

A furoviral replicase recruits host HSP70 to membranes for viral RNA replication

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Running title: A furoviral replicase recruits HSP70 to membranes for replication

Supplementary materials

Supplementary Table

Table S1 Primers used in this study.

Supplementary Figures

Figure S1 Western blotting assays showing inhibition of NbHSP70 by quercetin treatment (A) and over-expression of TaHSP70 by Agrobacterium infiltration of 35S:TaHSP70 (B) in *N. benthamiana* plants.

Figure S2 Sequence alignment of TaHSP70 and NbHSP70 showing that they are highly conserved.

Figure S3 Recombinant expression of GST-tagged Rep¹⁻³³³ (GST-Rep¹⁻³³³) and 6 x His-tagged TaHSP70 (His-TaHSP70) in *E. coli* BL21DE3 for ELISA-base binding assays. M, protein Marker; Lane 1, Protein sample extracted from *E. coli* BL21DE3 expressing GST-Rep¹⁻³³³; Lane 2, Protein sample extracted from *E. coli* BL21DE3; Lane 3, Protein sample extracted from *E. coli* BL21DE3 expressing His-TaHSP70. White arrows point to the recombinant proteins GST-Rep¹⁻³³³ and His-TaHSP70, respectively.

Table S1 Primers used in this study.

Primers	Sequences (5'-3')	Restriction sites (underlined)	The purpose of the primers
Nb70F	CTAG <u>T</u> CTAGATATGCATAACACATGAGG	XbaI	Vector TRV:HSP70
Nb70R	CGGGGTACCTTAGTCGACCTCCTCAAT	KpnI	
BDTa70N	GGAATTCCATATGATGGCCAAGGGCGAGGGG	NdeI	Bait plasmid BD-TaHSP70
BDTa70C	CGCGGATCCGTCCACCTCC TCGATCTT	BamHI	
BDNb70N	GGAATTCCATATGATGGCAGGAAAAGGTGAA	NdeI	Bait plasmid BD-NbHSP70
BDNb70C	CGCGGAT <u>C</u> GTGACCTCC TCAATCTT	BamHI	
ADRep ¹⁻⁶⁷⁰ N	TCCCCACC <u>CGGG</u> ATGCCGATCGATAGCAGT	XmaI	Prey plasmid AD- Rep ¹⁻⁶⁷⁰
ADRep ¹⁻⁶⁷⁰ C	CGCGGAT <u>CC</u> CTCCTTCATTACATGGAC	BamHI	
ADRep ⁶⁷⁰⁻¹⁴³⁰ N	TCCCCACC <u>CGGG</u> AGGAGAAATACTCTGAT	XmaI	Prey plasmid ADRep ⁶⁷⁰⁻¹⁴³⁰
ADRep ⁶⁷⁰⁻¹⁴³⁰ C	CGCGGAT <u>CCC</u> AAACCCGTTGTCTTG	BamHI	
ADRep ¹⁴³⁰⁻¹⁸⁵⁸ N	TCCCCACC <u>CGGG</u> TTGGTACCGGTATGCGG	XmaI	Prey plasmid ADRep ¹⁴³⁰⁻¹⁸⁵⁸
ADRep ¹⁴³⁰⁻¹⁸⁵⁸ C	CGCGGAT <u>CCC</u> CATTCAAAGTTCTATC	BamHI	
ADRep ¹⁻¹⁶⁷ N	TCCCCACC <u>CGGG</u> ATGCCGATCGATAGCAGT	XmaI	Prey plasmid ADRep ¹⁻¹⁶⁷
ADRep ¹⁻¹⁶⁷ C	CGCGGAT <u>CC</u> CTGGTATCTCGTCCTCTC	BamHI	
ADRep ¹⁶⁷⁻³³³ N	TCCCCACC <u>CGGG</u> CCCACCGAAGTCGGTGAA	XmaI	Prey plasmid ADRep ¹⁶⁷⁻³³³
ADRep ¹⁶⁷⁻³³³ C	CGCGGAT <u>CCC</u> GTCCGTCAATTGTGAAGAA	BamHI	
ADRep ³³³⁻⁶⁷⁰ N	TCCCCACC <u>CGGG</u> GACGCAACGGAAAGCGAGG	XmaI	Prey plasmid ADRep ³³³⁻⁶⁷⁰
ADRep ³³³⁻⁶⁷⁰ C	CGCGGAT <u>CCC</u> TCATTACATGGACCAT	BamHI	
pETNb70N	CGCGGATCCATGGCAGGAAAAGGTGAA	BamHI	Plasmid pET28(a)-Nb70
pETNb70C	ATTIGCGGCCGCAGTCGACCTCCTCAATCTT	NotI	
pETTa70N	CGCGGATCCATGGCCAAGGGCGAGGG	BamHI	Plasmid pET28(a)-Ta70
pETTa70C	ATTIGCGGCCGCAGTCACCTC CTCGATCTT	NotI	
p6P1Rep ¹⁻⁶⁷⁰ N	CGCGGATCCATGCCGATCGATAGCAGT	BamHI	Plasmid pGEX-Rep ¹⁻⁶⁷⁰
p6P1Rep ¹⁻⁶⁷⁰ C	CCGAATT <u>CTTA</u> ATTCTCCTTCATTCAC	EcoRI	
Rep ¹⁻¹³⁵⁰ -GFPN	AAAAAGCAGGCTCATGCCGATCGATAGCAGT		Plasmids Rep ¹⁻¹³⁵⁰ -GFP
Rep ¹⁻¹³⁵⁰ -GFPC	AGAAAGCTGGTCTTGTGAATTGGGACA		
Rep ¹⁻¹³⁵⁰ -mCherryN	AAAAAGCAGGCTCATGCCGATCGATAGCAGT		Plasmids Rep ¹⁻¹³⁵⁰ -mCherry
Rep ¹⁻¹³⁵⁰ -mCherryC	AGAAAGCTGGTCTTGTGAATTGGGACA		
Nb70-GFPN	AA AAAGCAGGCTCATGCCAAGGGCGAG		Plasmids NbHSP70-GFP
Nb70-GFPC	AGAAAGCTGGTCGACCTC CTCAATCTT		
Ta70-GFPN	AA AAAGCAGGCTCATGCCAAGGGCGAG		Plasmids TaHSP70-GFP
Ta70-GFPC	AGAAAGCTGGTCGACCTC CTCGATCTT		
attB1	ACAAGTTGTACAAAAAGCAGGCTCC		Gateway vector
attB2	ACCACTTGTACAAGAAAGCTGGGTC		
BRepF	CGCGGATCCATGCCGATCGATAGCAGT	BamHI	Plasmids pCV-nYFP-Rep ¹⁻⁶⁷⁰
BRepR	CGAGCTCCCTTCATTACATGGAC	SacI	
BTa70F	CGCGGATCCATGGCCAAGGGCGAGGGG	BamHI	Plasmids pCV-cYFP-TaHSP70
BTa70R	CGAGCTGTCCACCTC CTCGATCTT	SacI	
BNb70F	CGCGGATCCATGGCAGGAAAAGGTGAA	BamHI	Plasmids pCV-cYFP-NbHSP70
BNb70R	ATTIGCGGCCGCAGTCACCTCCTCAATCTT	NotI	

