Interaction of heat shock protein 60 (HSP60) with microRNA in Chinese mitten crab during *Spiroplasma eriocheiris* infection

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Fig. S1 Nucleotide sequence of the cDNA encoding *EsHSP60* and its deduced amino acid sequence. The nucleotide sequence is numbered from the 5' end, and the amino acid code is presented below the corresponding codon. The sequence contains a 25 amino acid extension at the N terminus (indicated by light gray). The classical mt-HSP60 signature motifs are underlined. The ATP-binding motif is bold. The typical GGM repeat motif at the C terminus is in italics.

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S. paramamosain (AGI74967)
                        MYRAASILIRLPASRRVAOHLAARSYAKDVKFGSEVRAMMLOGVDVLTDAVAVTMGPKGRNVTIEOSWGSPKITKDGVTVAKAVELKDKFONIGAKLVODVANNTNERAGDGTTTATVLAR 120
P. trituberculatus (AFA36427) MYRAASLLRLPASRQVPQRLAIRSYAKDVKFG SEVRAMMLQGVDVLTDAVAVTMGPKGRNVIIDQSWGSPKITKDGVTVAKAVELKDKFQNIGAKLWQDVANNTNEEAGDGTTTATVLAR 120
                        MHRAASLLRTPVARQATRYCLARHYAKDVKFGTEVRALMLQGVDVLTDAVAVTMGPKGRNVTIEQSWGSPKITKDGVTVAKAVELKDKFQNIGAKLVQDVANNTNEEAGDGTTTATVLAR 120
M. japonicus (AGD79959)
L. vannamei (ACN30235)
                        MHRAASILRTPVARQATRHYLARHYAKDVKFGTEVRALMLQGVDVLTDAVAVTMGPKGRNVLIEQSWGSPKITKDGVTVAKAVELKDKSQNIGAKLVQDVANNTNEEAGDGTTTATVLAR 120
E. sinensis (KP642083)
                        MYRAASLLRLPATRRAVOHLTARSYAKDVKFGSEVRAMMLOGVDVLTDAVAVTMGPKGRNVLIEQSWGSPKITKDGVTVAKAVELKDKFONIGAKLVODVANNTNEEAGDGTTTATVLAR 120
                        *: ****** *. : *: . :
                                         S. paramamosain (AG174967) TIAKEGFDRISKGANPIEIRRGVMLAVEATIDHLRSLSRQVTTPAEITQVATISANGDHEWGELISAAMEKVGRNGVITVKDGKTLKDELEVIEGMKFDRGYISPYFINTAKGAKVEYQD 240
P. trituberculatus (AFA36427) TIAKEGFDKISKGANPVEIRRGVMLAVEAVIDHLRSLSRQVITPVEIAQVATISANGDIEWGELISAAMEKVGREGVITVKDGKTLKDELEVIEGMKFDRGYISPYFINTAKGAKVEYQD 240
M japonicus (AGD79959)
                        TIAKEGFEKISKGANPVEIRRGVMMAVDAIVDHLKTLSKPVTTPAEIAQVATISANGDTEVGNLISAAMEKVGREGVITVKDGKTLKDELEVIEGMKFDRGYISPYFINSSKGAKVEYQD 240
L. vannamei (ACN30235)
                        TIAKEGFDRISKGANPVEIRRGVMLAVDAIVAHLKTLSKPVTTPAEIAQVATISANGDIEVGSLISAAMEKVGREGVITVKDGKTLKDELEVIEGMKFDRGYISPYFINSSKGAKVEYQG 240
E. sinensis (KP642083)
                       TIAKEGFDRISKGANPIEIRRGVMLAVDAVIEHLRTLSROVTTPEEIAOVATISANGDSEVGOLISAAMEKVGRNGVITVKDGKTLKDELEVIEGMKFDRGVISPYFINTSKGAKVEYOD 240
                        S. paramamosain (AGI74967) ALVILSEKKISSIQSIIPALEIANAORKPILIIAEDVDGEALSTLVVNRLKIGLQIAAVKAPGFGDNRKNTIQDIAIATGALVFNDEASMVKIEDVOVHDLGMVGEVQITKDDTLLLKGK 360
