				95% Confidence Interval of the Difference				
	Mean	Std. Deviation	Std. Error Mean	Lower	Upper			
sodA Mycelium-Conidia	-0.230	0.170	0.120	-1.755	1.295	-1.917	1	0.306
Conidia-Yeast	-0.215	0.035	0.025	-0.533	0.103	-8.600	1	0.074
Mycelium-Yeast	-0.445	0.035	0.0250	-0.762	-0.127	-17.800	1	0.036*
cpeA Mycelium-Conidia	-0.320	0.042	0.030	-0.701	0.061	-10.667	1	0.060
Conidia-Yeast	-0.380	0.014	0.010	-0.507	-0.253	-38.000	1	0.017*
Mycelium-Yeast	0.700	0.282	0.200	-0.954	0.446	-35.000	1	0.018*
hsp70 Mycelium-Conidia	-0.020	0.014	0.010	-0.147	0.107	-2.000	1	0.295
Conidia-Yeast	-0.060	0.014	0.010	-0.187	0.067	-6.000	1	0.105
Mycelium-Yeast	0.800	0.141	0.100	-0.047	0.207	8.000	1	0.079
acuD Mycelium-Conidia	-0.015	0.050	0.035	-0.460	0.430	-0.429	1	0.742
Conidia-Yeast	-0.040	0.014	0.010	-0.167	0.087	-4.000	1	0.156
Mycelium-Yeast	-0.055	0.035	0.025	-0.372	0.262	-2.200	1	0.272
gapdh Mycelium-Conidia	-0.140	0.028	0.020	-0.394	0.114	-7.000	1	0.090
Conidia-Yeast	0.230	0.085	0.060	-0.532	0.992	3.833	1	0.162
Mycelium-Yeast	0.090	0.056	0.040	-0.418	0.598	2.250	1	0.266

*$P<0.05$

5. Relative genes expression levels of *P. marneffei* during macrophage infection

Table D-9 Paired Samples statistics of relative *sodA* expression during macrophage infection

	Mean	N	Std. Deviation	Std. Error Mean
Pair 1 Control 2 h	0.290	2	0.028	0.020
Infect 2 h	0.515	2	0.035	0.025
Pair 2 Control 4 h	0.510	2	0.014	0.010
Infect 4 h	0.675	2	0.007	0.005
Pair 3 Control 8 h	0.425	2	0.035	0.025
Infect 8 h	0.760	2	0.014	0.010

Table D-10 Statistic significance of relative *sodA* expression during macrophage infection by Paired Samples Test

	Paired Differences					t	df	Sig. (2-tailed)
	Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference				
				Lower	Upper			
Pair 1 Ctl-Inf 2 h	-0.225	0.007	0.005	-0.289	-0.161	-45.000	1	0.014*
Pair 2 Ctl-Inf 4 h	-0.165	0.007	0.005	-0.229	-0.102	-33.000	1	0.019*
Pair 3 Ctl-Inf 8 h	-0.335	0.021	0.015	-0.526	-0.144	-22.333	1	0.028*

$^*P<0.05$

Table D-11 Paired Samples statistics of relative *cpeA* expression during macrophage infection

	Mean	N	Std. Deviation	Std. Error Mean
Pair 1 Control 2 h	0.065	2	0.007	0.005
Infect 2 h	0.630	2	0.000	0.000
Pair 2 Control 4 h	0.430	2	0.014	0.010
Infect 4 h	0.600	2	0.000	0.000
Pair 3 Control 8 h	0.445	2	0.021	0.015
Infect 8 h	0.560	2	0.000	0.000

Table D-12 Statistic significance of relative *cpeA* expression during macrophage infection by Paired Samples Test

	Paired Differences					t	df	Sig. (2-tailed)
				95% Confidence Interval of the Difference				
	Mean	Std. Deviation	Std. Error Mean	Lower	Upper			
Pair 1 Ctl-Inf 2 h	-0.565	0.007	0.005	-0.6285	-0.5015	-113.00	1	0.006*
Pair 2 Ctl-Inf 4 h	-0.170	0.014	0.010	-0.2971	-0.0429	-17.000	1	0.037*
Pair 3 Ctl-Inf 8 h	-0.115	0.021	0.015	-0.3056	0.0756	-7.667	1	0.083

