

APPENDIX

1. Full-Length Sequence of A.cam-like_C16 and A.cam-like_C27 cDNAs

>A.cam-like_C16

```
CAATAAAACTTTTTTTTTTTTTCTCGGGAGCGCGCCATTGTGTTGGTACCCGGGAATTCGGCCATTACGGC
CGGGGGTCAGTACACCGAGGGAAAAATGTATCTTAAGGTCTTTTCCAGCTTCTTGTTCGCATGGGGCTAT
GTTAGCATTGTTTCAGTCGGCTAAAACGGTGAAGGACTGCGAAAAAAGCTCCCAGCATCGCTGAAGGGAC
GGTTGTGCAAAATTCGTCAGTACAAAATCATCGATGGACCGGACATGGAAAAGCACACGGAGGGCGTCTCT
AAACGCATTAGGATTTCTCGACAAGGAGGGTCTTGGGGATTACCACTCATTGCATGATCCGATGACCGCG
ATCAAGGAGGACATGAGACATGGGTAAACCTGGAAGACTGCGTCGCAAACACACTCGACATGCCCAAAT
CCCCAAAGCGGGCGCGTGAGTTCTACAAATGTATGCTGAAATCGACCTCTGCTGATGCATTCCGTAAGGT
TTTCGATTTGACGGAGCTCATTAAAGCTGGGAAGCTTCCCGAGGGTTCAAGCTACGCAACAAAGTAGACA
AAATGATTAAGGCTATCGATAAAAAAGTGTGCAATAATTTTGGGGAAATTTTCGTCAAACCGTGTGGGC
AAATAAATGCAGACCATCGTATGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAACTTTGCCCCCCCC
CGCCCCTTTATTTTACTCCAAAAATTTTTTTTTGGGGCCCATTTTGGCTTTTGGCAATTTCCCTAGG
GGGGCTTTTAAATTCGGGGCGCTTTTAAAAAAAAAAATTTATTTTATTAAATCCTTTCCACAACATGT
CACTATTACTCTCATTTTCTCCAGATACCCACGCACCAC
```

>A.cam-like_C27

```
GCCAAGGCAAACTTTTTTTTTTTTCTCGGGAAGCGCGCCATTGTGTTGGTACCCGGGAATTCGGCCATT
ACGGCCGGGGTTCAGTACACCGAGGGAAAGATGTATCTTAAGGTCTTTTCCAGCTTCTTGTTCATGGT
GCTTTGTTAGCATTGTTTCAGTCGGCTAAAACGGTGAAGGACTGCGAGAAAAAGCTCCCAGCATCCCTGAA
GGGACGGTTGTGCGAAATTCGTCAGTACAAAATCATCGATGGACCGGACATGGAAAAGCACACGGAGTGC
GTCCTAAACGCATTAGGATTTCTCGACGAGGAGGGTCTTGGGGATTACCACTCATTGCATGATCCGATGA
CCGCGATCAAGGAGGACATGAGACATGGGTAAACCTGGAAGACTGCGTCGCAAACACACTCGACATGCC
CAAATCCCCAAAGCGGGCGCATGAGTTCTACAAATGTATGCTGAAATCGACCTCTGCTGATGCATTCCGT
AAGTTTTTCGATTTGACGGAGCTCATTAAAGCTGGGAAGCTTCCCGAGGGTTCAAGCTACAGCAACAAAG
TAGACAAAATGATTAAGGCTATCGATAAGAAAGTGTGAAATAATTTTGGGGAAATTTTCGTCAAACCGTG
TGGGCAAATAAATGCAAACCATCGTATGATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAATTTGGGGGCC
CCCCGGCCCCAAAAATTTATAATTTAAAAATTTTTGTTGGGGCCCCTTTTGGGCCCTCTTGGGCA
ATCTCCCCTTAAGAGGGGGCCTATTAATAATTCGGGGCGGCCCTTTTAAAAAAAAAAGAAATAAATTA
AATTTTTTCTCCCCTCTCCCCCTATCCCCCTTCTGGAAGCCCACTACCCTTTCCCCTCTTA
```

ลิขสิทธิ์มหาวิทยาลัยเชียงใหม่
Copyright© by Chiang Mai University
All rights reserved

2. Similar DNA and Nucleotide Sequence of A.cam-like_C16 and A.cam-like_C27 in GenBank for Comparing with A.cam-like_C16 and A.cam-like_C27.

>A.anta348

ATGGACAAACACATGGACTGCGTCATGAAAACAATAGGATTTGTCGACAAGGATGGCCGAGGAGATTACC
ACAAGCTGATCAAGCCTCTGAATGCCATCGAGAAAGATAGGAAGCACGATATGAATCTGGAGACTTGCAT
GGGAAAAACGTTTCGCTACCAAATGAAGGCAGCCGAGCGAACGCATTCTACAAGTGCATGCTGCAGTCC
AATTCGGCAGAGTCGTTCAAGAAGGTGTTTCGATCTGACCGAGTTGGTCCTGGCGGGCAAACCTCCGGCAG
GTGCCCAGTACAATAACAAAGTGGCCAACATGATGAAGAAAATTGATGCGAAAATTTGCAAGTAA

