APPENDICES

APPENDIX A

Biochem identification of *S. suis* isolates in this study

Table 14 Biochemical reactions and optochin disc diffusion test of 35 *S. suis* isolates

Clinical isolates	Biochemical reactions							Optochin
	Bile Esculin	Esculin	Trehalose	Mannitol	Raffinose	Lactose	Sorbitol	
H15/52 MNCH	-	+	+	-	+	+	-	R
H23/52 MNCH	-	+	+	-	+	+	-	R
H26/52 LPH	-	+	+	-	+	+	-	R
H29/52 LPH	-	+	+	-	+	+	-	R
H85/53 MNCH	-	+	+	-	+	+	-	R
H110/53 LPH	-	+	+	-	+	+	-	R
H131/53 MNCH	-	+	+	-	+	+	-	R
H132/53 MNCH	-	+	+	-	+	+	-	R
H148/53 LPH	-	+	+	-	+	+	-	R
H150/53 LPH	-	+	+	-	+	+	-	R
H153/53 MNCH	-	+	+	-	+	+	-	R
H155/53 LPH	-	+	+	-	+	+	-	R
H156/53 MNCH	-	+	+	-	+	+	-	R
H163/53 LPH	-	+	+	-	+	+	-	R
H179/53 LPH	-	+	+	-	+	+	-	R
H186/53 LPH	-	+	+	-	+	+	-	R
H187/53 LPH	-	+	+	-	+	+	-	R
H193/53 LPH	-	+	+	-	+	+	-	R
H194/53 LPH	-	+	+	-	+	+	-	R

R=resistant; S=sensitive

Table 14 Continued

Clinical isolates	Biochemical reactions							Optochin
	Bile Esculin	**Esculin**	**Trehalose**	**Mannitol**	**Raffinose**	**Lactose**	**Sorbitol**	
H203/53 LPH	-	+	+	-	+	+	-	R
H210/53 LPH	-	+	+	-	+	+	-	R
H218/53 LPH	-	+	+	-	+	+	-	R
H219/53 MNCH	-	+	+	-	+	+	-	R
H240/53 LPH	-	+	+	-	+	+	-	R
H244/54 LPH	-	+	+	-	+	+	-	R
H252/54 LPH	-	+	+	-	+	+	-	R
H272/54 LPH	-	+	+	-	+	+	-	R
H286/54 LPH	-	+	+	-	+	+	-	R
H290/54 MNCH	-	+	+	-	+	+	-	R
H291/54 SPT	-	+	+	-	+	+	-	R
H301/54 MNCH	-	+	+	-	+	+	-	R
H302/54 MNCH	-	+	+	-	+	+	-	R
H303/54 MNCH	-	+	+	-	+	+	-	R
H304/54 MNCH	-	+	+	-	+	+	-	R
H307/54 MNCH	-	+	+	-	+	+	-	R

R=resistant; S=sensitive

APPENDIX B

Viable count of sensitivity and specificity of PCR condition in hemoculture

Table 15 Viable count of sensitivity of PCR condition in hemoculture

***S. suis* P1/7**	**Cell dilutions**	**10^{-6}**	**10^{-7}**	**10^{-8}**	**10^{-9}**	**10^{-10}**
	Number of colony (duplicate) (colonies/50ul)	>300	288	23	1	0
						
***S. suis* MNCM07**	**Cell dilutions**	**10^{-6}**	**10^{-7}**	**10^{-8}**	**10^{-9}**	**10^{-10}**
	Number of colony (duplicate) (colonies/50ul)	>300	102	11	0	0
						

Table 16 Viable count of specificity of PCR condition in hemoculture

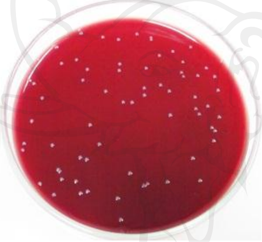
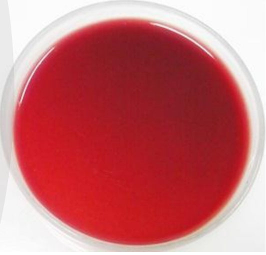
S. pneumoniae	**Cell dilutions**	**10^{-5}**	**10^{-6}**	**10^{-7}**	**10^{-8}**	**10^{-9}**
	Number of colony (colonies/50ul)	>300	64	6	0	0
						
Viridans streptococci	**Cell dilutions**	**10^{-5}**	**10^{-6}**	**10^{-7}**	**10^{-8}**	**10^{-9}**
	Number of colony (colonies/50ul)	>300	92	9	0	0
						

Table 16 Continued

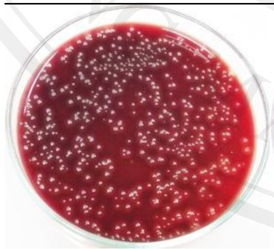
S. bovis	**Cell dilutions**	**10^{-5}**	**10^{-6}**	**10^{-7}**	**10^{-8}**	**10^{-9}**
	Number of colony (colonies/50ul)	>300	123	8	0	0
						
S. pyogenes	**Cell dilutions**	**10^{-4}**	**10^{-5}**	**10^{-6}**	**10^{-7}**	**10^{-8}**
	Number of colony (colonies/50ul)	>300	110	12	0	0
						

Table 16 Continued

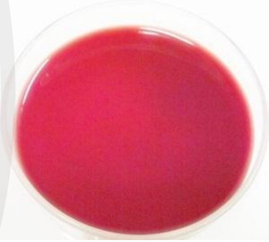
E. faecalis	**Cell dilutions**	**10^{-5}**	**10^{-6}**	**10^{-7}**	**10^{-8}**	**10^{-9}**
	Number of colony (colonies/50ul)	>300	104	22	1	0
						
S. aureus **ATCC 25923**	**Cell dilutions**	**10^{-4}**	**10^{-5}**	**10^{-6}**	**10^{-7}**	**10^{-8}**
	Number of colony (colonies/50ul)	>300	44	0	0	0
						

Table 16 Continued

E. coli **ATCC 25922**	**Cell dilutions**	**10^{-5}**	**10^{-6}**	**10^{-7}**	**10^{-8}**	**10^{-9}**
	Number of colony **(duplicate)** **(colonies/50ul)**	>300	108	12	1	0
						

APPENDIX C

Alignment of deduced amino acid sequences on database

A. Nucleotide alignment sequences of 16S rRNA gene of *S. suis*

1. H 23/52 MNCH

<u>Sequence:</u>

GTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACG
CGGCGTTGCTCGGTCAGGGTTGCCCCCATTGCCGAAGATTCCCTACTGCTG
CCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCC
TCTCAGGTCGGCTATGTATCGAAGCCTTGGTGAGCCGTTACCTCACCAACT
AGCTAATACAACGCAGGTCCATCTCATAGTGAAGCAGTTGCTCCTTTCAA
ATATCTACCATGCGGTAAATACAGA

> <u>gb|CP002640.1|</u> *Streptococcus suis* SS12, complete genome; Length=2096866

Score = 505 bits (273), Expect = 7e-140

Identities = 275/276 (99%), Gaps = 0/276 (0%)

Strand=Plus/Minus

```
Query  1      GTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGTTGC  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17428  GTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCACGCGGCGTTGC  17369

Query  61     TCGGTCAGGGTTGCCCCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17368  TCGGTCAGGGTTGCCCCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGTAGGAGTCTGG  17309

Query  121    GCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGAAGCCT  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17308  GCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGTATCGAAGCCT  17249

Query  181    TGGTGAGCCGTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCATAGTGAAGCA  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17248  TGGTGAGCCGTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCATAGTGAAGCA  17189

Query  241    GTTGCTCCTTTCAAATATCTACCATGCGGTAAATAC  276
               |||||||||||||||||||||||||||||||||||
Sbjct  17188  ATTGCTCCTTTCAAATATCTACCATGCGGTAAATAC  17153
```

2. H 29/52 LPH

<u>Sequence:</u>

TTTGGAAAGGCATTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGCAACCCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAACAGAAGAACT

> <u>gb|CP002651.1|</u> *Streptococcus suis* ST1, complete genome; Length=2034321

Score = 444 bits (240), Expect = 1e-121

Identities = 242/243 (99%), Gaps = 0/243 (0%)

Strand=Plus/Plus

```
Query  12     ATTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCAC  71
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17291  ATTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCAC  17350

Query  72     CAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG  131
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17351  CAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG  17410

Query  132    GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGCAACCCTGACC  191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17411  GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGCAACCCTGACC  17470

Query  192    GAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAACAGAAGA  251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Sbjct  17471  GAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGA  17530

Query  252    ACT  254
              |||
Sbjct  17531  ACT  17533
```

3. H 85/53 MNCH

Sequence:

TTTAAAGGGCATTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGT
TGGTGAGGTAACGGCTCACCAAGGCTTCGATACATAGCCGACCTGAGAGG
GTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC
AGCAGTAGGGAATCTTCGGCAATGGGGGCAACCCTGACCGAGCAACGCC
GCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGA

>gb|CP002651.1| *Streptococcus suis* ST1, complete genome; Length=2034321

Score = 448 bits (242), Expect = 1e-122

Identities = 247/249 (99%), Gaps = 2/249 (1%)

Strand=Plus/Plus

```
Query  4      AAAGG-GC-ATTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTA  61
              ||||| || |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17282  AAAGGAGCAATTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTA  17341

Query  62     ACGGCTCACCAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGAC  121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17342  ACGGCTCACCAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGAC  17401

Query  122    TGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGCA  181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17402  TGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGCA  17461

Query  182    ACCCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGT  241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17462  ACCCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGT  17521

Query  242    AAGAGAAGA  250
              |||||||||
Sbjct  17522  AAGAGAAGA  17530
```