Figure S1

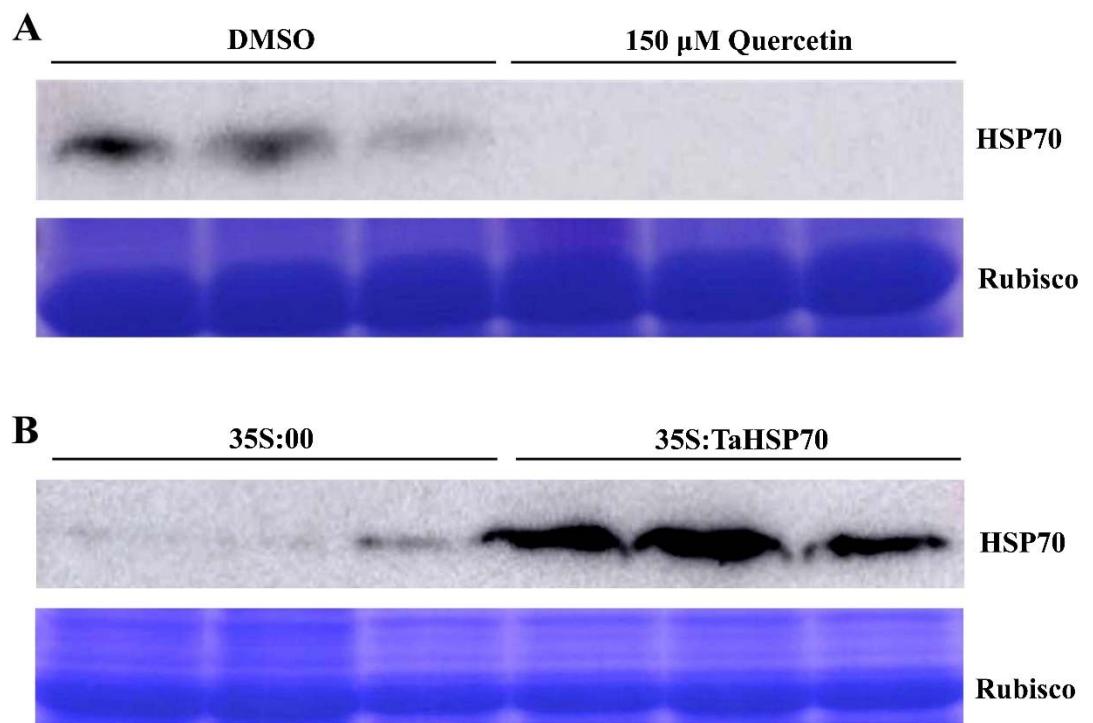


Figure S2

NbHSP70	MAGKGE GPAIG IDL GTT YSCGV VQ HDR VE II I AND QGN RTT P SYV GFT D T E R L I G D A K N Q V A M N P I N T V F D A K R L I G R R F A D A S V Q S D I K H W P F K V I P G	100
TaHSP70	MA-KGE GPAIG IDL GTT YSCGV VQ HDR VE II I AND QGN RTT P SYV A F T D T E R L I G D A K N Q V A M N P T N T V F D A K R L I G R R F S D P S V Q S D M K L W P F K V I P G	99
Consensus	MA KGE GPAIG IDL GTT YSCGV VQ HDR VE II I AND QGN RTT P SYV F T D T E R L I G D A K N Q V A M N P N T V F D A K R L I G R R F D S V Q S D K W P F K V I P G	93
NbHSP70	PGDKPMIVVNYKGEEKQFAAEEISSMVLIKMREIAEAFLGSTVKNAVTVPAYFNDNSQRQATKDAGVIAGLNVLRIINEPTAAAIAYGLDKKATSVGEKN	200
TaHSP70	PADKPMIVVNYKGEEKQFAAEEISSMVLIKMREIAEAFLGNSVKNAVTVPAYFNDNSQRQATKDAGAIAGLNVLRIINEPTAAAIAYGLDKKATSTGEKN	199
Consensus	P DKPMIVVNYKGEEKQFAAEEISSMVLIKMREIAEAFLG VKNAVTVPAYFNDNSQRQATKDAG IAGLNVLRIINEPTAAAIAYGLDKKATSGEKN	188
NbHSP70	VLI FDLGGGTFDVSLLTIEEGI FEVKA TAGD THLGGEFDNRMVNHFVQE FKR KNKKD I SGNP RALR RLRTACE RAKRT LSSTA QTTIEIDS LYEGIDFY	300
TaHSP70	VLI FDLGGGTFDVSLLTIEEGI FEVKA TAGD THLGGEFDNRMVNHFVQE FKR KKDI T GNP RALR RLRTACE RAKRT LSSTA QTTIEIDS LYEGVDFY	299
Consensus	VLI FDLGGGTFDVSLLTIEEGI FEVKA TAGD THLGGEFDNRMVNHFVQE FKR KKKDI GNPR ALR RLRTACE RAKRT LSSTA QTTIEIDS LYEG DFY	285
NbHSP70	STI T RARFEELNMDLFRKCME PVEK CLR DAKMDK STI HDV VL VGG STR I PKV QQL LQDFFNG KEL CKS I N PDE A V A Y GAA V QAA I L S GEG NE KV QD LLLL	400