>A.funshortD7r4

ATGGATAAGCATATCGATTGCGTTATGAAGGCGGTTCGGATTTCGTATACAGCGATGGTCGGGGAGATTATC
ACAAACTGTACGATCCACTGAATGCGATCGAGGAGGACCGTAGACATGATGTTAATCTCGAAAACATGCAT
CGGTGAATCGGTACGTGTTCTGCAAGCCAGCGCGCACATGTGTTCTACAAGTGTTCGTAACACCACA
TCCGGTCAACGTTTAAAGAAGGTGTTTGATCTTAAAGGAATTGGTGAAGGCTGGAAAAGTGCCAAAGCAGC
CCAGATATACGGCCGAAGTCGCTCAAATGATGAAGGACATTGATGCGAAAATTGTGCTAA

>A.steD7-short

ATGTACAGTCACATCGATTGTTGCATGAAGGCGGTTGATTTTGTGGAGAAAGATGGAACCTGGAGATTATC
ACAAGCTGTATGAGCTGCTGAATGACATCGAGAAGCATCGTAAACATGATATAAAATCTGGAAATGTGCGT
CGGTGAATCTATGGACGCTCAGGCAAACCAGCGGGCGTACGCTTACTACAAGTGTTCGTAACCAACC
TCGGCTGATGCGTTCAAGAAGGCGTTTGAATTTAAGGGAACCTGATCAAGGCTAACAAGCTTCCACCAGGCA
CCAGATACAGCTCGGAGGTCGACAAGCAGATGAAGAAAATTGATGACAACATATGTAA

>A.steD7-rel

1ATGTACAGTCACATCGATTGTTGCATGAAGGCGGTCGATTTTGTGGAGAAAGATGGAACCTGGAGATTAT
CACAAGCTGTATGAGCTGCTGAATGACATCGAGAAGCATCGTAAACATGATATAAAATCTGGAGACGTGCG
TCGGTGAATCCATGGACGCTCAGGCAAACCAGCGAGCGTACGCGTTCTACAAGTGTTCGTAACCAACC
CTCGGCGGACGCGTTCAAGAAGGCGTTTGAATTTGAGGGAACCTGATCAAGGCTAATAAGCTTCCACCAGGCA
ACCAGATACAGCTCGGAGGTCGACAAGCAGATGAAGAAAATTGATGACAACATATGTAA

>An.funeshortD7prot1

ATGGATAAGCATATGGACTGTGTGATGAAGACACTTAAATTCGTTTCGTGCTGATGGAACCTGGAGATTACC
ACCAGCTAATCAAACCACTGAATGCGATCGAGAAGGATCGTAAAGCACGATTTCAATCTGGAAAAGTGCGG
AGGAGACACGATGCACCTACCAGTAGGTAAACGAGCGAATGCCTACTACAAGTGTCTGCTGAACTCGTTCG
TCCAGTGAATCGTTCAAGAAGGTGTTTCGATCTGACGGAGCTGGTAAAGGCTGGCAAACCTACCGGCTACGG
CACCGTACAGTGGTGCAGTAGAGAAGCTGATGAAGAAAATTGATCAAAAGATTTGCAAATGA

>An.gambAGAP8283

ATGGACAGTCACATGCAGTGCCTACTGGAAGTGTGGGCTTTGTGGAAGATAACGGGGAGCTTGTGTTCC
AGGAGCTTCTTGGTGTGCTGAAAATGGTTGATCCCAGTGGGGATCACGCTAGCAGTATGAAAAAGTGTA
CGCCGAAGCTGAGAAGGTGGATACTTCTAGCAAAGCGAACACCTTCTACACGTGCTTTTTGGGTACGAGC
TCGGCACAGGCTTTCAAGTACGCGGTGGACTACGTGGAGCTGCTGCGCGCTGGAAAGCTGGACATGGGAA
CAACCTTCAACGCTGGCCAGGTGTCAGCATTGATGAAGCAAATTGATGATGGGCTGTGTAACCTGA

>An.arabshortD7r3

ATGGACAGTCACATGCAGTGCCTACTGGAAGTGTGGGCTTTGTGGAATATAACGGGGAACTTTTGTTC
AGGAGCTTCTTGGTGTGCTGAAAATGGTTGATCCCAGTGGGGATCACGCTGGCAGTATGAAAAAGTGTA
CGCCGAAGCAGAGAAGGTGGATACTTCTAGCAAAGCGAACACCTTCTACACGTGCTTTTTGGGTACGAGC
TCGGCGCAGGCATTCAAGTACGCGGTGGACTACGTGGAGCTGCTGCGCGCTGGAAAGCTGGACATGGGAA
CAACCTTCAACGCTGGCCAGGTGTCAGCATTGATGAAGCAAATTGATGATGGGCTGTGTAACCTGA

>An.gambAGAP8281

ATGGACAAGCACATTCATTGCGTGATGCGAGCACTTGACTTTGTCTATGAGGATGGTCGTGGAGATTACC
ATAAGCTGTACGATCCATTGAACATTATCGAGCTGGACAAAAGACACGATGTGAATCTTGAGAAGTGTAT
TGGCGAATGCGTACAAGTCCCAGCAAGCGAGCGTGTCTCACGTGTTCTACAAATGTCTCTGAAATCAACC