4. H 131/53 MNCH

Sequence:

TCTTCTCCAGTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCTT
CACTCACGCGGCGTTGCTCGGTCAGGGTTGCCCCCATTGCCGAAGATTCCC
TACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCC
GATCACCCTCTCAGGTCGGCTATGTATCGAAGCCTTGGTGAGCCGTTACCT
CACCAACTAGCTAATACAACGCAGGTCCATCTCATAGTGAAGCAGTTGCT
CCTTTCAAATATCTACCATGCGGTAAATACTGA

> gb|CP002640.1| *Streptococcus suis* SS12, complete genome; Length=2096866

Score = 520 bits (281), Expect = 3e-144

Identities = 286/288 (99%), Gaps = 1/288 (0%)

Strand=Plus/Minus

```
Query  1      TCTTCTC-CAGTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCAC  59
              ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17438  TCTTCTCACAGTTCTTCTCTTACAACAGAGCTTTACGATCCGAAAACCTTCTTCACTCAC  17379

Query  60     GCGGCGTTGCTCGGTCAGGGTTGCCCCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGT  119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17378  GCGGCGTTGCTCGGTCAGGGTTGCCCCCATTGCCGAAGATTCCCTACTGCTGCCTCCCGT  17319

Query  120    AGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGT  179
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17318  AGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCCGATCACCCTCTCAGGTCGGCTATGT  17259

Query  180    ATCGAAGCCTTGGTGAGCCGTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCA  239
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17258  ATCGAAGCCTTGGTGAGCCGTTACCTCACCAACTAGCTAATACAACGCAGGTCCATCTCA  17199

Query  240    TAGTGAAGCAGTTGCTCCTTTCAAATATCTACCATGCGGTAAATACTG  287
              |||||||||| |||||||||||||||||||||||||||||||||||||
Sbjct  17198  TAGTGAAGCAATTGCTCCTTTCAAATATCTACCATGCGGTAAATACTG  17151
```

5. H 148/53 LPH

Sequence:

ACTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGT
AACGGCTCACCAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGG
CCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTA
GGGAATCTTCGGCAATGGGGGCAACCCTGACCGAGCAACGCCGCGTGAG
TGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGA
GAAGAGTGGAAAACTTTCCACT

> gb|CP002641.1| *Streptococcus suis* D9, complete genome; Length=2177656

Score = 481 bits (260), Expect = 3e-132

Identities = 267/270 (99%), Gaps = 2/270 (1%)

Strand=Plus/Plus

```
Query  1      ACTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCAC  60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17402  ACTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCAC  17461

Query  61     CAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG  120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17462  CAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG  17521

Query  121    GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGCAACCCTGACC  180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17522  GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGCAACCCTGACC  17581

Query  181    GAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGA  240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17582  GAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGA  17641

Query  241    ACTGTGAGAAGAGTGGAAAACTTTC-CACT  269
              |||||||||||||||||||  |||| ||||
Sbjct  17642  ACTGTGAGAAGAGTGGAAAG-TTTCTCACT  17670
```

6. H 156/53 MNCH

Sequence:

TTGAAGGGGACTGCTTCCTATGAGATGGACCTGCGTTGTATTAGCTAGTTG
GTGAGGTAACGGCTCACCAAGGCTTCGATACATAGCCGACCTGAGAGGGT
GATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCA
GCAGTAGGGAATCTTCGGCAATGGGGGCAACCCTGACCGAGCAACGCCG
CGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAA
CTGTGAG

>gb|CP002641.1| *Streptococcus suis* D9, complete genome; Length=2177656

Score = 451 bits (244), Expect = 9e-124

Identities = 247/248 (99%), Gaps = 1/248 (0%)

Strand=Plus/Plus

```
Query  10     ACTGCTTC-CTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCAC  68
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17402  ACTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCAC  17461

Query  69     CAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG  128
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17462  CAAGGCTTCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG  17521

Query  129    GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGCAACCCTGACC  188
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17522  GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGCAACCCTGACC  17581

Query  189    GAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGA  248
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  17582  GAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGA  17641

Query  249    ACTGTGAG  256
              ||||||||
Sbjct  17642  ACTGTGAG  17649
```

B. Nucleotide alignment sequences of *gdh* gene of *S. suis*

1. H23/52 LPH

Sequence:

GANTGGTCTNTCTNGCAGCGTATTCTGTCAAACGAGCGCGGCGTTTTNCTT
TGATGTCCACCAAGAGGTCGAAGTCGATACCAGTTTCGTCAATGATGTAA
CCATTTGAGTCTGAAACAGAAATAACTTTTGCACCAAGTTCAGTCGCTTTT
CGAACAGCATATTGGGCAACGTTACCAGAACCTGAGATTAGGACAGTTTG
GTCTTTGAAGGATTTACCGTTTGCTGCCAACATGTTATCAGTGAAGTAAAC
CAAACCGTAACCAGTTGCTTCTGGGCGGATCAATGAACCACCGAAGCCAA
GAGGTTTACCAGTCAAGACACCTGCATCAAACTGGCGGAGGCGTTTGTAT
TGACCGTACATGTAACCGATCTCACGACCACCGACACCGATGTCACCAGC
AGGGACGTCAAGTGAAGGTCCGATGTGTTTTTGCAATTCAGTCATGAAGC
TTTGGCAGAAGCGCATGATTTCAGCATCAGTTTTTCCTTTAGGATCAAAGT
CTGAACCACCTTTACCACCGCCGATTGGAAGACCTGTCAAGACG

> gb|EF073054.1| *Streptococcus suis* strain SH031238 glutamate dehydrogenase gene, partial cds; Length=689

Score = 977 bits (529), Expect = 0.0

Identities = 532/534 (99%), Gaps = 0/534 (0%)

Strand=Plus/Plus

```
Query  15   GCAGCGTATTCTGTCAAACGAGCGCGGCGTTTTNCTTTGATGTCCACCAAGAGGTCGAAG  74
            ||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Sbjct  1    GCAGCGTATTCTGTCAAACGAGCGCGGCGTTTTTCTTTGATGTCCACCAAGAGGTCGAAG  60

Query  75   TCGATACCAGTTTCGTCAATGATGTAACCATTTGAGTCTGAAACAGAAATAACTTTTGCA  134
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  61   TCGATACCAGTTTCGTCAATGATGTAACCATTTGAGTCTGAAACAGAAATAACTTTTGCA  120

Query  135  CCAAGTTCAGTCGCTTTTCGAACAGCATATTGGGCAACGTTACCAGAACCTGAGATTAGG  194
            |||||||||||||||||| |||||||||||||||||||||||||||||||||||||||||
Sbjct  121  CCAAGTTCAGTCGCTTTTTGAACAGCATATTGGGCAACGTTACCAGAACCTGAGATTAGG  180

Query  195  ACAGTTTGGTCTTTGAAGGATTTACCGTTTGCTGCCAACATGTTATCAGTGAAGTAAACC  254
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  181  ACAGTTTGGTCTTTGAAGGATTTACCGTTTGCTGCCAACATGTTATCAGTGAAGTAAACC  240

Query  255  AAACCGTAACCAGTTGCTTCTGGGCGGATCAATGAACCACCGAAGCCAAGAGGTTTACCA  314
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241  AAACCGTAACCAGTTGCTTCTGGGCGGATCAATGAACCACCGAAGCCAAGAGGTTTACCA  300

Query  315  GTCAAGACACCTGCATCAAACTGGCGGAGGCGTTTGTATTGACCGTACATGTAACCGATC  374
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  301  GTCAAGACACCTGCATCAAACTGGCGGAGGCGTTTGTATTGACCGTACATGTAACCGATC  360

Query  375  TCACGACCACCGACACCGATGTCACCAGCAGGGACGTCAAGTGAAGGTCCGATGTGTTTT  434
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  361  TCACGACCACCGACACCGATGTCACCAGCAGGGACGTCAAGTGAAGGTCCGATGTGTTTT  420

Query  435  TGCAATTCAGTCATGAAGCTTTGGCAGAAGCGCATGATTTCAGCATCAGTTTTTCCTTTA  494
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  421  TGCAATTCAGTCATGAAGCTTTGGCAGAAGCGCATGATTTCAGCATCAGTTTTTCCTTTA  480

Query  495  GGATCAAAGTCTGAACCACCTTTACCACCGCCGATTGGAAGACCTGTCAAGACG  548
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  481  GGATCAAAGTCTGAACCACCTTTACCACCGCCGATTGGAAGACCTGTCAAGACG  534
```

2. H29/52 LPH

Sequence:

TTTACTGGTCTTCCAATCGGCGGTGGTAAAGGTGGTTCAGACTTTGATCCT
AAAGGAAAAACTGATGCTGAAATCATGCGCTTCTGCCAAAGCTTCATGAC
TGAATTGCAAAAACACATCGGACCTTCACTTGACGTCCCTGCTGGTGACA
TCGGTGTCGGTGGTCGTGAGATCGGTTACATGTACGGTCAATACAAACGC
CTCCGCCAGTTTGATGCAGGTGTCTTGACTGGTAAACCTCTTGGCTTCGGT
GGTTCATTGATCCGCCCAGAAGCAACTGGTTACGGTTTGGTTTACTTCACT
GATAACATGTTGGCAGCAAACGGTAAATCCTTCAAAGACCAAACTGTCCT
TATCTCAGGTTCTGGTAACGTTGCCCAATATGCTGTTCAAAAAGCGACTGA
ACTTGGTGCAAAAGTTATTTCTGTTTCAGACTCAAATGGTTACATCATTGA
CGAAACTGGTATCGACTTCGACCTCTTGGTGGACATCAAAGAAAAACGCC
GCGCTCGTTTGACAGAATACGCTGCAGAAAAATCAACTGCTAAGTACTTC
AAAGGTTCTGTATGG

