```
                10        20        30        40        50        60        70        80        90       100       110       120
1       ATGAAGGTGAAAATGTCACGATCAAACGGATTATTTGTGGTGCTCGTTATTGGTGTTTGCTGTGAGTTTGTAAGTTCTCAAGATATCCTCAAGACGTCGACGGCGTCCGCAAAGGACGGG
1        M  K  V  K  M  S  R  S  N  G  L  F  V  V  L  V  I  G  V  C  C  E  F  V  S  S  Q  D  I  L  K  T  S  T  A  S  A  K  D  G
                130       140       150       160       170       180       190       200       210       220       230       240
121     ACCACACCGACCCCGAGAGTGAAAAAAAGACAAGGAGGAGCGACGGATCAGTCGACCGCAGAGTCTTGGTGGAGGCCGCCCACGCAGTCATTCGTCGACACCCCGTACTCGGCCACTCAC
41       T  T  P  T  P  R  V  K  K  R  Q  G  G  A  T  D  Q  S  T  A  E  S  W  W  R  P  P  T  Q  S  F  V  D  T  P  Y  S  A  T  H
                250       260       270       280       290       300       310       320       330       340       350       360
241     GGCCTCGTCCAGACCCACCCTGCAGGCTTCGGCTCCACCGGTAACAGCATAGGTGCTGGTGATCAGTTGGCCGCTGTGTCAGAGGATGGCTCGACCCTGGGCTACACGTCTCTGGACTTC
81       G  L  V  Q  T  H  P  A  G  F  G  S  T  G  N  S  I  G  A  G  D  Q  L  A  A  V  S  E  D  G  S  T  L  G  Y  T  S  L  D  F
                370       380       390       400       410       420       430       440       450       460       470       480
361     GACAAACACGGACTCGACGAGCTGAGGCGCAACCCGCTTCTGTCTTCACCCGAGGAGTGCGCCCGTGCCTGCAGAGAGGGCGAACCCCCCAGGATTTGTTACTACCACTTCACCCTCGAA
121      D  K  H  G  L  D  E  L  R  R  N  P  L  L  S  S  P  E  E  C  A  R  A  C  R  E  G  E  P  P  R  I  C  Y  Y  H  F  T  L  E
                490       500       510       520       530       540       550       560       570       580       590       600
481     CTTTACACTGTTCTCGGAGCTGCTTGCCAAGTGTGCGTTCCCAATGCGACAAACACAGTATGGAGCCACTGTCAGTGTGTCTTAGCTGATGGAGTAGAAAGAGGAATTTTGACAGTCAAC
161      L  Y  T  V  L  G  A  A  C  Q  V  C  V  P  N  A  T  N  T  V  W  S  H  C  Q  C  V  L  A  D  G  V  E  R  G  I  L  T  V  N
                610       620       630       640       650       660       670       680       690       700       710       720
601     AGAATGATCCCTGGACCTAGTATACAAGTTTGTGAAGGAGACAAAGTTGTTGTAGACGTCAGGAACCAGATGGAAGGTCTAGAAGTCACGATCCACTGGCACGGTATCACCCAACGTGGA
201      R  M  I  P  G  P  S  I  Q  V  C  E  G  D  K  V  V  V  D  V  R  N  Q  M  E  G  L  E  V  T  I  H  W  H  G  I  T  Q  R  G
                730       740       750       760       770       780       790       800       810       820       830       840
721     ACTCAGTACTCCGATGGTGTTCCCATGGTTACGCAGTGCCCCATCTTACAAGGAAACACTTTCCGGTATCAATGGTACGCGAACGCTGGTACTCACTTCTGGCACGCTCACACTGGAGTC
241      T  Q  Y  S  D  G  V  P  M  V  T  Q  C  P  I  L  Q  G  N  T  F  R  Y  Q  W  Y  A  N  A  G  T  H  F  W  H  A  H  T  G  V