*$P<0.05$

Table D-13 Paired Samples statistics of relative *hsp70* expression during macrophage infection

	Mean	N	Std. Deviation	Std. Error Mean
Pair 1 Control 2 h	0.740	2	0.156	0.110
Infect 2 h	0.825	2	0.219	0.155
Pair 2 Control 4 h	0.710	2	0.099	0.070
Infect 4 h	0.870	2	0.170	0.120
Pair 3 Control 8 h	0.550	2	0.042	0.030
Infect 8 h	0.705	2	0.163	0.115

Table D-14 Statistic significance of relative *hsp70* expression during macrophage infection by Paired Samples Test

	Paired Differences					t	df	Sig. (2-tailed)
	Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference				
				Lower	Upper			
Pair 1 Ctl-Inf 2 h	-0.0850	0.064	0.045	-0.657	0.487	-1.889	1	0.310
Pair 2 Ctl-Inf 4 h	-0.1600	0.071	0.050	-0.795	0.475	-3.200	1	0.193
Pair 3 Ctl-Inf 8 h	-0.1550	0.120	0.085	-1.235	0.925	-1.824	1	0.319

Table D-15 Paired Samples statistics of relative *acuD* expression during macrophage infection

	Mean	N	Std. Deviation	Std. Error Mean
Pair 1 Control 2 h	0.270	2	0.000	0.000
Infect 2 h	0.295	2	0.064	0.045
Pair 2 Control 4 h	0.305	2	0.078	0.055
Infect 4 h	0.340	2	0.000	0.000
Pair 3 Control 8 h	0.400	2	0.071	0.050
Infect 8 h	0.395	2	0.007	0.005

Table D-16 Statistic significance of relative *acuD* expression during macrophage infection by Paired Samples Test

	Paired Differences					t	df	Sig. (2-tailed)
	Mean	Std. Deviation	Std. Error Mean	95% Confidence Interval of the Difference				
				Lower	Upper			
Pair 1 Ctl-Inf 2 h	-0.025	0.064	0.045	-0.597	0.547	-.0556	1	0.677
Pair 2 Ctl-Inf 4 h	-0.035	0.078	0.055	-0.734	0.664	-0.636	1	0.639
Pair 3 Ctl-Inf 8 h	0.005	0.078	0.055	-0.694	0.704	0.091	1	0.942

Table D-17 Paired Samples statistics of relative *gapdh* expression during macrophage infection

	Mean	**N**	**Std. Deviation**	**Std. Error Mean**
Pair 1 Control 2 h	0.360	2	0.113	0.080
Infect 2 h	0.370	2	0.156	0.110
Pair 2 Control 4 h	0.395	2	0.191	0.135
Infect 4 h	0.550	2	0.156	0.110
Pair 3 Control 8 h	0.680	2	0.085	0.060
Infect 8 h	0.625	2	0.148	0.105

Table D-18 Statistic significance of relative *gapdh* expression during macrophage infection by Paired Samples Test

	Paired Differences					**t**	**df**	**Sig. (2-tailed)**
	Mean	**Std. Deviation**	**Std. Error Mean**	**95% Confidence Interval of the Difference**				
				Lower	**Upper**			
Pair 1 Ctl-Inf 2 h	-0.010	0.042	0.030	-0.391	0.371	-0.333	1	0.795
Pair 2 Ctl-Inf 4 h	-0.155	0.035	0.025	-0.473	0.163	-6.200	1	0.102
Pair 3 Ctl-Inf 8 h	0.055	0.064	0.045	-0.517	0.627	1.222	1	0.437

APPENDIX E

RECIPES

1. Culture Media

Brain heart infusion (BHI) agar

BHI agar (dehydrated)	52.00	g
Distilled water	1,000.00	ml

Melt, disperse in tubes and autoclave at 121 °C 15 lb/sq.in. for 15 min. Allow tubes to cool in slant position. Or, after autoclave, pour plates and allow cooling.