> gb|CP002570.1| *Streptococcus suis* A7, complete genome; Length=2038409

Score = 1048 bits (567), Expect = 0.0

Identities = 567/567 (100%), Gaps = 0/567 (0%)

Strand=Plus/Minus

```
Query  4       ACTGGTCTTCCAATCGGCGGTGGTAAAGGTGGTTCAGACTTTGATCCTAAAGGAAAAACT  63
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241256  ACTGGTCTTCCAATCGGCGGTGGTAAAGGTGGTTCAGACTTTGATCCTAAAGGAAAAACT  241197

Query  64      GATGCTGAAATCATGCGCTTCTGCCAAAGCTTCATGACTGAATTGCAAAAACACATCGGA  123
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241196  GATGCTGAAATCATGCGCTTCTGCCAAAGCTTCATGACTGAATTGCAAAAACACATCGGA  241137

Query  124     CCTTCACTTGACGTCCCTGCTGGTGACATCGGTGTCGGTGGTCGTGAGATCGGTTACATG  183
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241136  CCTTCACTTGACGTCCCTGCTGGTGACATCGGTGTCGGTGGTCGTGAGATCGGTTACATG  241077

Query  184     TACGGTCAATACAAACGCCTCCGCCAGTTTGATGCAGGTGTCTTGACTGGTAAACCTCTT  243
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241076  TACGGTCAATACAAACGCCTCCGCCAGTTTGATGCAGGTGTCTTGACTGGTAAACCTCTT  241017

Query  244     GGCTTCGGTGGTTCATTGATCCGCCCAGAAGCAACTGGTTACGGTTTGGTTTACTTCACT  303
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  241016  GGCTTCGGTGGTTCATTGATCCGCCCAGAAGCAACTGGTTACGGTTTGGTTTACTTCACT  240957

Query  304     GATAACATGTTGGCAGCAAACGGTAAATCCTTCAAAGACCAAACTGTCCTTATCTCAGGT  363
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240956  GATAACATGTTGGCAGCAAACGGTAAATCCTTCAAAGACCAAACTGTCCTTATCTCAGGT  240897

Query  364     TCTGGTAACGTTGCCCAATATGCTGTTCAAAAAGCGACTGAACTTGGTGCAAAAGTTATT  423
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240896  TCTGGTAACGTTGCCCAATATGCTGTTCAAAAAGCGACTGAACTTGGTGCAAAAGTTATT  240837

Query  424     TCTGTTTCAGACTCAAATGGTTACATCATTGACGAAACTGGTATCGACTTCGACCTCTTG  483
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240836  TCTGTTTCAGACTCAAATGGTTACATCATTGACGAAACTGGTATCGACTTCGACCTCTTG  240777

Query  484     GTGGACATCAAAGAAAAACGCCGCGCTCGTTTGACAGAATACGCTGCAGAAAAATCAACT  543
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  240776  GTGGACATCAAAGAAAAACGCCGCGCTCGTTTGACAGAATACGCTGCAGAAAAATCAACT  240717

Query  544     GCTAAGTACTTCAAAGGTTCTGTATGG  570
               |||||||||||||||||||||||||||
Sbjct  240716  GCTAAGTACTTCAAAGGTTCTGTATGG  240690
```

C. Nucleotide alignment sequences of 16S rRNA gene of 11 non-*S. suis* isolates

1. H 24/52 MNCH

Sequence:

TTTTTAGGAACATTGCTTCCTATGAGTGGACCTGCGTTGTATTAGCTAGTT
GGTGAGGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGG
GTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGC
AGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCC
GCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGA
ACTGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACAACAGAG
A

>gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 510 bits (276), Expect = 2e-141

Identities = 286/290 (99%), Gaps = 3/290 (1%)

Strand=Plus/Plus

```
Query  6    AGGAAC-ATTGCTTC-CTATGAG-TGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAAC  62
            |||| | |||||||| ||||||| ||||||||||||||||||||||||||||||||||||
Sbjct  202  AGGAGCAATTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAAC  261

Query  63   GGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTG  122
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262  GGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTG  321

Query  123  AGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAAC  182
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322  AGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAAC  381

Query  183  CCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAA  242
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382  CCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAA  441

Query  243  GAGAAGAACTGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  292
            ||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  442  GAGAAGAACTGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  491
```

2. H 32/52 LPH

Sequence:

CANTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGT
AACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGC
CACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAG
GGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGCGTGAGTG
AAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGA
AGAGTGGAAAGTTTCTCACTTGACGGTATCTTACCACAGAG

> gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 523 bits (283), Expect = 2e-145

Identities = 283/283 (100%), Gaps = 0/283 (0%)

Strand=Plus/Plus

```
Query  4    TGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCA  63
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  211  TGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCA  270

Query  64   AGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC  123
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  271  AGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC  330

Query  124  CCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGA  183
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331  CCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGA  390

Query  184  GCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC  243
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  391  GCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC  450

Query  244  TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACCA  286
            |||||||||||||||||||||||||||||||||||||||||||
Sbjct  451  TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACCA  493
```

3. H 37/52 LPH

Sequence:

CATTGCTTCCTATGAGANGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTA
ACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCC
ACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGG
GAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGCGTGAGTGA
AGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGAA
GAGTGGAAAGTTTCTCACTTGACGGTATCTTACCACA

> gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 516 bits (279), Expect = 4e-143

Identities = 283/285 (99%), Gaps = 1/285 (0%)

Strand=Plus/Plus

```
Query  2    ATTGCTTC-CTATGAGANGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCAC  60
            |||||||| |||||||| ||||||||||||||||||||||||||||||||||||||||||
Sbjct  209  ATTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCAC  268

Query  61   CAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  269  CAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACG  328

Query  121  GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACC  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  329  GCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACC  388

Query  181  GAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  389  GAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGA  448

Query  241  ACTGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACCA  285
            |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  449  ACTGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACCA  493
```

4. H 66/52 MNCH

Sequence:

TTTTAAGGACATTGCTTCCTATGAGTGGACTGCGTTGTATTAGCTAGTTGG
TGAGGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTG
ATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG
CAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGC
GTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC
TGTGAGAAGAGTGGAAA

> gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 416 bits (225), Expect = 3e-113

Identities = 229/231 (99%), Gaps = 0/231 (0%)

Strand=Plus/Plus

```
Query  34   GCGGTGTATTAGCTAGTTGGTGAGGTAACGGATCACCAAGGCATCGATACATAGCCGACC  93
            ||| ||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Sbjct  233  GCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCATCGATACATAGCCGACC  292

Query  94   TGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC  153
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  293  TGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGC  352

Query  154  AGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGCGTGAGTGAAGAA  213
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  353  AGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGCGTGAGTGAAGAA  412

Query  214  GGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGAAGAGTG  264
            |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  413  GGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGAAGAGTG  463
```

5. H 84/53 MNCH

Sequence:

TTTAAAGGAAATGCTTCCTATGAGTGGACCTGCGTTGTATTAGCTAGTTGG
TGAGGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTG
ATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG
CAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGC
GTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC
TGTGAGAAGAGTG

> gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445
Score = 455 bits (246), Expect = 7e-125
Identities = 259/264 (98%), Gaps = 5/264 (2%)
Strand=Plus/Plus

```
Query  4    AAAGGA--AA-TGCTTC-CTATGAG-TGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTA  58
            ||||||  || |||||| ||||||| ||||||||||||||||||||||||||||||||||
Sbjct  200  AAAGGAGCAATTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTA  259

Query  59   ACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGAC  118
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  260  ACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGAC  319

Query  119  TGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCA  178
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  320  TGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCA  379

Query  179  ACCCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGT  238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  380  ACCCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGT  439

Query  239  AAGAGAAGAACTGTGAGAAGAGTG  262
            ||||||||||||||||||||||||
Sbjct  440  AAGAGAAGAACTGTGAGAAGAGTG  463
```

6. H 103/53 MNCH

Sequence:

TTTTTAAGGGAAAGTGCTTACATCTGTATTGGACTGCGTTGTATTAGCTAG
TTGGTGAGGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAG
GGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAG
GCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACG
CCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAA
GAACTGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACAACAG
AGAGCTTT

> gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 484 bits (262), Expect = 1e-133

Identities = 265/266 (99%), Gaps = 1/266 (0%)

Strand=Plus/Plus

```
Query  30   TGGA-CTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCATCGATACATA  88
            |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  226  TGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCATCGATACATA  285

Query  89   GCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGG  148
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  286  GCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGG  345

Query  149  AGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGCGTGAG  208
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  346  AGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGCGTGAG  405

Query  209  TGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGAAGAGTGGA  268
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  406  TGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGAAGAGTGGA  465

Query  269  AAGTTTCTCACTTGACGGTATCTTAC  294
            ||||||||||||||||||||||||||
Sbjct  466  AAGTTTCTCACTTGACGGTATCTTAC  491
```

7. H 106/53 MNCH

Sequence:

TTTTAAGACATGCTCCTATGAGTGGACCTGCGTTGTATTAGCTAGTTGGTG
AGGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGAT
CGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCA
GTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGCGTG
AGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGT
GAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACAACAGAGAGCTT
T

> gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 499 bits (270), Expect = 4e-138

Identities = 273/274 (99%), Gaps = 1/274 (0%)