ACCGGACGCACGTTCAAGAAGGTGTTTCGATCTGATGGAATTGAAACAGGCTGGCAAAGTGCCACAGCATC
AACGGTACACTGCAGAGTTTGTGCAAATCATGAAGGATTATGATAAGGCATTAACACTGCTGA

>A.gamD7r4

ATGGACAAGCACATTCATTGCGTGATGCGAGCACTTGACTTTGTCTATGAGGATGGTTCGTGGAGATTACC
ATAAGCTGTACGATCCATTGAACATTATCGAGCTGGACAAAAGACACGATGTGAATCTTGAGAAGTGTAT
TGGCGAATGCGTACAAGTCCCAGCAAGCGAGCGTGCTCACGTGTTCTACAAATGTCTGCTGAAATCAACC
ACCGGGCGCACGTTCAAGAAGGTGTTTCGATCTGATGGAATTGAAAAAGGCTGGCAAAGTTCACAACATC
AACGGTACACTGCTGAGTTTGTGCAAATCATGAAGGATTATGATAAGGCATTAACACTGCTGA

>An.gambD7-rel2

ATGGACAAGCACATGCAGTGCCTGGAGGTGGTTGGATTTGTGGATGGAAATGGAGAAGTTAAGGAAA
GCGTTCCTGCTAGAATTGCTGCAGCGCGTGCAGAGTGGCGTCAATCATGCGGCCAACATGAAGAAGTGTGT
GACGGAAGCATCGACTTCGGGCAGTGACAAGAAAGCCAACACTTTCTACACGTGCTTTTTGGGTACGAGC
TCATTGGCCGGGTTTAAGAATGCGGTGCGACTACAACGAGCTACTGAAGGCTGGCAAGATGCAGACGAGCG
ATCCGTTTCGATATGAACCGTGTGGCTGCGCTGATCAAGGAAATCGATGATGGTTTTGTGCTAGTAG

>An.gambD7-rel3

ATGGACAGTCACATGCAGTGCCTGACTGGAAGTGCCTGGGCTTTGTGGAAGATAACGGGGAACTTGTGTTCC
AGGAGCTTCTTGGTGTGCTGAAAATGGTTGATCCCGATGGGGATCACGCAGGCAGTATGAAAAAGTGTA
CGCCGAAGCTGAGAAGGTGGATACTTCTAGCAAAGCGAACACCTTCTACACGTGCTTTTTGGGTACGAGC
TCGGCACAGGCTTTCAAGTACGCGGTGGACTACGTGGAGCTGCTGCGCGCTGGAAAGCTGGACATGGGAA
CAACCTTCAATGCTGGCCAGGTGTCAGCATTGATGAAGCAAATTGATGATGGGCTGTGTAATTGA

>An.gambAGAP8282

ATGGACAAGCACATGCAGTGCCTGGAGGTGGTTGGATTTGTGGATGGAAATGGAGAAGTTAAGGAAA
GCGTTCCTGCTAGAATTGCTGCAGCGCGTGCAGAGTGGCGTCAATCATGCGGCCAACATGAAGAAGTGTGT
GACGGAAGCATCGACTTCGGGCAGTGACAAGAAAGCCAACACTTTCTACACGTGCTTTTTGGGTACGAGC
TCATTGGCCGGGTTTAAGAATGCGGTGCGACTACAACGAGCTACTGAAGGCTGGCAAGATGCAGACGAGCG
ATCCGTTTCGATATGAACCGTGTGGCAGCGCTGATCAAGGAAATCGATGATGGTTTTGTGCTAGTAG

>An.arabshortD7r2

ATGGACAAGCACATGCAGTGCCTGGAGGTGGTTGGATTTGTGGATGGAAATGGAGAAGTTAAGGAAA
GCGTTCCTGCTAAAATTGCTGCAGCGCGTGCAGAGTGGCGTCAATCATGCGGCCAACATGAAGAAGTGTGT
GACGGAAGCATCGACTTCGGGCAGTGACAAGAAAGCCAACACTTTCTACACGTGCTTTTTGGGTACGAGC
TCATTGGCCGGGTTTAAGAATGCGGTGCGACTACAACGAGCTACTGAAGGCTGGCAAGATGCAGACGAGCG
ATCCGTTTCGATATGAACCGTGTGGCAGCGCTGATCAAGGAAATCGATGATGGTTTTGTGCTAGTAG

ลิขสิทธิ์มหาวิทยาลัยเชียงใหม่
Copyright© by Chiang Mai University
All rights reserved