BHI broth

BHI	37.00	g
Distilled water	1,000.00	ml

Dissolve, disperse 30 ml in each 125 ml-Erlenmeyer flask.cSterile by autoclaving for 20 min at 15 lb/sq. in. on liquid cycle.

Luria-Bertani (LB) Medium

LB	20.00	g
Deionized H_2O up to	1,000.00	ml

Shake until the solutes are dissolved. Sterilize by autoclaving for 20 min at 15 lbs on liquid cycle. To make an agar medium add 20 g of agar to the 1 L solution and sterile by autoclave.

Sabouraud Dextrose Agar (SDA)

Dehydrated SDA agar (Becton Dickinson)	65.00	g
Distilled water	1,000.00	ml

Suspend 65 g of the powder in 1 liter of distilled water. Mix thoroughly, heat with frequent agitation and boil for 1 min to completely dissolve the powder. Autoclave at 121 °C 15 l bs. for 15 min.

SOC medium

Per liter:

To 950 ml of deionized water, add:

Tryptone	20	g
Yeast extract	5	g
NaCl	0.5	g

Shake until the solutes are dissolved. Adjust the pH to 7.0 with 5 N NaOH. Adjust the volume of the solution to 980 ml with the deionized water. Sterile by autoclaving, allow it to cool to 60°C or less and then add 20 ml of a sterile 1 M solution of glucose.

The glucose solution is made by dissolving 18 g of glucose in 90 ml of deionized water. After the sugar is dissolved, adjust the volume of the solution to 100 ml and sterile by filtration through a 0.2-μm filter.

2. Solutions for working with bacteriophage λ

20 % Maltose

Maltose	20	g
H_2O to	100	ml

Sterilize the solution by filtration through a 0.2-μM filter. Store the sterile solution at room temperature.

SM

Per liter:

NaCl	5.8	g
$MgSO_4 \bullet 7H_2O$	2	g
1 M Tris-Cl (pH 7.5)	50	ml
2 % gelatin solution	5	ml
H_2O to	1	L

Sterilize the buffer by autoclaving for 20 min ar 15 lb/sq.in. on liquid cycle. After the solution is cooled, dispense 50-ml aliquots into sterile containers. SM may be stored indefinitely at room temperature.

A 2 % gelatin solution is made by adding 2 g of gelatin to a total volume of 100 ml of H_2O and autoclaving the solution for 15 min at 15 lb/sq.in. on liquid cycle.

10 mM $MgSO_4$ (λ diluent)

Per liter:

1 M Tris-Cl (pH 7.5)	10	ml
$MgSO_4 \bullet 7H_2O$	2	g
H_2O to	1	L

Sterilize the buffer by autoclaving for 20 min at 15 lb/sq.in. on liquid cycle. After the dilution has cooled, dispense 50-ml aliquots into sterile containers. λ diluent may be stored indefinitely at room temperature.

3. Alkaline lysis buffers for minipreparation of plasmid DNA

Solution I

50 mM glucose
25 mM Tris-Cl (pH 8.0)
10 mM EDTA (pH 8.0)

Sterilize by autoclaving for 20 min at 15 lb/sq.in. on liquid cycle and store at 4^oC.

Solution II

0.2 N NaOH (freshly diluted from a 10 N stock)
1 % SDS

Solution III

5 M potassium acetate	60	ml
Glacial acetic acid	11.5	ml
H_2O	28.5	ml

The resulting solution is 3 M with respect to potassium and 5 M with respect to acetate.

4. Reagents

50X Tris-acetate (TAE) buffer

Tris base	242	g
Glacial acetic acid	57.1	ml
0.5 M EDTA	100	ml

The working solution (1X) contains 0.04 M Tris acetate and 0.0001 M EDTA

6X agarose gel-loading buffer

Bromophenol blue	0.025	g
Xylene cyanol FF	0.025	g
Glycerol	3	ml
Distilled water	6.95	ml

5. Tissue culture medium

ATCC complete growth medium

Dulbecco's modified Eagle's medium (4 mM L-glutamine and 4.5% g/l glucose)	90%
Fetal bovine serum	10%

Freeze medium

Complete growth medium	85%
Fetal bovine serum	10%
DMSO	5%

Storage in liquid nitrogen vapor phase

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