Strand=Plus/Plus

```
Query  16   CTATGAG-TGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCATC  74
            ||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  218  CTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCATC  277

Query  75   GATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACT  134
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  278  GATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACT  337

Query  135  CCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGC  194
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  338  CCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGC  397

Query  195  CGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGA  254
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  398  CGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGA  457

Query  255  AGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  288
            ||||||||||||||||||||||||||||||||||
Sbjct  458  AGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  491
```

8. H 137/53 MNCH

Sequence:

TTTTAAGGGGCATGCTCCTATGAGTGGACCTGCGTTGTATTAGCTAGTTGG
TGAGGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTG
ATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG
CAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGC
GTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC
TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACAACAGAGAG

>gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 499 bits (270), Expect = 4e-138

Identities = 273/274 (99%), Gaps = 1/274 (0%)

Strand=Plus/Plus

```
Query  18   CTATGAG-TGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCATC  76
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  218  CTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCATC  277

Query  77   GATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACT  136
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  278  GATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACT  337

Query  137  CCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGC  196
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  338  CCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGC  397

Query  197  CGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGA  256
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  398  CGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGA  457

Query  257  AGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  290
            ||||||||||||||||||||||||||||||||||
Sbjct  458  AGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  491
```

9. H 151/53 DSK

<u>Sequence:</u>

TTTTAGACATGCTCCTATGAGTGGACCTGCGTTGTATTAGCTAGTTGGTGA
GGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATC
GGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAG
TAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGCGTGA
GTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTG
AGAAGAG

> <u>gb|HM590020.1|</u> *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 444 bits (240), Expect = 1e-121

Identities = 243/244 (99%), Gaps = 1/244 (0%)

Strand=Plus/Plus

```
Query  15   CTATGAG-TGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCATC  73
            ||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  218  CTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCATC  277

Query  74   GATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACT  133
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  278  GATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCCCAGACT  337

Query  134  CCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGC  193
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  338  CCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGC  397

Query  194  CGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGA  253
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  398  CGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACTGTGAGA  457

Query  254  AGAG  257
            ||||
Sbjct  458  AGAG  461
```

10. H197/53 LPH

Sequence:

TTTTAAGGAAATGCTTCCTATGAGTGGACCTGCGTTGTATTAGCTAGTTGG
TGAGGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTG
ATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG
CAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGC
GTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC
TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACAACAGAGAG
C

> gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 507 bits (274), Expect = 2e-140

Identities = 279/281 (99%), Gaps = 2/281 (1%)

Strand=Plus/Plus

```
Query  12   TGCTTC-CTATGAG-TGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCA  69
            |||||| ||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  211  TGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCA  270

Query  70   AGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC  129
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  271  AGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC  330

Query  130  CCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGA  189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331  CCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGA  390

Query  190  GCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC  249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  391  GCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC  450

Query  250  TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  290
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  451  TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  491
```

11. H 205/53 LPH

Sequence:

TTTTAAGGAAATGCTTCCTATGAGTGGACCTGCGTTGTATTAGCTAGTTGG
TGAGGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTG
ATCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAG
CAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAGCAACGCCGC
GTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC
TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACAACAGAGAG

> gb|HM590020.1| *Streptococcus suis* culture-collection DMST:22215 16S ribosomal RNA gene, partial sequence; Length=1445

Score = 507 bits (274), Expect = 2e-140

Identities = 279/281 (99%), Gaps = 2/281 (1%)

Strand=Plus/Plus

```
Query  12   TGCTTC-CTATGAG-TGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCA  69
            |||||| ||||||| |||||||||||||||||||||||||||||||||||||||||||||
Sbjct  211  TGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCA  270

Query  70   AGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC  129
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  271  AGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGC  330

Query  130  CCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGA  189
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  331  CCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGA  390

Query  190  GCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC  249
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  391  GCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAAC  450

Query  250  TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  290
            |||||||||||||||||||||||||||||||||||||||||
Sbjct  451  TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTAC  491
```

D. Nucleotide alignment sequences of *sod*A gene of *S. bovis* biotype II/2

1. H24/52 MNCH

Sequence:

GTGGGAAATTAGCTGTCGAGAGCACTTCAAGTTTGCCATTTTCATTCACCA
CAAGCCAAGCCCAACCTGATCCAAAGCGAGTTGTCGCAGCTTGCGTGAAA
GCAGCTTTGAATTCATCAAATGAGCCAAAAGCTTCCTCAATCGCAGCCAA
CACTTGTGTTGTTGGTTCTTGTTTTTCAGGTGATAACAATTCCCAGAAAAG
GGCGTGGTTCAAATGCCCACCACCATTATTAATCACCGCTTGACGGATATC
TGTTGGAATACTATCAACATCTGCCAACAAAGCTTCCAAATCATCTCCAAT
TTCTGGATGCTTTTCAAGCGCCGCATTTACATTTGCCACATAAGTAGCATG
ATGTTTATCATGGTGAATTGTCATTGAAGA

>gb|GU991770.1| *Streptococcus pasteurianus* strain LMG 22784 manganese-dependent superoxide dismutase (sodA) gene, partial cds ; Length=419

Score = 691 bits (374), Expect = 0.0

Identities = 374/374 (100%), Gaps = 0/374 (0%)

Strand=Plus/Minus

```
Query  8    ATTAGCTGTCGAGAGCACTTCAAGTTTGCCATTTTCATTCACCACAAGCCAAGCCCAACC  67
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  382  ATTAGCTGTCGAGAGCACTTCAAGTTTGCCATTTTCATTCACCACAAGCCAAGCCCAACC  323

Query  68   TGATCCAAAGCGAGTTGTCGCAGCTTGCGTGAAAGCAGCTTTGAATTCATCAAATGAGCC  127
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  322  TGATCCAAAGCGAGTTGTCGCAGCTTGCGTGAAAGCAGCTTTGAATTCATCAAATGAGCC  263

Query  128  AAAAGCTTCCTCAATCGCAGCCAACACTTGTGTTGTTGGTTCTTGTTTTTCAGGTGATAA  187
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  262  AAAAGCTTCCTCAATCGCAGCCAACACTTGTGTTGTTGGTTCTTGTTTTTCAGGTGATAA  203

Query  188  CAATTCCCAGAAAAGGGCGTGGTTCAAATGCCCACCACCATTATTAATCACCGCTTGACG  247
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  202  CAATTCCCAGAAAAGGGCGTGGTTCAAATGCCCACCACCATTATTAATCACCGCTTGACG  143

Query  248  GATATCTGTTGGAATACTATCAACATCTGCCAACAAAGCTTCCAAATCATCTCCAATTTC  307
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  142  GATATCTGTTGGAATACTATCAACATCTGCCAACAAAGCTTCCAAATCATCTCCAATTTC  83

Query  308  TGGATGCTTTTCAAGCGCCGCATTTACATTTGCCACATAAGTAGCATGATGTTTATCATG  367
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  82   TGGATGCTTTTCAAGCGCCGCATTTACATTTGCCACATAAGTAGCATGATGTTTATCATG  23

Query  368  GTGAATTGTCATTG  381
            ||||||||||||||
Sbjct  22   GTGAATTGTCATTG  9
```

2. H84/53 MNCH

Sequence:

GTAATGATAGCTGTCGAGAGCACTTCAAGTTTGCCATTTTCATTCACCACAAGCCAAGCCCAACCTGACCCAAAGCGAGTTGTCGCAGCTTGCGTGAAAGCAGCTTTGAATTCGTCAAATGAGCCAAAAGCTTCCTCAATTGCAGCCAACACTTGTGTTGTTGGTTCTTGTTTTTCAGGTGATAATAATTCCCAGAAAAGGGCGTGGTTCAAATGCCCACCACCATTATTAATCACCGCTTGACGGATATCTGTTGGAATACTATCAACATCTGCCAACAAAGCTTCCAAATCATCTCCAATTTCTGGATGCTTTTCAAGCGCCGCATTTACATTTGCCACATAAGTAGCATGATGTTTATCATGGTGAATTGTCATTGAG

>gb|GU991757.1| *Streptococcus pasteurianus* strain LMG 14865 manganese-dependent superoxide dismutase (sodA) gene, partial cds; Length=409

Score = 688 bits (372), Expect = 0.0

Identities = 375/376 (99%), Gaps = 1/376 (0%)

Strand=Plus/Minus

```
Query  5      TGA-TAGCTGTCGAGAGCACTTCAAGTTTGCCATTTTCATTCACCACAAGCCAAGCCCAA  63
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  376    TGATTAGCTGTCGAGAGCACTTCAAGTTTGCCATTTTCATTCACCACAAGCCAAGCCCAA  317

Query  64     CCTGACCCAAAGCGAGTTGTCGCAGCTTGCGTGAAAGCAGCTTTGAATTCGTCAAATGAG  123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  316    CCTGACCCAAAGCGAGTTGTCGCAGCTTGCGTGAAAGCAGCTTTGAATTCGTCAAATGAG  257

Query  124    CCAAAAGCTTCCTCAATTGCAGCCAACACTTGTGTTGTTGGTTCTTGTTTTTCAGGTGAT  183
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  256    CCAAAAGCTTCCTCAATTGCAGCCAACACTTGTGTTGTTGGTTCTTGTTTTTCAGGTGAT  197

Query  184    AATAATTCCCAGAAAAGGGCGTGGTTCAAATGCCCACCACCATTATTAATCACCGCTTGA  243
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  196    AATAATTCCCAGAAAAGGGCGTGGTTCAAATGCCCACCACCATTATTAATCACCGCTTGA  137

Query  244    CGGATATCTGTTGGAATACTATCAACATCTGCCAACAAAGCTTCCAAATCATCTCCAATT  303
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  136    CGGATATCTGTTGGAATACTATCAACATCTGCCAACAAAGCTTCCAAATCATCTCCAATT  77

Query  304    TCTGGATGCTTTTCAAGCGCCGCATTTACATTTGCCACATAAGTAGCATGATGTTTATCA  363
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  76     TCTGGATGCTTTTCAAGCGCCGCATTTACATTTGCCACATAAGTAGCATGATGTTTATCA  17

Query  364    TGGTGAATTGTCATTG  379
              ||||||||||||||||
Sbjct  16     TGGTGAATTGTCATTG  1
```