3. CLUSTAL Multiple Sequence Alignment of *Anopheles* D7 protein

```

An.gambD7-re12      ATGGACAAGCACATGCAGTGCCTGGAGGTGGTTGGATTTGTGGATGAAATGGAGAA 60
An.gambAGAP8282    ATGGACAAGCACATGCAGTGCCTGGAGGTGGTTGGATTTGTGGATGAAATGGAGAA 60
An.arabshortD7r2   ATGGACAAGCACATGCAGTGCCTGGAGGTGGTTGGATTTGTGGATGAAATGGAGAA 60
An.arabshortD7r3   ATGGACAGTCACATGCAGTGCCTGGAGGTGGTTGGATTTGTGGATGAAATGGAGAA 60
An.gambAGAP8283    ATGGACAGTCACATGCAGTGCCTGGAGGTGGTTGGATTTGTGGATGAAATGGAGAA 60
An.gambD7-re13     ATGGACAAGCACATGCAGTGCCTGGAGGTGGTTGGATTTGTGGATGAAATGGAGAA 60
A.cam-likeC16      ATGGAAAAGCACACGGAGGGCGTCTAAACGCATTAGGATTTCTCGACAAAGGAGGCTT 60
A.cam-likeC27      ATGGAAAAGCACACGGAGTGCCTAAACGCATTAGGATTTCTCGACGAGGAGGCTT 60
A.anta348          ATGGACAACACATGGACTGCGTCATGAAAACAATAGGATTTGTGCAAGGATGGCCGA 60
An.funeshortD7prot1 ATGGATAAGCATATGGACTGTGTGATGAAGACACTTAAATTCGTTCTGCTGATGGA 60
A.steD7-short      ATGTACAGTCACATCGATTGTTGCATGAAGGCGGTCGATTTTGTGGAGAAAGATG 60
A.steD7-re11       ATGTACAGTCACATCGATTGTTGCATGAAGGCGGTCGATTTTGTGGAGAAAGATG 60
A.funshortD7r4     ATGGATAAGCATATCGATTGCGTGTGAAGGCGGTCGATTCGATACAGCGATGGTC 60
An.gambAGAP8281    ATGGACAAGCACATTCATTGCGTGTGCGAGCACTTGACTTTGTCTATGAGGATGG 60
A.gamD7r4          ATGGACAAGCACATTCATTGCGTGTGCGAGCACTTGACTTTGTCTATGAGGATGG 60
                    * * * * *
GTTAAGGAAAGCGTCTGCTAGAATTGCTGCAGCGCGTCGACAGTGGCGTCAATCATG 120
An.gambD7-re12     GTTAAGGAAAGCGTCTGCTAGAATTGCTGCAGCGCGTCGACAGTGGCGTCAATCATG 120
An.gambAGAP8282    GTTAAGGAAAGCGTCTGCTAGAATTGCTGCAGCGCGTCGACAGTGGCGTCAATCATG 120
An.arabshortD7r2   GTTAAGGAAAGCGTCTGCTAGAATTGCTGCAGCGCGTCGACAGTGGCGTCAATCATG 120
An.arabshortD7r3   CTTTGTGCCAGGAGCTTCTGTTGGTGTGCTGAAAATGGTTGATCCCGATGGGGAT 120
An.gambAGAP8283    CTTTGTGCCAGGAGCTTCTGTTGGTGTGCTGAAAATGGTTGATCCCGATGGGGAT 120
An.gambD7-re13     CTTTGTGCCAGGAGCTTCTGTTGGTGTGCTGAAAATGGTTGATCCCGATGGGGAT 120
A.cam-likeC16      GGGGATTACCACCTCATTGCATGATCCGATGACCCGCGATCAAGGAGGACATGAG 120
A.cam-likeC27      GGGGATTACCACCTCATTGCATGATCCGATGACCCGCGATCAAGGAGGACATGAG 120
A.anta348          GGAGATTACCACAAGCTGTATCAAGCTCTGAATGCCATCGAGAAGATAGGAAGCAC 120
An.funeshortD7prot1 GGAGATTACCACCAGCTAATCAAACCACTGAATGCCATCGAGAAGGATCGTAAGC 120
A.steD7-short      GGAGATTATCACAAGCTGTATGAGCTGCTGAATGACATCGAGAAGCATCGTAAAC 120
A.steD7-re11       GGAGATTATCACAAGCTGTATGAGCTGCTGAATGACATCGAGAAGCATCGTAAAC 120
A.funshortD7r4     GGAGATTATCACAAGCTGTATGAGCTGCTGAATGACATCGAGAAGCATCGTAAAC 120
An.gambAGAP8281    GGAGATTACCATAAGCTGTACGATCCATTGAACATTATCGAGCTGGACAAAAGAC 120
A.gamD7r4          GGAGATTACCATAAGCTGTACGATCCATTGAACATTATCGAGCTGGACAAAAGAC 120
                    * * * * *
GCCAACATGAAGAAGTGTGTGACGGAAGCATCGACTTCGGGC---AGTGACAAGAAAGCC 177
An.gambD7-re12     GCCAACATGAAGAAGTGTGTGACGGAAGCATCGACTTCGGGC---AGTGACAAGAAAGCC 177
An.gambAGAP8282    GCCAACATGAAGAAGTGTGTGACGGAAGCATCGACTTCGGGC---AGTGACAAGAAAGCC 177
An.arabshortD7r2   GGCAGTATGAAAAGTGTAAACGCCGGAAGCAGAGAAGGTGGAT---ACTTCTAGCAAAGCC 177
An.arabshortD7r3   AGCAGTATGAAAAGTGTAAACGCCGGAAGTGTGAGAAGGTGGAT---ACTTCTAGCAAAGCC 177
An.gambAGAP8283    GGCAGTATGAAAAGTGTAAACGCCGGAAGTGTGAGAAGGTGGAT---ACTTCTAGCAAAGCC 177