                850       860       870       880       890       900       910       920       930       940       950       960
841     CAAAAGATGGATGGTATCTACGGAAGTATCGCCGTGCGACAAGCTCCTTCAGAGGACCCCAACAGCCACCTTTACGACTACGATTTAACGACTCACGTCATGCTCCTCTCGGATTGGATG
281      Q  K  M  D  G  I  Y  G  S  I  A  V  R  Q  A  P  S  E  D  P  N  S  H  L  Y  D  Y  D  L  T  T  H  V  M  L  L  S  D  W  M
                970       980       990      1000      1010      1020      1030      1040      1050      1060      1070      1080
961     CACGAAGACGCTTTGGAGAGGTTCCCCGGAAGACTTGCCGCCAACACTGGTCAGGATCCTGAGACTCTGCTCATCAACGGAAAAGGACAGTTCACGGATCCAATGACCGGCTACAGCACC
321      H  E  D  A  L  E  R  F  P  G  R  L  A  A  N  T  G  Q  D  P  E  T  L  L  I  N  G  K  G  Q  F  T  D  P  M  T  G  Y  S  T
               1090      1100      1110      1120      1130      1140      1150      1160      1170      1180      1190      1200
1081    AACACCCCCTTGGAAACATTCACGATCACTCCTGGCAGAAGGTACAGATTCCGTATGATCAACTCTTTGGCTAGTGTCTGCCCAGCTCAACTGACTGTTCAAGGTCATCCCCTCATCCTC
361      N  T  P  L  E  T  F  T  I  T  P  G  R  R  Y  R  F  R  M  I  N  S  L  A  S  V  C  P  A  Q  L  T  V  Q  G  H  P  L  I  L
               1210      1220      1230      1240      1250      1260      1270      1280      1290      1300      1310      1320
1201    ATCGCCACCGATGGAGAGCCAGTCCACCCTGTTGTTGTAAACACCATCATCTCTTTCTCAGGAGAAAGATACGATTTCGTGATCAATGCCGAACAGCCCGTCGGAGCTTACTGGATCCAA
401      I  A  T  D  G  E  P  V  H  P  V  V  V  N  T  I  I  S  F  S  G  E  R  Y  D  F  V  I  N  A  E  Q  P  V  G  A  Y  W  I  Q
               1330      1340      1350      1360      1370      1380      1390      1400      1410      1420      1430      1440
1321    GTTCGAGGACTCGGAGAATGTGGTAACAAACGAGTGCAGCAATTGGCCATCCTCCGGTACGCTCGAGGACCCTACCAACCCACTTCCCGTGCTCCCACCTACGATATTGGAATCCCACAA
441      V  R  G  L  G  E  C  G  N  K  R  V  Q  Q  L  A  I  L  R  Y  A  R  G  P  Y  Q  P  T  S  R  A  P  T  Y  D  I  G  I  P  Q
               1450      1460      1470      1480      1490      1500      1510      1520      1530      1540      1550      1560
1441    GGAGTCGTTCTTAACCCGTTGGATGCCGTCTGCAACAGACCGAGAACCGATGCCATTTGCATAAACCAATTGAAAAACGCCAAAAAGGTAGATAAGGCTTTACTCCAAGAACTGCCCGAC
481      G  V  V  L  N  P  L  D  A  V  C  N  R  P  R  T  D  A  I  C  I  N  Q  L  K  N  A  K  K  V  D  K  A  L  L  Q  E  L  P  D
               1570      1580      1590      1600      1610      1620      1630      1640      1650      1660      1670      1680
1561    ATCAAGATCTTCTTGCCGTTCAAATTCTTGTTCTACCGACCTGAGGAAATCTTCACACCACACACTTACAACAGATTCTTGGTTGCTCCGGGTGGTGGAGATCATGTCATCAGTTTAGTG
521      I  K  I  F  L  P  F  K  F  L  F  Y  R  P  E  E  I  F  T  P  H  T  Y  N  R  F  L  V  A  P  G  G  G  D  H  V  I  S  L  V