3. H103/53 MNCH

Sequence:

GCTGTCGAGAGCACTTCAAGTTTGCCATTTTCATTCACCACAAGCCAAGCC
CAACCTGATCCAAAGCGAGTTGTCGCAGCTTGCGTGAAAGCAGCTTTGAA
TTCATCAAATGAGCCAAAAGCTTCCTCAATCGCAGCCAACACTTGTGTTGT
TGGTTCTTGTTTTTCAGGTGATAACAATTCCCAGAAAAGGGCGTGGTTCAA
ATGCCCACCACCATTATTAATCACCGCTTGACGGATATCTGTTGGAATACT
ATCAACATCTGCCAACAAAGCTTCCAAATCATCTCCAATTTCTGGATGCTT
TTCAAGCGCCGCATTTACATTTGCCACATAAGTAGCATGATGTTTATCATG
GTGAATTGTCATTGAAT

>gb|GU991770.1| *Streptococcus pasteurianus* strain LMG 22784 manganese-dependent superoxide dismutase (sodA) gene, partial cds; Length=419

Score = 684 bits (370), Expect = 0.0

Identities = 370/370 (100%), Gaps = 0/370 (0%)

Strand=Plus/Minus

```
Query  1    GCTGTCGAGAGCACTTCAAGTTTGCCATTTTCATTCACCACAAGCCAAGCCCAACCTGAT  60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  378  GCTGTCGAGAGCACTTCAAGTTTGCCATTTTCATTCACCACAAGCCAAGCCCAACCTGAT  319

Query  61   CCAAAGCGAGTTGTCGCAGCTTGCGTGAAAGCAGCTTTGAATTCATCAAATGAGCCAAAA  120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  318  CCAAAGCGAGTTGTCGCAGCTTGCGTGAAAGCAGCTTTGAATTCATCAAATGAGCCAAAA  259

Query  121  GCTTCCTCAATCGCAGCCAACACTTGTGTTGTTGGTTCTTGTTTTTCAGGTGATAACAAT  180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  258  GCTTCCTCAATCGCAGCCAACACTTGTGTTGTTGGTTCTTGTTTTTCAGGTGATAACAAT  199

Query  181  TCCCAGAAAAGGGCGTGGTTCAAATGCCCACCACCATTATTAATCACCGCTTGACGGATA  240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  198  TCCCAGAAAAGGGCGTGGTTCAAATGCCCACCACCATTATTAATCACCGCTTGACGGATA  139

Query  241  TCTGTTGGAATACTATCAACATCTGCCAACAAAGCTTCCAAATCATCTCCAATTTCTGGA  300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  138  TCTGTTGGAATACTATCAACATCTGCCAACAAAGCTTCCAAATCATCTCCAATTTCTGGA  79

Query  301  TGCTTTTCAAGCGCCGCATTTACATTTGCCACATAAGTAGCATGATGTTTATCATGGTGA  360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct  78   TGCTTTTCAAGCGCCGCATTTACATTTGCCACATAAGTAGCATGATGTTTATCATGGTGA  19

Query  361  ATTGTCATTG  370
            ||||||||||
Sbjct  18   ATTGTCATTG  9
```

E. Alignment of 16S rRNA primers of *S. suis* to 16S ribosomal RNA gene (partial sequence) of *S. bovis* strain FMA766

GenBank Accession No.: HQ721264

>gi|327494323|gb|HQ721264.1| *Streptococcus bovis* strain FMA766 16S ribosomal RNA gene, partial sequence

```
GGCATACGGGTCTATAATGCAGTGGACGCATGATTGATACCGGAGCTTGCTCCACCATTAATCATGAGTC
GCGAACGGGTGAGTAACGCGTAGGTAACCTACCTCATAGCGGGGGATAACTATTGGAAACGATAGCTAAT
ACCGCATAACAGTATTTATCGCATGGTAAATGCTTGAAAGGAGCAACTGCTTCACTATGAGATGGACCTG
CGTTGTATTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGA
TCGGCCACACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATG
GGGGGAACCCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGA
GAAGAACGTGTGTGAGAGTGGAAAGTTCACACAGTGACGGTAACTTACCAGAAAGGGACGGCTAACTACG
TGCCAGCAGCCGCGGTAATACGTAGGTCCCGAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGG
CGGTTTGATAAGTCTGAAGTAAAAGGCTGTGGCTTAACCATAGTATGCTTTGGAAACTGTCAAACTTGAG
TGCAGAAGGGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGC
GAAAGCGGCTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACC
CTGGTAGTCCACGCCGTAAACGATGAGTGCTAGGTGTTGGGTCCTTTCCGGGACTCAGTGCCGTAGCTAA
CGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGGTTGAAACTCAAAGGAATTGACGGGGGCCCG
CACAAGCGGTGGAGCATGTGGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCCAG
TGACCGTCCTAGAGATAGGATTTTTCTTCGGAACACTGGAGACAGGTGGTGCATGGTTGTCGTCAGCTCG
TGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACCCCTATTGTTAGTTGCCATCATTCAGTTGG
GCACTCTAGCGAGACTGCCGGTAATAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTA
TGACCTGGGCTACACACGTGCTACAATGGCTGGTACAACGAGTCGCAAGTCGGTGACGACAAGCTAATCT
CTTAAAGCCAGTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGTCGGAATCGCTAGTAATCG
CGGATCAGCACGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTG
TAACACCCGAAGTCGGTGAGGTAACCATTTGGAGCCAGCCGCCTAAGGTGGGATAGATGATTGGGGGAAG
TCGAACAAGACGCATGCC
```

Sequence alignment of 16S rRNA forward primer to 16S ribosomal RNA gene of *S. bovis* strain FMA766

```
16S rRNA gene   GGCATACGGGTCTATAATGCAGTGGACGCATGATTGATACCGGAGCTTGCTCCACCATTA
primer          ------------------------------------------------------------

16S rRNA gene   ATCATGAGTCGCGAACGGGTGAGTAACGCGTAGGTAACCTACCTCATAGCGGGGGATAAC
primer          ------------------------------------------------------------

16S rRNA gene   TATTGGAAACGATAGCTAATACCGCATAACAGTATTTATCGCATGGTAAATGCTTGAAAG
primer          -----------------------------CAGTATTTACCGCATGGTAGATAT-------
                                             ********* *********.**.
16S rRNA gene   GAGCAACTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGGGGTAACGG
primer          ------------------------------------------------------------

16S rRNA gene   CTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAG
primer          ------------------------------------------------------------

16S rRNA gene   ACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGGAACCC
primer          ------------------------------------------------------------

16S rRNA gene   TGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGA
primer          ------------------------------------------------------------

16S rRNA gene   GAAGAACGTGTGTGAGAGTGGAAAGTTCACACAGTGACGGTAACTTACCAGAAAGGGACG
primer          ------------------------------------------------------------

16S rRNA gene   GCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTCCCGAGCGTTGTCCGGATTTATT
primer          ------------------------------------------------------------

16S rRNA gene   GGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGTAAAAGGCTGTGGCTTAACCA
primer          ------------------------------------------------------------

16S rRNA gene   TAGTATGCTTTGGAAACTGTCAAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGT
primer          ------------------------------------------------------------

16S rRNA gene   AGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGTCTG
primer          ------------------------------------------------------------

16S rRNA gene   TAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCC
primer          ------------------------------------------------------------

16S rRNA gene   ACGCCGTAAACGATGAGTGCTAGGTGTTGGGTCCTTTCCGGGACTCAGTGCCGTAGCTAA
primer          ------------------------------------------------------------

16S rRNA gene   CGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGGTTGAAACTCAAAGGAATTGAC
primer          ------------------------------------------------------------

16S rRNA gene   GGGGGCCCGCACAAGCGGTGGAGCATGTGGGTTTAATTCGAAGCAACGCGAAGAACCTT
primer          ------------------------------------------------------------

16S rRNA gene   ACCAGGTCTTGACATCCCAGTGACCGTCCTAGAGATAGGATTTTTCTTCGGAACACTGGA
primer          ------------------------------------------------------------

16S rRNA gene   GACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAA
primer          ------------------------------------------------------------
```