An.gambD7-re13     TTAACCTGGAAGACTGCGTGCAAAACACACTCGACATGCCCAAATCCCAAAGCGGGCG 180
A.cam-likeC16      TTAACCTGGAAGACTGCGTGCAAAACACACTCGACATGCCCAAATCCCAAAGCGGGCG 180
A.cam-likeC27      ATGAATCTGGAGACTTGCATGGGAAAAACGTTTCGCCTACCAAATGAAGGCAGCCGAG 180
A.anta348          TTAACCTGGAAGACTGCGTGCAAAACACACTCGACATGCCCAAATCCCAAAGCGGGCG 177
An.funeshortD7prot1 ATAAATCTGGAAATGTGCGTGGTGAATCTATGGACGCTCAG---GCAAACAGCGGGCG 177
A.steD7-short      ATAAATCTGGAGACTGCGTGGTGAATCTATGGACGCTCAG---GCAAACAGCGGGCG 177
A.steD7-re11       GTTAATCTGAAACATGCATCGGTGAATCGGTACGTTCTCT---GCAAGCAGCGGGCG 177
A.funshortD7r4     GTGAATCTGGAAGTGTATTGGCGAATGCGTACAAAGTCCCG---ACAAGCAGCGGTGCT 177
An.gambAGAP8281    GTGAATCTGGAAGTGTATTGGCGAATGCGTACAAAGTCCCG---ACAAGCAGCGGTGCT 177
A.gamD7r4          GTGAATCTGGAAGTGTATTGGCGAATGCGTACAAAGTCCCG---ACAAGCAGCGGTGCT 177
                    * * * * *
AACACTTCTACACGTGCTTTTGGGTACGAGCTCATTGGCCGGGTTTAAAGATGCGGTC 237
An.gambD7-re12     AACACTTCTACACGTGCTTTTGGGTACGAGCTCATTGGCCGGGTTTAAAGATGCGGTC 237
An.gambAGAP8282    AACACTTCTACACGTGCTTTTGGGTACGAGCTCATTGGCCGGGTTTAAAGATGCGGTC 237
An.arabshortD7r2   AACACTTCTACACGTGCTTTTGGGTACGAGCTCATTGGCCGGGTTTAAAGATGCGGTC 237
An.arabshortD7r3   AACACTTCTACACGTGCTTTTGGGTACGAGCTCATTGGCCGGGTTTAAAGATGCGGTC 237
An.gambAGAP8283    AACACTTCTACACGTGCTTTTGGGTACGAGCTCATTGGCCGGGTTTAAAGATGCGGTC 237
An.gambD7-re13     AACACTTCTACACGTGCTTTTGGGTACGAGCTCATTGGCCGGGTTTAAAGATGCGGTC 237
A.cam-likeC16      CGTGAGTTCTACAAATGTATGCTGAAATCGACCTCTGCTGATGCATTCGTAAGGTTTC 240
A.cam-likeC27      CATGAGTTCTACAAATGTATGCTGAAATCGACCTCTGCTGATGCATTCGTAAGGTTTC 240
A.anta348          AACGCATCTACAAGTGCATGCTGAGTCCAATTCGGCAGAGTCTGTTCAAGAAGGTGTT 240
An.funeshortD7prot1 AATGCTACTACAAGTGTCTGCTGAACTCGTCCAGTGAATCGTTCAAGAAGGTGTT 237
A.steD7-short      TACGCTTACTACAAGTGTGCTGAAATCAACCTCGGCTGATGCGTTCAAGAAGGCGTT 237
A.steD7-re11       TACGCTTACTACAAGTGTGCTGAAATCAACCTCGGCTGATGCGTTCAAGAAGGCGTT 237
A.funshortD7r4     CATGTGTTCTACAAGTGTGCTGAAATCAACCTCGGCTGATGCGTTCAAGAAGGTT 237
An.gambAGAP8281    CACGTGTTCTACAAGTGTGCTGAAATCAACCTCGGCTGATGCGTTCAAGAAGGTT 237
A.gamD7r4          CACGTGTTCTACAAGTGTGCTGAAATCAACCTCGGCTGATGCGTTCAAGAAGGTT 237
                    * * * * *
GACTACAACGAGCTACTGAAGGCTGGCAAGATGCAGACGAGCGATCCCGTTCGATATGA 297
An.gambD7-re12     GACTACAACGAGCTACTGAAGGCTGGCAAGATGCAGACGAGCGATCCCGTTCGATATGA 297
An.gambAGAP8282    GACTACAACGAGCTACTGAAGGCTGGCAAGATGCAGACGAGCGATCCCGTTCGATATGA 297
An.arabshortD7r2   GACTACAACGAGCTACTGAAGGCTGGCAAGATGCAGACGAGCGATCCCGTTCGATATGA 297
An.arabshortD7r3   GACTACGTGGAGCTGCTGCGCGCTGGAAGCTGGACATGGGAACAACCTTCAACGCTGG 297
An.gambAGAP8283    GACTACGTGGAGCTGCTGCGCGCTGGAAGCTGGACATGGGAACAACCTTCAACGCTGG 297
An.gambD7-re13     GACTACGTGGAGCTGCTGCGCGCTGGAAGCTGGACATGGGAACAACCTTCAATGCTGG 297
A.cam-likeC16      GATTTGACGGAGCTCATTAAAGCTGGGAAGCTTCCCGAGGGTTCAAGCTACAGCAACA 298
A.cam-likeC27      GATTTGACGGAGCTCATTAAAGCTGGGAAGCTTCCCGAGGGTTCAAGCTACAGCAACA 298
A.anta348          GATCTGACCGAGTTGGTCTGGCGGCAACCTTCCCGAGGGTCCAGTACATAACA 298
An.funeshortD7prot1 GATCTGACGGAGCTGGTAAAGCTGGCAACCTACCAGCTACGGCACCCTACAGTGGT 295
A.steD7-short      GATTTAAGGGAAGTGAAGGCTTAAAGCTTCCACCAGGCAACAGATACAGCTCGG 295