               1690      1700      1710      1720      1730      1740      1750      1760      1770      1780      1790      1800
1681    GACAACATTTCGTACGTTTCGCCACCAGCTCCACCTCTAAGTCAGATCGACGACATCCCACCAGAGATGTTCTGCAACGGAGACAACAGGCCAGCAGACTGTGGAAGGAACTGTATGTGC
561      D  N  I  S  Y  V  S  P  P  A  P  P  L  S  Q  I  D  D  I  P  P  E  M  F  C  N  G  D  N  R  P  A  D  C  G  R  N  C  M  C
               1810      1820      1830      1840      1850      1860      1870      1880      1890      1900      1910      1920
1801    ACACACAAGGTGGACATTCCTCTTCACGCTATTGTAGAGGTCGTTCTCGTCGACGAGGTACAACAACCAAACTTGAGTCATCCGTTCCATTTGCACGGTTACACATTCAATGTCATCGGT
601      T  H  K  V  D  I  P  L  H  A  I  V  E  V  V  L  V  D  E  V  Q  Q  P  N  L  S  H  P  F  H  L  H  G  Y  T  F  N  V  I  G
               1930      1940      1950      1960      1970      1980      1990      2000      2010      2020      2030      2040
1921    ATGGGTCGATCACCAGACAAGAACGTTAAGAAAATCAACTTGAAACACGCATTAGATCTTGACAGGCGAGGACTGTTGGACAGACACTTCAACCTTCCTCCCGGCAAGGACACAATTGCA
641      M  G  R  S  P  D  K  N  V  K  K  I  N  L  K  H  A  L  D  L  D  R  R  G  L  L  D  R  H  F  N  L  P  P  G  K  D  T  I  A
               2050      2060      2070      2080      2090      2100      2110      2120      2130      2140      2150      2160
2041    GTACCAAACAACGGATACGTTGTCTTTAGGTTTAGGGCAGACAATCCAGGTTACTGGTTGTTCCACTGTCACTTCTTGTTCCACATTCTCATCGGTATGAACTTAGTCCTTCACGTAGGT
681      V  P  N  N  G  Y  V  V  F  R  F  R  A  D  N  P  G  Y  W  L  F  H  C  H  F  L  F  H  I  L  I  G  M  N  L  V  L  H  V  G
               2170      2180      2190      2200      2210      2220      2230
2161     ACTCACGCCGACCTACCACCAGTGCCAGAAGGTTTCCCTCGATGTGGAGACTTCTTACCCCCGGTCAGTTTACATTGA
721       T  H  A  D  L  P  P  V  P  E  G  F  P  R  C  G  D  F  L  P  P  V  S  L  H  *
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Figure S1. The protein-coding DNA sequence and amino acid sequence for *B. tabaci* MEAM1 *Lac2* gene. Note: start codon (ATG); stop codon (TGA); glycosylation sites are double-underlined; blue areas are signal peptide site; yellow areas represent copper ion domains

GATCGACGACATCCCACCAGAGATGTTCTGCAACGGAGACAACAGGCCAGCAGACTGTGGAAGGA
ACTGTATGTGCACACACAAGGTGGACATTCCTCTTCACGCTATTGTAGAGGTCGTTCTCGTCGACGA
GGTACAACAACCAAACTTGAGTCATCCGTTCCATTTGCACGGTTACACATTCAATGTCATCGGTATG
GGTCGATCACCAGACAAGAACGTTAAGAAAATCAACTTGAAACACGCATTAGATCTTGACAGGCG
AGGACTGTTGGACAGACACTTCAACCTTCCTCCCGGCAAGGACACAATTGCAGTACCAAACAACGG
ATACGTTGTCTTTAGGTTTAGGGCAGACAATCCAGGTTACTGGTTGTTCCACTGTCACTTCTTGTTCC
ACATTCTCATCGGTATGAACTTAGTCCTTCACGTAGGTACTCACGCCGACCTACCACCAGTGCCAGA
AGGTTTCCCTCGAT

Figure S2. The sequence of the gene region used for dsRNA syhthesis.