Sequence alignment of 16S rRNA reverse primer to 16S ribosomal RNA gene of

S. bovis strain FMA766

```
primer          ------------------------------------------------------------
16S rRNA gene   GGCATACGGGTCTATAATGCAGTGGACGCATGATTGATACCGGAGCTTGCTCCACCATTA

primer          ------------------------------------------------------------
16S rRNA gene   ATCATGAGTCGCGAACGGGTGAGTAACGCGTAGGTAACCTACCTCATAGCGGGGGATAAC

primer          ------------------------------------------------------------
16S rRNA gene   TATTGGAAACGATAGCTAATACCGCATAACAGTATTTATCGCATGGTAAATGCTTGAAAG

primer          ------------------------------------------------------------
16S rRNA gene   GAGCAACTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGGGGTAACGG

primer          ------------------------------------------------------------
16S rRNA gene   CTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAG

primer          ------------------------------------------------------------
16S rRNA gene   ACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGGAACCC

primer          ------------------------------------------------------------
16S rRNA gene   TGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGA

primer          -------------------------TTCTCACT-TGACGGTATCTTAC------------
16S rRNA gene   GAAGAACGTGTGTGAGAGTGGAAAGTTCACACAGTGACGGTAACTTACCAGAAAGGGACG
                                         ***:***: ********:*****

primer          ------------------------------------------------------------
16S rRNA gene   GCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTCCCGAGCGTTGTCCGGATTTATT

primer          ------------------------------------------------------------
16S rRNA gene   GGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGTAAAAGGCTGTGGCTTAACCA

primer          ------------------------------------------------------------
16S rRNA gene   TAGTATGCTTTGGAAACTGTCAAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTGT

primer          ------------------------------------------------------------
16S rRNA gene   AGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGTCTG

primer          ------------------------------------------------------------
16S rRNA gene   TAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCC

primer          ------------------------------------------------------------
16S rRNA gene   ACGCCGTAAACGATGAGTGCTAGGTGTTGGGTCCTTTCCGGGACTCAGTGCCGTAGCTAA

primer          ------------------------------------------------------------
16S rRNA gene   CGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGGTTGAAACTCAAAGGAATTGAC

primer          ------------------------------------------------------------
16S rRNA gene   GGGGGCCCGCACAAGCGGTGGAGCATGTGGGTTTAATTCGAAGCAACGCGAAGAACCTT

primer          ------------------------------------------------------------
16S rRNA gene   ACCAGGTCTTGACATCCCAGTGACCGTCCTAGAGATAGGATTTTTCTTCGGAACACTGGA

primer          ------------------------------------------------------------
16S rRNA gene   GACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAA
```

Sequence alignment of *S. suis* H23/52 MNCH 16S rRNA sequence product to 16S ribosomal RNA gene of *S. bovis* strain FMA766

Sequence 1: Bovis 1488 bp

Sequence 2: H23 279 bp

Aligned. Score: 25.448

```
Bovis           GGCATACGGGTCTATAATGCAGTGGACGCATGATTGATACCGGAGCTTGCTCCACCATTA
H23             ------------------------------------------------------------


Bovis           ATCATGAGTCGCGAACGGGTGAGTAACGCGTAGGTAACCTACCTCATAGCGGGGGATAAC
H23             ------------------------------------------------------------


Bovis           TATTGGAAACGATAGCTAATACCGCATAACAGTATTTATCGCATGGTAAATGCTTGAAAG
H23             -------------------------------GTTCTTCTCTTACAACAGAGCTTTACGAT
                                               **  ** **  *    * *   **   *

Bovis           GAGCAACTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGGGGTAACGG
H23             CCGAAAACCTTCTTCACTCACGCGGCGTTGCTCGGTCAGGGTTGCCCCCATTGCCGAAGA
                  * **    *   *  * *   **   ***   **    * *         *   * *

Bovis           CTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAG
H23             TTCCCTACTGCTGCCTCCCGTAGGAGTCTGGGCCGTGTC-TCAGTCCCAGTGTGGCCGAT
                 ** * *  **  *    * ***  * *  *   * **  ** * * ** ** * * **

Bovis           ACACGGCCCAGACTC-CTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGGAACC
H23             CACCCTCTCAGGTCGGCTATGTATCGAAGCCTTGGTGAGCCGTTACCTCACCAACTAGCT
                   *  * ***     *** *    * ***  * * **  * *   *         * *

Bovis           CTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAG
H23             AATACAACGCAGGTCCATCTCATAGTGAAGCAGTTGCTCCTTTCAAATATCTACCATGCG
                   **   ***   **   * *  *   *    ** *   *   ***  ***    *  *

Bovis           AGAAGAACGTGTGTGAGAGTGGAAAGTTCACACAGTGACGGTAACTTACCAGAAAGGGAC
H23             GTAAATACAGA-------------------------------------------------
                  **  **

Bovis           GGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTCCCGAGCGTTGTCCGGATTTAT
H23             ------------------------------------------------------------


Bovis           TGGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGTAAAAGGCTGTGGCTTAACC
H23             ------------------------------------------------------------


Bovis           ATAGTATGCTTTGGAAACTGTCAAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTG
H23             ------------------------------------------------------------


Bovis           TAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGTCT
H23             ------------------------------------------------------------


Bovis           GTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTC
H23             ------------------------------------------------------------


Bovis           CACGCCGTAAACGATGAGTGCTAGGTGTTGGGTCCTTTCCGGGACTCAGTGCCGTAGCTA
H23             ------------------------------------------------------------


Bovis           ACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGGTTGAAACTCAAAGGAATTGA
H23             ------------------------------------------------------------
```

```
Bovis           CGGGGGGCCCGCACAAGCGGTGGAGCATGTGGGTTTAATTCGAAGCAACGCGAAGAACCT
H23             ------------------------------------------------------------

Bovis           TACCAGGTCTTGACATCCCAGTGACCGTCCTAGAGATAGGATTTTTCTTCGGAACACTGG
H23             ------------------------------------------------------------

Bovis           AGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCA
H23             ------------------------------------------------------------

Bovis           ACGAGCGCAACCCCTATTGTTAGTTGCCATCATTCAGTTGGGCACTCTAGCGAGACTGCC
H23             ------------------------------------------------------------

Bovis           GGTAATAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGG
H23             ------------------------------------------------------------

Bovis           CTACACACGTGCTACAATGGCTGGTACAACGAGTCGCAAGTCGGTGACGACAAGCTAATC
H23             ------------------------------------------------------------

Bovis           TCTTAAAGCCAGTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGTCGGAATC
H23             ------------------------------------------------------------

Bovis           GCTAGTAATCGCGGATCAGCACGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGC
H23             ------------------------------------------------------------

Bovis           CCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCATTTGGAGCCAGC
H23             ------------------------------------------------------------

Bovis           CGCCTAAGGTGGGATAGATGATTGGGGGAAGTCGAACAAGACGCATGCC
H23             -------------------------------------------------
```

Sequence alignment of *S. bovis* H24/52 MNCH 16S rRNA sequence product to 16S ribosomal RNA gene of *S. bovis* strain FMA766

```
Sequence 1: Bovis      1488 bp
Sequence 2: H24         300 bp
Aligned. Score: 85.3333

Bovis           GGCATACGGGTCTATAATGCAGTGGACGCATGATTGATACCGGAGCTTGCTCCACCATTA
H24             ------------------------------------------------------------


Bovis           ATCATGAGTCGCGAACGGGTGAGTAACGCGTAGGTAACCTACCTCATAGCGGGGGATAAC
H24             ------------------------------------------------------------


Bovis           TATTGGAAACGATAGCTAATACCGCATAACAGTATTTATCGCATGGTAAATGCTTGAAAG
H24             -----------------------------------------------------TTTTTAG
                                                                      **   **

Bovis           GAGCAACTGCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGGGGTAACGG
H24             GAACA-TTGCTTC-CTATGAG-TGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGG
                ** **  ****** ******* ***************************** ********

Bovis           CTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAG
H24             CTCACCAAGGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAG
                ************************************************************

Bovis           ACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGGGGGAACCC
H24             ACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCC
                ************************************************* **** *****

Bovis           TGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGA
H24             TGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGA
                ************************************************************

Bovis           GAAGAACGTGTGTGA-GAGTGGAAAGTTCACACAGTGACGGTAACTTACCAGAAAGGGAC
H24             GAAGAAC-TGTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACAACAGAGA---
                ******* **** ** ************       ******** ***** * * **

Bovis           GGCTAACTACGTGCCAGCAGCCGCGGTAATACGTAGGTCCCGAGCGTTGTCCGGATTTAT
H24             ------------------------------------------------------------


Bovis           TGGGCGTAAAGCGAGCGCAGGCGGTTTGATAAGTCTGAAGTAAAGGCTGTGGCTTAACC
H24             ------------------------------------------------------------


Bovis           ATAGTATGCTTTGGAAACTGTCAAACTTGAGTGCAGAAGGGGAGAGTGGAATTCCATGTG
H24             ------------------------------------------------------------


Bovis           TAGCGGTGAAATGCGTAGATATATGGAGGAACACCGGTGGCGAAAGCGGCTCTCTGGTCT
H24             ------------------------------------------------------------


Bovis           GTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTC
H24             ------------------------------------------------------------


Bovis           CACGCCGTAAACGATGAGTGCTAGGTGTTGGGTCCTTTCCGGGACTCAGTGCCGTAGCTA
H24             ------------------------------------------------------------


Bovis           ACGCATTAAGCACTCCGCCTGGGGAGTACGACCGCAAGGGTTGAAACTCAAAGGAATTGA
H24             ------------------------------------------------------------
```

```
Bovis           CGGGGGGCCCGCACAAGCGGTGGAGCATGTGGGTTTAATTCGAAGCAACGCGAAGAACCT
H24             ------------------------------------------------------------

Bovis           TACCAGGTCTTGACATCCCAGTGACCGTCCTAGAGATAGGATTTTTCTTCGGAACACTGG
H24             ------------------------------------------------------------

Bovis           AGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCA
H24             ------------------------------------------------------------

Bovis           ACGAGCGCAACCCCTATTGTTAGTTGCCATCATTCAGTTGGGCACTCTAGCGAGACTGCC
H24             ------------------------------------------------------------

Bovis           GGTAATAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGG
H24             ------------------------------------------------------------

Bovis           CTACACACGTGCTACAATGGCTGGTACAACGAGTCGCAAGTCGGTGACGACAAGCTAATC
H24             ------------------------------------------------------------

Bovis           TCTTAAAGCCAGTCTCAGTTCGGATTGTAGGCTGCAACTCGCCTACATGAAGTCGGAATC
H24             ------------------------------------------------------------

Bovis           GCTAGTAATCGCGGATCAGCACGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGC
H24             ------------------------------------------------------------

Bovis           CCGTCACACCACGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCATTTGGAGCCAGC
H24             ------------------------------------------------------------

Bovis           CGCCTAAGGTGGGATAGATGATTGGGGGAAGTCGAACAAGACGCATGCC
H24             -------------------------------------------------
```