```

A.steD7-re11 GATTGAGGGAACCTGATCAAGGCTAATAAGCTTCCACCGGGCACCAGATACAGCTCGG--295
 A.funshortD7r4 GATCTTAAGGAATTGGTGAAGGCTGAAAAGTGCCAAAGCACGCCAGATATACGGCCG--295
 An.gambAGAP8281 GATCTGATGGAATTGAAACAGGCTGGCAAAGTGCCACAGCATCAACGGTACACTGCAG--295
 A.gamD7r4 GATCTGATGGAATTGAAAAGGCTGGCAAAGTCCACACATCAACGGTACACTGCTG--295
 ** * * * * *
 An.gambD7-re12 CGTGTGGCTGCGCTGATCAAGGAAATCGATGATGGTTTGTGCTAGTAG 345
 An.gambAGAP8282 CGTGTGGCAGCGCTGATCAAGGAAATCGATGATGGTTTGTGCTAGTAG 345
 An.arabshortD7r2 CGTGTGGCAGCGCTGATCAAGGAAATCGATGATGGTTTGTGCTAGTAG 345
 An.arabshortD7r3 CAGGTGTCAGCATTGATGAAGCAAATTGATGATGGGCTGTGTAAGTGA 345
 An.gambAGAP8283 CAGGTGTCAGCATTGATGAAGCAAATTGATGATGGGCTGTGTAAGTGA 345
 An.gambD7-re13 CAGGTGTCAGCATTGATGAAGCAAATTGATGATGGGCTGTGTAAGTGA 345
 A.cam-likeC16 -AAGTAGACAAAATGATTAAGGCTATCGATAAAAAAGTGTGCAAAATA 345
 A.cam-likeC27 -AAGTAGACAAAATGATTAAGGCTATCGATAAAGAAAAGTGTGAAATAA 345
 A.anta348 -AAGTGGCCAACATGATGAAGAAAATTGATGCGAAAATTGCAAGTAA 345
 An.funshortD7prot1 -CAGTAGAGAAGCTGATGAAGAAAATTGATCAAAAGATTGCAAAATGA 342
 A.steD7-short -AGGTGCGACAAGCAGATGAAGAAAATTGATGACAACATATGTAA---- 338
 A.steD7-re11 -AGGTGCGACAAGCAGATGAAGAAAATTGATGACAACATATGTAA---- 338
 A.funshortD7r4 -AAGTCGCTCAAATGATGAAGGACATTGATGCGAAATTGTGCTAA--- 339
 An.gambAGAP8281 -AGTTTGTGCAAATCATGAAGGATTATGATAAGGCATTAACACTGCTGA 342
 A.gamD7r4 -AGTTTGTGCAAATCATGAAGGATTATGATAAGGCATTAACACTGCTGA 342



ลิขสิทธิ์มหาวิทยาลัยเชียงใหม่
 Copyright© by Chiang Mai University
 All rights reserved

4. BLASTx Search Results

A.cam-like_C16

a348 [*Anopheles anthropophagus*]

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
139 bits(350)	1e-41()	Compositional matrix adjust.	62/114(54%)	84/114(73%)	0/114(0%)	+1

Features:

Query	1	MEKHTEGVLNALGFLDKEGLGDYHSLHDPMTAIKEDMRHGLNLEDCVANTLDMPKSPKRA	180
		M+KH + V+ +GF+DK+G GDYH L P+ AI++D +H +NLE C+ T +P RA	
Sbjct	53	MDKHMDVCMKTIGFVDKDGGRGDYHKLKPLNAIEKDRKHDNMLETGKTFRLPNEGSR	112

Query	181	REFYKMLKSTSAADAFKRVFDLTELKAGKLEGGSSYSNKVDKMIKAIKDKVCK	342
		FYKML+S SA++F+KVFDLTEL+ AGKLP G+ Y+NKV M+K ID K+CK	
Sbjct	113	NAFYKMLQNSAESFKKVFDELTELVLGKLPAGAQQNNKVNMMKKIDAKICK	166

short form D7 salivary protein [*Anopheles stephensi*]

