FIGURE S1. Nucleotide and deduced amino acid sequences of genes encoding small heat shock proteins (sHSPs) in *Bemisia tabaci*. The three sHSP genes include *Bthsp19.5* (A); *Bthsp19.2* (B); and *Bthsp21.3* (C). HSP20 family profiles and α-crystallin domains are underscored.

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1       ATCAACGCAGAGTACATGGGATTCAATAGAAATGGCTTTGCTACCGTACTTGTTGGAAGA
1                                       M  A  L  L  P  Y  L  L  E  E
61      GCTGAACCGACCAACCATCTACGATCAGAACTTTGGTCTAGGATTGTTCAATGATGATTT
11        L  N  R  P  T  I  Y  D  Q  N  F  G  L  G  L  F  N  D  D  F
121     CCCGTCTGCTGTTGGATCTCTGCGCCCTTACTACCTGAGACCATGGAGACTGTTTCCCCA
31        P  S  A  V  G  S  L  R  P  Y  Y  L  R  P  W  R  L  F  P  H
181     CGATGAAAGTGGCATTTCTTCAGTACAGCATGACAAAGATGGATTTAAGGTGAATTTAGA
51        D  E  S  G  I  S  S  V  Q  H  D  K  D  G  F  K  V  N  L  D
241     CGTACAGCAATTCAAGCCAGAGGAGGTCAACGTGAAAATAGCTGACAACTATGTCATCGT
71        V  Q  Q  F  K  P  E  E  V  N  V  K  I  A  D  N  Y  V  I  V
301     CAACGCTAAACATGAGGAGCGTAGTGATGAACATGGCTTCATTTCACGAGAATTCACCCG
91        N  A  K  H  E  E  R  S  D  E  H  G  F  I  S  R  E  F  T  R
361     CCGTTACCTTCTGCCAAAAGACGTAAACGCTGAGGCCTTGACTTCATCTCTCTCTTCCGA
111       R  Y  L  L  P  K  D  V  N  A  E  A  L  T  S  S  L  S  S  D
421     CGGAGTTCTTTCCATCCAGGCTCCACCAAAGGCAATCACCAACGATAAGGGAAATGAGCG
131       G  V  L  S  I  Q  A  P  P  K  A  I  T  N  D  K  G  N  E  R
481     TCAAATTCCAGTCACCAAAACCAACGCCCCAGCAATCAAACAACAACAACAACAACAGAA
151       Q  I  P  V  T  K  T  N  A  P  A  I  K  Q  Q  Q  Q  Q  Q  K
541     GAAGTAAATTATCGTGAATGACATTTACTCTCATCTTAAGTATTTATTTTTACGTCATCT
171       K  *
601     TTCTAAGGTGAATATCTCTTACATTTTTAATGTTACTATGTAACCGACTATGTTATTACT
661     CTTTATGATAATCTAATTTTAAGTTCCTATCCATGAATAGTTTTTAATTTAGTCCCATTT
721     CAAATTTTGTCTGACTGTACATGTGTCCATTCATTAATCTTCAAAATATTAAGTTACAAA
781     TTTTCATCTTTCATACTTATTAAGGAGAAAATGTTTTCAACCGTATGCAGAGCTAGACCA
841     TTCATTGTCACATTTTACTGAATTTGACATCTTCTCAGGGATATATAGGATTCAAATTTT
901     CATCTAGTTTAGTCTAGCTGTGCTCTCTGAGAAATATGAATATTAAGTGAAATTAAGTAC
961     AATTTTCTTTCTTGTTATTCTTTTTGAACTCTCAACTTGGATCAGTAAAATGTCATTCAA
1021    TACTCAAATAATTACTTAATGCTGTTGAATTATTCTGTTCAACTGTTAAAGTCATCAGAC
1081    TTCACCCTAGTTAGTGTATTAAGATTGTTTGTATAAATTATATTGTAAGGAAGATTTATT
1141    ACTTTTTAATAAAGGTGTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
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A