F. Alignment of 16S rRNA primers of *S. suis* to 16S ribosomal RNA gene (partial sequence) of *E. faecalis* strain FUA3372

GenBank Accession No.: JN102567

>gi|355336804|gb|JN102567.1| *Enterococcus faecalis* strain FUA3372 16S ribosomal RNA gene, partial sequence

```
TACATGCAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCACTCAATTGGAAAGAGGAGTGGCGGACGGGT

GAGTAACACGTGGGTAACCTACCCATCAGAGGGGGATAACACTTGGAAACAGGTGCTAATACCGCATAAC

AGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTTCGGGTGTCGCTGATGGATGGACCCGCGGTGCAT

TAGCTAGTTGGTGAGGTAACGGCTCACCAAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCAC

ACTGGGACTGAGACACGGCCCAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAG

TCTGACCGAGCAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGAACA

AGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAACTACGTGCCAGCAG

CCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAAGCGAGCGCAGGCGGTTTCTT

AAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTCATTGGAAACTGGGAGACTTGAGTGCAGAAG

AGGAGAGTGGAATTCCATGTGTAGCGGTGAAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGG

CTCTCTGGTCTGTAACTGACGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGT

CCACGCCGTAAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCAAACGCATTAA

GCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCGCACAAGCGGT

GGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTGACATCCTTTGACCACTCTAG

AGATAGAGCTTTCCCTTCGGGGACAAAGTGACAGGTGGTGCATGGTTGTCGTCAGCTCGTGTCGTGAGAT

GTTGGGTTAAGTCCCGCAACGAGCGCAACCCTTATTGTTAGTTGCCATCATTTAGTTGGGCACTCTAGCG

AGACTGCCGGTGACAAACCGGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCT

ACACACGTGCTACAATGGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGCAAATCTCTTAAAGCTTC

TCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGCGGATCAGCAC

GCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCACGAGAGTTTGTAACACCCGAA

GTCGGTGAGGTAACCTTTTTGGAGCCAGCCGCCTAAGGTGGGATAGATGATTGGGGTGAAGTCGT
```

Sequence alignment of 16S rRNA forward primer to 16S ribosomal RNA gene of *E. faecalis* strain FUA3372

```
Entero          TACATGCAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCACTCAATTGGAAAGAGGAGTG
primer          ------------------------------------------------------------


Entero          GCGGACGGGTGAGTAACACGTGGGTAACCTACCCATCAGAGGGGGATAACACTTGGAAAC
primer          ------------------------------------------------------------


Entero          AGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTTCGG
primer          -------------------CAGTATTTACCGCATGGTAGATAT-----------------
                                   **** * * ******** * *

Entero          GTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAA
primer          ------------------------------------------------------------


Entero          GGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCC
primer          ------------------------------------------------------------


Entero          CAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACCGAG
primer          ------------------------------------------------------------


Entero          CAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGAACA
primer          ------------------------------------------------------------


Entero          AGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAACTAC
primer          ------------------------------------------------------------


Entero          GTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAA
primer          ------------------------------------------------------------


Entero          GCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
primer          ------------------------------------------------------------


Entero          ATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGA
primer          ------------------------------------------------------------


Entero          AATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAACTGAC
primer          ------------------------------------------------------------


Entero          GCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTA
primer          ------------------------------------------------------------


Entero          AACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCAAACGCATTAA
primer          ------------------------------------------------------------


Entero          GCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCG
primer          ------------------------------------------------------------


Entero          CACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTG
primer          ------------------------------------------------------------


Entero          ACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGACAAAGTGACAGGTGGTG
primer          ------------------------------------------------------------


Entero          CATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC
primer          ------------------------------------------------------------


Entero          CTTATTGTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGACTGCCGGTGACAAACCG
primer          ------------------------------------------------------------


Entero          GAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGC
primer          ------------------------------------------------------------


Entero          TACAATGGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGCAAATCTCTTAAAGCTTC
primer          ------------------------------------------------------------


Entero          TCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGC
primer          ------------------------------------------------------------
```

Sequence alignment of 16S rRNA reverse primer to 16S ribosomal RNA gene of *E. faecalis* strain FUA3372

```
Entero          TACATGCAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCACTCAATTGGAAAGAGGAGTG
primer          ------------------------------------------------------------

Entero          GCGGACGGGTGAGTAACACGTGGGTAACCTACCCATCAGAGGGGGATAACACTTGGAAAC
primer          ------------------------------------------------------------

Entero          AGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTTCGG
primer          ------------------------------------------------------------

Entero          GTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAA
primer          ------------------------------------------------------------

Entero          GGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCC
primer          ------------------------------------------------------------

Entero          CAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACCGAG
primer          ------------------------------------------------------------

Entero          CAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGAACA
primer          ---------------------------------GTAAGATACCGTCAAGTGAGAA-----
                                                 **** *  * **     *****
Entero          AGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAACTAC
primer          ------------------------------------------------------------

Entero          GTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAA
primer          ------------------------------------------------------------

Entero          GCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
primer          ------------------------------------------------------------

Entero          ATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGA
primer          ------------------------------------------------------------

Entero          AATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAACTGAC
primer          ------------------------------------------------------------

Entero          GCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTA
primer          ------------------------------------------------------------

Entero          AACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCAAACGCATTAA
primer          ------------------------------------------------------------

Entero          GCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCG
primer          ------------------------------------------------------------

Entero          CACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTG
primer          ------------------------------------------------------------

Entero          ACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGACAAAGTGACAGGTGGTG
primer          ------------------------------------------------------------

Entero          CATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC
primer          ------------------------------------------------------------

Entero          CTTATTGTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGACTGCCGGTGACAAACCG
primer          ------------------------------------------------------------

Entero          GAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTGC
primer          ------------------------------------------------------------

Entero          TACAATGGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGCAAATCTCTTAAAGCTTC
primer          ------------------------------------------------------------

Entero          TCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCGC
primer          ------------------------------------------------------------
```

Sequence alignment of *S. suis* H23/52 MNCH 16S rRNA sequence product to 16S ribosomal RNA gene of *E. faecalis* strain FUA3372

```
Sequence 1: Entero      1465 bp
Sequence 2: SS23         279 bp
Aligned. Score: 22.9391


Entero          TACATGCAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCACTCAATTGGAAAGAGGAGTG
SS              ------------------------------------------------------------

Entero          GCGGACGGGTGAGTAACACGTGGGTAACCTACCCATCAGAGGGGGATAACACTTGGAAAC
SS              ------------------------------------------------------------

Entero          AGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTTCGG
SS              ------------------------------------------------------------

Entero          GTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAA
SS              ------------------------------------------------------------

Entero          GGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCC
SS              ------------------------------------------------------------

Entero          CAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACCGAG
SS              ------------------------------------------------------------

Entero          CAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGAACA
SS              ------------------------------------------------------------

Entero          AGGACGTTAGTAACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAACTAC
SS              ------------------------------------------------------------

Entero          GTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAAA
SS              ------------------------------------------------------------

Entero          GCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGTC
SS              ------------------------------------------------------------

Entero          ATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTGA
SS              ------------------------------------------------------------

Entero          AATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAACTGAC
SS              ------------------------------------------------------------

Entero          GCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGTA
SS              ------------------------------------------------------------

Entero          AACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCAAACGCATTAA
SS              ------------------------------------------------------------

Entero          GCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCCG
SS              ------------------------------------------------------------

Entero          CACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTTG
SS              --------------------GTTCTTCTCTTA-CAAC----AGAGCTTTAC--GATCCGA
                                    ***    **  * ****    *** * ****  * **
```

```
Entero          ACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGACAAAGTGACAGGTGGTG
SS              AAACCTTCT--TCACTC---ACGCGGCGTTGCTCGGTCAGGGTTGCCCCCATTGCCGAAG
                * * * * *   *****   *    * * *   *  ** ***        *  *  *  *

Entero          CATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAACC
SS              ATTCCCTACTGCTGCCTC---CCGTAGGAGTCTGGGCCGTGTCTCAGTCCCAGTGTGGCC
                  *   *   *    ***    ***  **   ****    *** *    * ** *   **

Entero          C-TTATTGTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGACTGCCGGTGACAAACC
SS              GATCACCCTCTCAGGTCGGC-TATGTATCGAAGCCTTGGTGAGCCGTTACCTCACCAACT
                  * *   *     * *  * * *   * *   *  * * *** *      * ** ***

Entero          GGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTG
SS              AGCTAATACAACGCAGGTC--CATCTCATAGTGAAGCAGTTGCTCCTTTCAA-ATATCTA
                 *   *      * * * *  **  ****  **   *   **  *    * * * *  *

Entero          CTACAATGGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGCAAATCTCTTAAAGCTT
SS              CCATG-CGGTAAATACAGA-----------------------------------------
                * *    ** ** ****

Entero          CTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCG
SS              ------------------------------------------------------------

Entero          CGGATCAGCACGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCA
SS              ------------------------------------------------------------

Entero          CGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTTTGGAGCCAGCCGCCTAAGGT
SS              ------------------------------------------------------------

Entero          GGGATAGATGATTGGGGTGAAGTCGT
SS              --------------------------
```