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
119 bits(298)	8e-34	Compositional matrix adjust.	56/114(49%)	82/114(71%)	1/114(0%)	+1

Query	1	MEKHTEGVLNALGFLDKEGLGDYHSLHDPMTAIKEDMRHGLNLEDCVANTLDMPKSPKRA	180
		M H + + A+ F++K+G GDYH L++ + I++ +H +NLE CV ++D ++ +RA	
Sbjct	53	MYSHIDCCMKAVDFVEKDGTDYHKLKPLNIEKHKRKHNDINLEMCVGSMD-AQANQRA	111

Query	181	REFYKMLKSTSAADAFKRVFDLTELKAGKLEGGSSYSNKVDKMIKAIKDKVCK	342
		+YKC+LKSTSAADAF+K FDL ELIKA KLP G+ YS++VDK +K ID +CK	
Sbjct	112	YAYYKCLLKSTSAADAFKAFDLRELKANKLPPGTRYSSSEVDKQMKKIDDNICK	165

A.cam-like_C27

a348 [*Anopheles anthropophagus*]

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
136 bits(343)	2e-40()	Compositional matrix adjust.	60/114(53%)	84/114(73%)	0/114(0%)	+1

Features:

Query	1	MEKHTECVLNALGFLDEEGLGDYHSLHDPMTAIKEDMRHGLNLEDCVANTLDMPKSPKRA	180
		M+KH +CV+ +GF+D++G GDYH L P+ AI++D +H +NLE C+ T +P RA	
Sbjct	53	MDKHMDVCMKTIGFVDKDGGRGDYHKLKPLNAIEKDRKHDNMLETGKTFRLPNEGSR	112

Query	181	HEFYKMLKSTSAADAFKRVFDLTELKAGKLEGGSSYSNKVDKMIKAIKDKSVK	342
		+ FYKML+S SA++F+KVFDLTEL+ AGKLP G+ Y+NKV M+K ID + K	
Sbjct	113	NAFYKMLQNSAESFKKVFDELTELVLGKLPAGAQQNNKVNMMKKIDAKICK	166

D7-related 1 protein [*Anopheles stephensi*]

Alignment statistics for match #1

Score	Expect	Method	Identities	Positives	Gaps	Frame
120 bits(300)	4e-34	Compositional matrix adjust.	55/109(50%)	81/109(74%)	1/109(0%)	+1

Query	1	MEKHTECVLNALGFLDEEGLGDYHSLHDPMTAIKEDMRHGLNLEDCVANTLDMPKSPKRA	180
		M H +C + A+ F++++G GDYH L++ + I++ +H +NLE CV ++D ++ +RA	
Sbjct	53	MYSHIDCCMKAVDFVEKDGTDYHKLKPLNIEKHKRKHNDINLETGCVGSMD-AQANQRA	111

Query	181	HEFYKMLKSTSAADAFKRVFDLTELKAGKLEGGSSYSNKVDKMIKAIK	327
		+ FYKC+LKSTSAADAF+K FDL ELIKA KLP G+ YS++VDK +K ID	
Sbjct	112	YAFYKCLLKSTSAADAFKAFDLRELKANKLPPGTRYSSSEVDKQMKKID	160

5. BLASTn Search Results

A.cam-like_C16

Anopheles stephensi mRNA for D7-related 1 protein
Alignment statistics for match #1

	Score	Expect	Identities	Gaps	Strand	Frame	
	71.6 bits(78)	1e-11()	89/122(66%)	0/122(0%)	Plus/Plus		
Query	173	AGCGGGCGCGTGAGTTCTACAAATGTATGCTGAAATCGACCTCTGCTGATGCATTCCGTA	232				
Sbjct	344	AGCGAGCGTACGCGTTCTACAAGTGTGGCTGAAATCCACCTCGGCGGACGCGTTCAAGA	403				
Query	233	AGGTTTTTCGATTTGACGGAGCTCATTAAAGCTGGGAAGCTTCCCAGGGTTCAAGCTACA	292				
Sbjct	404	AGGCGTTTGATTTGAGGGAAGCTGATCAAGGCTAATAAGCTTCCACCGGGCACCAGATACA	463				
Query	293	GC	294				
Sbjct	464	GC	465				

A.cam-like_C27

Anopheles stephensi mRNA for D7-related 1 protein
Alignment statistics for match #1

	Score	Expect	Identities	Gaps	Strand	Frame	
	77.0 bits(84)	3e-13()	90/122(74%)	0/122(0%)	Plus/Plus		
Query	173	AGCGGGCGCATGAGTTCTACAAATGTATGCTGAAATCGACCTCTGCTGATGCATTCCGTA	232				
Sbjct	344	AGCGAGCGTACGCGTTCTACAAGTGTGGCTGAAATCCACCTCGGCGGACGCGTTCAAGA	403				
Query	233	AGGTTTTTCGATTTGACGGAGCTCATTAAAGCTGGGAAGCTTCCCAGGGTTCAAGCTACA	292				
Sbjct	404	AGGCGTTTGATTTGAGGGAAGCTGATCAAGGCTAATAAGCTTCCACCGGGCACCAGATACA	463				
Query	293	GC	294				
Sbjct	464	GC	465				