TaHSP70	TTI T RARFEELNMDLFRKCME PVEK CLR DAKMDK STV HDV VL VGG STR I PKV QQL LQDFFNG KEL CKS I N PDE A V A Y G A S V QAA I L S GEG NE KV QD LLLL	399
Consensus	TIT RARFEELNMDLFRKCME PVEK CLR DAKMDK ST HDV VL VGG STR I PKV QQL LQDFFNG KEL CKS I N PDE A V A Y G A V QAA I L S GEG NE KV QD LLLL	382
NbHSP70	DVTPLSLGLETAGGVMVTLIPRNTT IPTKKE QVF STY SDN QPGVLI QVY EGER ART RDNNLLGKFELSGIPPA PRGVPQITVCFDIDANGILNVSAEDKT	500
TaHSP70	DVTPLSLGLETAGGVM TTLIPRNTT IPTKKE QVF STY SDN QPGVLI QVY EGER ART RDNNLLGKFELSGIPPA PRGVPQITVCFDIDANGILNVSAEDKT	499
Consensus	DVTPLSLGLETAGGVM TLIPRNTT IPTKKE QVF STY SDN QPGVLI QVY EGER ART RDNNLLGKFELSGIPPA PRGVPQITVCFDIDANGILNVSAEDKT	479
NbHSP70	TGQKNKITITNDKGRLSKEEIEK MV QEA E KYK SE DEE HKKK V EA KNA LEN Y A Y NMR NT V K D E K I A SKL P E A D K K K I E D A I E S A I Q W L D A N Q L A E S D F E D	600
TaHSP70	TGQKNKITITNDKGRLSKEEIEK MV QEA E R YK A E D E E H K K K V D A K N A L E N Y A Y NMR NT V K D D K I A SKL G ADD K K K V E E A I E G T I S W L D A N Q L A E A D F E D	599
Consensus	TGQKNKITITNDKGRLSKEEIEK MV QEA E YK E D E E H K K K V A K N A L E N Y A Y NMR NT V K D K K I A SKL E A I E I W L D A N Q L A E D F E D	566
NbHSP70	KMKELESICNPIIAKMYQGAGGDMGGAMDDDAPPSGGSGAGPKIEEV D	649
TaHSP70	KMKELEGICNPIIAKMYQGAA PDMGGGMGDEDMPAGGGGAGPKIEEV D	648
Consensus	KMKELE ICNPIIAKMYQGA DMGG M D P GG GAGPKIEEV D	604

Figure S3