Sequence alignment of *E. faecalis* H32/52 LPH16S rRNA sequence product to 16S ribosomal RNA gene of *E. faecalis* strain FUA3372

```
Sequence 1: Entero      1465 bp
Sequence 2: H32          291 bp
Aligned. Score: 80.4124


Entero          TACATGCAGTCGAACGCTTCTTTCCTCCCGAGTGCTTGCACTCAATTGGAAAGAGGAGTG
H32             ------------------------------------------------------------


Entero          GCGGACGGGTGAGTAACACGTGGGTAACCTACCCATCAGAGGGGGATAACACTTGGAAAC
H32             ------------------------------------------------------------


Entero          AGGTGCTAATACCGCATAACAGTTTATGCCGCATGGCATAAGAGTGAAAGGCGCTTTCGG
H32             --------------------------------------------------------CANT


Entero          GTGTCGCTGATGGATGGACCCGCGGTGCATTAGCTAGTTGGTGAGGTAACGGCTCACCAA
H32             GCTTCACTATGAGATGGACCTGCGTTGTATTAGCTAGTTGGTGAGGTAACGGCTCACCAA
                *  ** **    ******** *** ** ********************************

Entero          GGCCACGATGCATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCC
H32             GGCATCGATACATAGCCGACCTGAGAGGGTGATCGGCCACACTGGGACTGAGACACGGCC
                ***  **** **************************************************

Entero          CAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATGGACGAAAGTCTGACCGAG
H32             CAGACTCCTACGGGAGGCAGCAGTAGGGAATCTTCGGCAATAGGGGCAACCCTGACCGAG
                ***************************************** *  * **  *********

Entero          CAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAACTCTGTTGTTAGAGAAGAACA
H32             CAACGCCGCGTGAGTGAAGAAGGTTTTCGGATCGTAAAGCTCTGTTGTAAGAGAAGAACT
                ************************************** ********* ********** 

Entero          AGGACGTTAGTA-ACTGAACGTCCCCTGACGGTATCTAACCAGAAAGCCACGGCTAACTA
H32             GTGAGAAGAGTGGAAAGTTTCTCACTTGACGGTATCTTACCACAGAG-------------
                  **    ***  *  *    ** * *********** **** * **

Entero          CGTGCCAGCAGCCGCGGTAATACGTAGGTGGCAAGCGTTGTCCGGATTTATTGGGCGTAA
H32             ------------------------------------------------------------


Entero          AGCGAGCGCAGGCGGTTTCTTAAGTCTGATGTGAAAGCCCCCGGCTCAACCGGGGAGGGT
H32             ------------------------------------------------------------


Entero          CATTGGAAACTGGGAGACTTGAGTGCAGAAGAGGAGAGTGGAATTCCATGTGTAGCGGTG
H32             ------------------------------------------------------------


Entero          AAATGCGTAGATATATGGAGGAACACCAGTGGCGAAGGCGGCTCTCTGGTCTGTAACTGA
H32             ------------------------------------------------------------


Entero          CGCTGAGGCTCGAAAGCGTGGGGAGCAAACAGGATTAGATACCCTGGTAGTCCACGCCGT
H32             ------------------------------------------------------------


Entero          AAACGATGAGTGCTAAGTGTTGGAGGGTTTCCGCCCTTCAGTGCTGCAGCAAACGCATTA
H32             ------------------------------------------------------------


Entero          AGCACTCCGCCTGGGGAGTACGACCGCAAGGTTGAAACTCAAAGGAATTGACGGGGGCCC
H32             ------------------------------------------------------------


Entero          GCACAAGCGGTGGAGCATGTGGTTTAATTCGAAGCAACGCGAAGAACCTTACCAGGTCTT
H32             ------------------------------------------------------------


Entero          GACATCCTTTGACCACTCTAGAGATAGAGCTTTCCCTTCGGGGACAAAGTGACAGGTGGT
H32             ------------------------------------------------------------
```

```
Entero          GCATGGTTGTCGTCAGCTCGTGTCGTGAGATGTTGGGTTAAGTCCCGCAACGAGCGCAAC
H32             ------------------------------------------------------------

Entero          CCTTATTGTTAGTTGCCATCATTTAGTTGGGCACTCTAGCGAGACTGCCGGTGACAAACC
H32             ------------------------------------------------------------

Entero          GGAGGAAGGTGGGGATGACGTCAAATCATCATGCCCCTTATGACCTGGGCTACACACGTG
H32             ------------------------------------------------------------

Entero          CTACAATGGGAAGTACAACGAGTCGCTAGACCGCGAGGTCATGCAAATCTCTTAAAGCTT
H32             ------------------------------------------------------------

Entero          CTCTCAGTTCGGATTGCAGGCTGCAACTCGCCTGCATGAAGCCGGAATCGCTAGTAATCG
H32             ------------------------------------------------------------

Entero          CGGATCAGCACGCCGCGGTGAATACGTTCCCGGGCCTTGTACACACCGCCCGTCACACCA
H32             ------------------------------------------------------------

Entero          CGAGAGTTTGTAACACCCGAAGTCGGTGAGGTAACCTTTTTGGAGCCAGCCGCCTAAGGT
H32             ------------------------------------------------------------

Entero          GGGATAGATGATTGGGGTGAAGTCGT
H32             --------------------------
```

APPENDIX D
Media and reagents

1. Culture media and biochemical test media

Todd-Hewitt broth (THB)

Todd-Hewitt broth	30.00	g
Distilled water	1,000	ml

Suspend 30 g of powder in 1 L of distilled water. Autoclave at 121 °C 15 lbs for 15 min.

Tripticase soy agar (TSA) with human blood

Tripticase soy agar	40.00	g
Distilled water	1,000	ml

Suspend 40 g of powder in 1 L of distilled water. Bring to the boil to dissolve completely. Autoclave at 121 °C 15 lbs for 15 min, cool to 50-55 °C before adding sterilized human blood (50 ml/L).

Bacterial Storage Media

Oxoid tryptone soyabroth	3.00	g
Glucose	0.50	g
Oxoid skim milk powder	2.00	g
Glycerol	10.00	ml

Double distilled water was added to 100 ml. The solution was dispensed in 1 ml amounts into cryotubes and autoclaved at 121 °C 15 lbs for 15 min and then stored at 4-6 °C.

Bile esculin slant

Bile esculin agar	4.35	g

Suspend the bile esculin agar in 100 ml of distilled water. Autoclave at 121 °C 15 lbs for 15 min.

Esculin slant

Heart infusion agar	4.00	g
Ammonium Ferric Citrate	0.05	g
Esculin	0.10	g

Suspend the above ingradients in 100 ml of distilled water. Autoclave at 121 °C 15 lbs for 15 min.

Trehalose, Manntol, Raffinose, Lactose and Sorbitol

CTA base agar	0.25	g

Suspend 1 g of each sugar (1%) and CTA agar in 100 ml of distilled water. Autoclave at 110 °C for 10 min.

2. Reagents and buffers

Phosphate buffer saline (PBS)

NaCl	8.00	g
KCl	0.20	g
Na_2HPO_4	1.44	g
KH_2PO_4	0.20	g

The above ingradients were suspended in 900 ml of distilled water. Adjust to pH 7.2 by using 1M NaOH or 1M HCl. Distilled water was added to 1,000 ml. Autoclave at 121 °C 15 lbs for 15 min.

Lysozyme solution (10 mg/ml)

Lysozyme	0.01	g
0.5M Tris-HCl (pH 7.5)	1.00	ml

Mix to dissolve completely.

Saturated NaCl

NaCl was added in 200 ml till undissolve. Filter and autoclave at 121°C 15 lbs for 15 min.

20% (w/v) Sodium dodecyl sulphate (SDS)

SDS	20.0	g
Distilled water	100.0	ml

Dissolve 20 g of SDS in 90 ml of distilled water with gentle stirring and bring to 100 ml with distilled water. Store at room temperature.

Tris-acetate (TAE) buffer

50x stock solution in 1 liter:

Tris-base	242.0	g
Glacial acetic acid	57.1	ml
0.5 M EDTA (pH 8.0)	100.0	ml

Suspend the above ingradients in 500 ml of distilled water. Adjust to pH 8.0. Distilled water was added to 1,000 ml and autoclave at 121 °C 15 lbs for 15 min.

Agarose gel electrophoresis (2.0%)

Agarose gel powder	2.00	g
TAE Buffer (1X)	100.0	ml

Suspend agarose gel powder in 100 ml TAE buffer. Bring to boil to dissolve completely.

Working 0.5 μg/ml Ethidium bromide

Stock 10 mg/ml Ethidium bromide	5.0	μl
Distilled water	100.0	ml

CURRICULUM VITAE

Name	Miss Wannisa Raksamat
Date of birth	March 16, 1986

Institution attended

2003	Certificated of Mathayomsuksa VI, Chomsurang Upatham School, Pranakorn Sri Ayutthaya, Thailand
2007	Bachelor of Science (Microbiology), Department of Microbiology, Faculty of Science, Burapha University, Chonburi, Thailand Project: Antimicrobial Activity of Curcuminoids from *Curcuma longa* Linn. on *Helicobacter pylori* Advisor: Assoc. Prof. Punnipa Siripermpool
2011	Master of Science (Microbiology), Department of Microbiology, Faculty of Medicine, Chiang Mai, University, Chiang Mai, Thailand

Publications and presentations

Wannisa Raksamat, Piyawan Takarn, Kwanjit Duangsonk, Anusorn Boonthum, and Prasit Tharavijitkul. Detection of *Streptococcus suis* serotype 2 isolated from Hemocultures by Polymerase Chain Reaction Method. Proceeding of the Burapha University National Conference 2011 (6-7 July 2011). Burapha University, Chonburi; 2011. HS (O-HS-025).