ลิขสิทธิ์มหาวิทยาลัยเชียงใหม่
Copyright© by Chiang Mai University
All rights reserved

CURRICULUM VITAE

Name Ms. Sriwatapron Sor-suwan

Date of birth April 9, 1986

Educational Background

2006-2009 B.Sc. (Animal Science) Faculty of Science and Agricultural Technology, Rajamongala University, Lumpang, Thailand

Research Emphasis Medical Parasitology

Grant Ph.D Scholarship, The Royal Golden Jubilee Ph.D Program (Grant No. PHD/0149/2551), Thailand Research Fund, Thailand

Faculty of Medicine Research Fund, Faculty of Medicine, Chiang Mai University, Thailand

Training Bioinformatics analysis of *Anopheles* mosquitoes, Division of Biomedical and Life Sciences, Faculty of Health and Medicine, Lancaster University, United Kingdom.

Publications

2012 Jariyapan N, Roytrakul S, Paemanee A, Junkum A, Saeung A, Thongsahuan S, **Sor-suwan S**, Phattanawiboon B, Poovorawan Y, Choochote W.

Proteomic analysis of salivary glands of female *Anopheles barbirostris* species A2 (Diptera: Culicidae) by two-dimensional gel electrophoresis and mass spectrometry. *Parasitology Research* 2012; 111: 1239-49.

2013

Sor-Suwan S, Jariyapan N, Roytrakul S, Paemanee A, Saeung A, Thongsahuan S, Phattanawiboon B, Bates PA, Poovorawan Y, Choochote W. Salivary gland proteome of the human malaria vector, *Anopheles campestris*-like (Diptera: Culicidae). *Parasitology Research* 2013; 112: 1065-75.

Jariyapan N, Saeung A, Intakhan N, Chanmol W, **Sor-Suwan S**, Phattanawiboon B, Taai K, Choochote W. Peritrophic matrix formation and *Brugia malayi* microfilaria invasion of the midgut of a susceptible vector, *Ochlerotatus togoi* (Diptera: Culicidae). *Parasitology Research* 2013; 112: 2431-40.

Wijit A, Saeung A, Baimai V, Otsuka Y, Thongsahuan S, Taai K, Srisuka W, Songsawatkiat S, **Sor-suwan S**, Hempolchom C, Somboon P, Choochote W. DNA barcoding for the identification of eight species members of the Thai Hyrcanus Group and investigation of their stenogamous behavior. *Comptes Rendus Biologies* 2013; 336: 449-56.

2014

Sor-suwan S, Jariyapan N, Roytrakul S, Paemanee A, Phumee A, Phattanawiboon B, Intakhan N, Chanmol W, Bates PA, Saeung A,

Choochote W. Identification of salivary gland proteins depleted after blood feeding in the malaria vector *Anopheles campestris*-like mosquitoes (Diptera: Culicidae) PLoS One 2014; 9: e90809.

Intakhan N, Jariyapan N, **Sor-Suwan S**, Phattanawiboon B, Taai K, Chanmol W, Saeung A, Choochote W, Bates PA. Exsheathment and midgut invasion of nocturnally subperiodic *Brugia malayi* microfilariae in a refractory vector, *Aedes aegypti* (Thailand strain). Parasitology Research 2014; 113: 4141-9.

Phattanawiboon B, Jariyapan N, Roytrakul, S, Paemane A, **Sor-suwan S**, Intakhan N, Chanmol W, Siriyasatien P, Saeung A, Choochote, W. Morphological and protein analyses of adult female salivary glands of *Anopheles barbirostris* species A1 (Diptera: Culicidae). Tropical Biomedicine 2014; 31: 813-27.

Oral Presentation

2013

Sriwatapron Sor-suwan, Narissara Jariyapan, Sittirak Roytrakul, Atchara Paemane, Atiporn Saeung, Benjarat Phattanawiboon, Paul A Bates, Yong Poovorawan, and Wej Choochote (2013) Changes in Salivary Gland Proteome after Blood Feeding in *Anopheles campestris*-like (Diptera: Culicidae) “RGJ-Ph.D. Congress XIV” 5-7 April 2013 in Chonburi, Thailand.

Poster Presentation

2010

Sriwatapron Sor-suwan, Visut Baimai, Wej Choochote, Sittirak Roytrakul, Atiporn Saeung, Sorawat Thongsahuan, Kritsana Taai, Yong Poovorawan, Narissara Jariyapan, (2010) Salivary Gland Protein of Human Malaria Vector *Anopheles campestris*-like (Diptera: Culicidae) “RGJ SEMINAR SERIES LXXIV” 16 September 2010 in Chiang Mai, Thailand.

2012

Sriwatapron Sor-suwan, Narissara Jariyapan Sittirak Roytrakul Visut Baimai, Atiporn Saeung, Benjarat Phattanaviboon, Paul A Bates, Yong Poovorawan, Wej Choochote, (2012) Changes in Salivary Gland Protein after Blood feeding in *Anopheles campestris*-like (Diptera: Culicidae) “Thailand Research Scholar Meeting 2012” 3 December 2012 in Chiang Mai, Thailand.



มหาวิทยาลัยเชียงใหม่
right © by Chiang Mai University
rights reserved