P. trituberculatus (AFA36427) ALVILSEKKISSIQSIIPALEIANAQRKPILIIAEDVDGEALSTLVVNRLKIGLQVAAVKAPGFGDNRKNTLQDIAIATGALVFNDEASMVKIEDVQAHDLGMVGEWQITKDDTLLLKGK 360
M japonicus (AGD79959) CLVLLSEKKISSIQSIIPVLELANAQRKPLLIIAEDIDGEALSTLVVNRLKIGLQVAAVKAPGFGDNRKNTLHDIAIATGAIVFNDEASMVKIEDVQVHDLGQVGEVQITKDDTLMLKGK 360
L. vannamei (ACN30235)
                        CLVLLSEKKISSIQSIIPVLELANAQRKPLLIIAEDIVGEALSTLVVNRLKIGLQVAAVKAPGFGDNRKNTLHDIAIATGAVVFNDEASMVKIEDVQVHDLGQVGEVQITKDDTLLLKGK 360
                        ALVILISEKKISSIQSTIPALEIANQORKPILIIAEDVDGEALSTLVVNRLKIGLQIAAVKAPGFGDNRKNTIQDIATATGALVFNDEASMVKMEDVOVHDLGMVGEWOITKDDTLLLKGK 360
E. sinensis (KP642083)
                        S. paramamosain (AG174967) GKSSDIERRINQIREQIEDSNSEYEKEKMQERMARLSNGVAVVKVGGSSEVEVNEKKDRVNDALCATR<u>AAIEBGIVPGGG</u>VALLRCLPALDNVKPANEDQKMGVDIIRKAIRTPCHTIVS 480
P. trituberculatus (AFA36427) GKSSDIERRIGQIREQIEDSNSEYEKEKMQERMARLSNGVAVVKVGGSSEVEVNEKKDRVNDALCATR<u>AAVEBGIVPGGG</u>VALLRCLPALDAVKAANEDQKIGVDIIRKAIRTPCYTIVT 480
M japonicus (AGD79959)
                        GNSSDIHRRVBQIKDQIAESSSEYEKEKMQERMARLASGVAVVKVGGSSEVEVNEKKDRVNDALCATRAAVEBGIVPGGGVALIRCLPALEAIAPANDDQKVGIEIVRKAIQTPCHTIAS 480
L. vannamei (ACN30235)
                        {\tt GNSSDIQRRVDQIKDQIADSSSEYEKEKMQERMARLASGVAVVKVGGSSEVEVNEKKDRVNDALCATR\underline{AAVEBGIVPGGGVALIRCLPALDTITPSNEDQKVGIEIVRKAIQTPCHTIAS} 480
                       GKSSDIERRVNQIREQIEDSNSEYEKEKMQERMARLSNGVAVVKVGGSSEVEVNEKKDRVNDALCATR<u>AAIEBGIVPGGG</u>VALLRCLPALEQLTPANEDQKMGIDIIRKAIRTPCHTIVT 480
E. sinensis (KP642083)
                       S. paramamosain (AG174967) NAGIDAAVIVNKVEEATGDYGYDAANGTFVNLVEAGIIDPTKVVRSALTDAAGVASLLTTAESVITEIPKEEPAG—G-MGGNGGNGGNGGNGGNGTNGTNG 576
M japonicus (AGD79959)
                        NAGVDASVIVNKVMEATGDNGYDAATGTFVNLVEAGIIDPTKVVRTALTDAAGVASLLTTAETVITEIPKEEPAGGNGGNGGNGGNGGNGGNGGNGGNGGNG
                        NAGVNASVIVNKVMEASGDVGYDAATGTFVNLVEAGIIDPTKVVRTALTDAAGVASLLTTAESVITEIPKEEPAG-WGGWGGWGGWGGWGGWGGWGFW578
L. vannamei (ACN30235)
E. sinensis (KP642083)
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Fig. S2 Multiple alignment of EsHSP60 amino acid sequence with other crustacean homologues: *Scylla paramamosain* HSP60 (AGI74967), *Portunus trituberculatus* HSP60 (AFA36427), *Macrophthalmus japonicus* HSP60 (AGD79959), *Litopenaeus vannamei* HSP60 (ACN30235). Identical (*) and similar (. or :) amino acid residues are indicated. Gaps (-) were introduced to maximize the alignment. The mitochondrial targeting signal sequence indicated by light gray. The ATP-binding motif is bold. The classical mt-HSP60 signature motifs are underlined. The typical GGM repeat motif is in italics.