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1       AGCGGTTCGATAAATCCACTGTGTATGTCTCTCTTGCCCTACTTGTTGGAAGAATTGAAC
1                                M  S  L  L  P  Y  L  L  E  E  L  N
61      CGTCCAACAGTGTATGACCAAAACTTCGGTGTTGGACTGTGGAATGATGATCTGCCATCT
13       R  P  T  V  Y  D  Q  N  F  G  V  G  L  W  N  D  D  L  P  S
121     ATCACTGCCATTCGCCCGTTTTATATGCGGCCATGGAGACTGCTTCCCCAAAATGAGAGT
33       I  T  A  I  R  P  F  Y  M  R  P  W  R  L  L  P  Q  N  E  S
181     GGGACTTCATCAGTACAGCACGATAAAGATGGATTTAAGGTGAACTTAGATGTGCAGCAG
53       G  T  S  S  V  Q  H  D  K  D  G  F  K  V  N  L  D  V  Q  Q
241     TTCAAACCTGAAGAAGTGAATGTCAAAGTCAGTGACAATTATGTTACCATCCACGCCAAA
73       F  K  P  E  E  V  N  V  K  V  S  D  N  Y  V  T  I  H  A  K
301     CACGAAGAACGCAGTGATGAGCATGGTTTTATTTCTCGGGAATTCACTAGGCGTTATCTC
93       H  E  E  R  S  D  E  H  G  F  I  S  R  E  F  T  R  R  Y  L
361     ATCCCTAAAGACGTCAATGCGGAAGCCTTGACTTCAAGTCTTTCATCTGATGGTGTTCTC
113      I  P  K  D  V  N  A  E  A  L  T  S  S  L  S  S  D  G  V  L
421     TCTGTACATGCTCCGCCAAAGGCTATCACCAATGAGAATGGCAGTGAGCGCCAAATTCCA
133      S  V  H  A  P  P  K  A  I  T  N  E  N  G  S  E  R  Q  I  P
481     ATTACTAAAACCAATGCTCCCGCAATCAAACAGGAACAAGCGAAGAAGAAGTAATCAATC
153      I  T  K  T  N  A  P  A  I  K  Q  E  Q  A  K  K  K  *
541     CTACCTTGATGTCTAATTGAGTTTTCCTCTTTCTCCTCAATGAGCTTCTTCCTTTTTCCT
601     TGTACTGTAAATATTTTCACTTACTTATTTTTGTTCCTATCATTGAGAACCAGCTTGTAT
661     CAAGAAATGTTAAACAGTGAAAGTGAAACATAAATTCCCTTTTAAATACTATTATGCCCC
721     GTCAATAATTGTACTATCGTTTTCACGGAGCAATAGTAAAATTCCTAAAAAAACCATGTA
781     TTTTTCATAACAGGATATCATCGTAAGTGTTGTGTAAGCAGAGTGCTACAGTTAGCACGT
841     GTTCTCTTTTCACCACCACCAAGAAATTACCACCGTGTGTTGTACTTATTTAACTTTTAG
901     AACTATTTTTAAGTCTGCTCCATTGTTACATTATACAAAGTAGTGATAAGAAATTCACTT
961     GGAAGGTATTTTGTTCTAGGTTATTGTCAACATGAAATGAATTACTGTACTGTTCTTGTG
1021    AGACTGCTACTATTTATGTAAATTTTATTATTTTTTTAAATAAAATTTCCAGACAAAAAA
1081    AAAAAAAAAAAAAAAAAAAAAAAAAAA
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B

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1         AGCGGTTCGATAAATCCACTGTGATATCTTCTGAGTTCGATACGTAGGTTGCGCAACCCT
61        CGAGAGGGTATACCAGCTGGACGTCCGCCGGCGCTTAAGTGTATGTCTCTCTTGCCCTAC
1                                                    M  S  L  L  P  Y
121       TTGTTGGAAGAATTGAACCGTCCAACAGTGTATGACCAAAACTTCGGTGTTGGACTGTGG
7          L  L  E  E  L  N  R  P  T  V  Y  D  Q  N  F  G  V  G  L  W
181       AATGATGATCTGCCATCTATCACTGCCATTCGCCCGTTTTATATGCGGCCATGGAGACTG
27         N  D  D  L  P  S  I  T  A  I  R  P  F  Y  M  R  P  W  R  L
241       CTTCCCCAAAATGAGAGTGGGACTTCATCAGTACAGCACGATAAAGATGGATTTAAGGTG
47         L  P  Q  N  E  S  G  T  S  S  V  Q  H  D  K  D  G  F  K  V
301       AACTTAGATGTGCAGCAGTTCAAACCTGAAGAAGTGAATGTCAAAGTCAGTGACAATTAT
67         N  L  D  V  Q  Q  F  K  P  E  E  V  N  V  K  V  S  D  N  Y
361       GTTACCATCCACGCCAAACACGAAGAACGCAGTGATGAGCATGGTTTTATTTCTCGGGAA
87         V  T  I  H  A  K  H  E  E  R  S  D  E  H  G  F  I  S  R  E
421       TTCACTAGGCGTTATCTCATCCCTAAAGACGTCAATGCGGAAGCCTTGACTTCAAGTCTT
107        F  T  R  R  Y  L  I  P  K  D  V  N  A  E  A  L  T  S  S  L
481       TCATCTGATGGTGTTCTCTCTGTACATGCTCCGCCAAAGGCTATCACCAATGAGAATGGC
127        S  S  D  G  V  L  S  V  H  A  P  P  K  A  I  T  N  E  N  G
541       AGTGAGCGCCAAATTCCAATTACTAAAACCAATGCTCCCGCAATCAAACAGGAACAAGCG
147        S  E  R  Q  I  P  I  T  K  T  N  A  P  A  I  K  Q  E  Q  A
601       AAGAGAGCAGAAACGCCAACACCAACGATGCCGTCACCGCTAACAACAAGCCCGACAGCG
167        K  R  A  E  T  P  T  P  T  M  P  S  P  L  T  T  S  P  T  A
661       AAGAAAGATTGAACGAATTCGTCCGCAAATCCTACGCCGGAATCAACAGTGCCTTCGTCA
187        K  K  D  *
721       ACGCCTTCGACTTCTCTGCCCAATTCCTTGGACAAAAGGAAGCCGACTACGTTTGCACCT
781       TTGCCTTCGCCCGCAGCCCAGTTGCTGAGAAATCTCGTTTCCTCTTCTACGGACACTACA
841       ACACTGCCAACAACAAGAAACAACAGTGCGCTTTCCACGCCTCCGCTGAGATGCCCAATG
901       TTCCCTTGACCAACCCTGCTGCCGCCATGAAGGCTGAGCCAGCTTCCAAGATCTACGCTA
961       ACTTCAAGTTCGGAGAATCTTTCGAAAATGCCGCCAAGGTTCACTTCAACGCTAACTTGA
1021      AGCAGAGCTCTGAACGCCGTCAATTCCTCCGCAACAACGCCCTCTACAAGCAATGCGAAT
1081      CCGAAATGGAACGTGGACAATACTTCCTCCCTGCTTGCCGTAACTTCACCGTTGCTGACA
1141      ACAGAATGAACGAATACTACTACAACTTCAACTTCCAAAAAAAAAAAAAAAAAAAAAAAA
1201      AAAAAAAAA
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C