Supporting Information for

Analysis of *Sogatella furcifera* proteome that interact with P10 protein of *Southern rice black-streaked dwarf virus*

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Supplemental Table-S1: Complete nucleotide sequence for each gene

Name	Complete nucleotide sequence
Vesicle-associated membrane protein 7 5' untranslated region [32 bp] CDS (33 bp-683 bp) [651 bp] 3' untranslated region [693 bp] Poly (A) tail [29 bp] Total [1405 bp]	atctcactttcatttgattaaatcgaataaaa**atg**cttatcctatacagtgtagttgcaagagggaccacggttctggcaaaatttgcaacatgcgctggaaatttttccgaggtgacagaacaaatcctggcgaaaattggtccagaaaacaggaggaagactctctctcacagtagctatttattccattacatatgtgaggacagaattgtttacatgtgtattgcggatgatgagtttgaacgaccaagagcgtttttatacttgaatgaaataaaaaagaggttccgttcaacatatggcagcagagctgacacggccattgcttatgccatgaactcagagtttggccctattttaggaaatgaaatgaaatactattcagaatcgaaggatattgacacaatttcacgagtacatggcgaattggatgaattgaaagatataatggttcacaatattgataacattgctatgagagatgaacgcctcgaattgctggttgataaaacagaaaatctaacagccagctctgtcacattccgagcaactagtagaaatttacagcgagctctcttctggaaaaatatgaaactctatatgataatctcagctattgttttggtaataatttatttcatcttagctatgtcttgtggatcgactttgtccagttgc**tga**aagactacagagtaacaatcacctgtacggtttaattataatccgatgtattcttcagtaaagagtcttccttgtgatatgttcaatgataaatttatactattcttctaaagtagcatgtaaaacataagctacggtactgtatttttttattttatccttatttcacggttcaattaatcaccagaaattattttgaataatccaatcatattcttaattattatatccataaacaaatggtaatgtgactgtatccactgtattaaataatagattgcaataaatttcaattaagagtttttttactgcagtttgagtaatacaaaatagatccgttttatattagttgtttatatttattcacagattgttttattgtcagagaagtgaaacattgtatttgcataaggaatgtatgatagatacctatgaagatattattttgaattattctattttcttgataaatattatgttcataaacaaagggaaatgtaaatgtattgtaatccactgttttagatcatagattgtaataaatttctattgaagtacggttttttagattgcagtttcagtaatacaaaatagaaccgtttttttattagttgcataaatttgaaaatatatatttctataaaaatattgttttattatcggagaattgaaacaatttatttgcataatgaaaataaaaaaaaaaaaaaaaaaaaaaaaaaa
Vesicle transport V-SNARE protein Vti1a 5' untranslated region [54 bp] CDS (55 bp-723 bp) [669 bp] 3' untranslated region [952 bp] Poly (A) tail [30 bp] Total [1705 bp]	aatgaaaaattattaataagttcaaactaatttagtagcctaaaacattagatt**atg**gctgctttaattgatgtttatgagcagcaatatgcagtcatcacagcagatgttacttcaaagattggaagattatcatctctttctggaggagaacgacgtcatgttatttcggaattggataagctgtttgatgaagccaaagagcttatggaacaaatgggccttgaagttcacgagttgaaatcagcagatcaatcaaaacttaagaacagaattgaaagttataaggcagaactgaaaagactagaacaagaatttactaatgctaaaaagaatatcaactcacaaaatggctacagcgataggatagaactgtatagcgaaagtataagcgtcaatgaggaacagaagcaaaggcttttggacaatgctgaaatggttgagcgcactggcaagaaattgactgctggctatcaagtgcttttggagactgaagatattggcaatcaagttctcagggacttgcattcgcagagggaaacgatacagaaatcgaggtctaggttaagagaaacaaacgccgagctgggaagaagtaacagaatcatcaattcgatgatcaacagatctctgcaacacaggttcatcttgacagctatcgccatcgtgttctgccttgtggtcgtgatcagcatctacatatcagctactcgctctcga**taa**actgcacttgtcaccatttagtactctactcggtgtatttcctaatcattctataattaaataatttattcactgctctagtatgaaattaaactaactatcattgaattgaactatcactgttgaaacaaacacctagtaaattattaattgtgtaaaagacaaaggacttcaatagctgtctgcctctctccgtcttaatataaaatgatctaataaaggattatctcatgctcaatatatgggtatcgtatgtgactatgattcttgatatcagtatttgaaaatgcattcatattttcctagaataataacttacgtctatcattgcacagtatattgtactaatttcataactcacatcatattgtttatcattttagatattttaaagtctgattgtgacttaattgtaacgaagatcattctggagctataaaatacttgagttattccaatatcttaattgctattgcaagaaaatgttatttgttttgtatgctgaatctattaaacgatagaaatctatgaaaagtttggat

	gctttttgtgatgtaaataaatagtaaatagtaagctagagtaataatcaattatcttgaaattaatacttgagtttcaaataaggatggatagtatatgcgtaagtatggctagatggatgataatagatggatagtatggctagtaagtttttttgttttatgttgtcctatacaaaatcttaattaattgatatctgattggaaactgctaattttattctatataccctcgtattgattcatgatgcaaatattttccaattattatactgtaagttactcatattctacttcacatgtctgttgaaaaatttgagaattgtccattttaatgtctttttgtgagttgtaaatatttcatgtgtaacttattattgtaaataaaataaatgtctcatttattgttcgaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
Growth hormone-inducible transmembrane protein 5' untranslated region [57 bp] CDS (58 bp-1083 bp) [1026 bp] 3' untranslated region [297 bp] Poly (A) tail [30 bp] Total [1410 bp]	tcatctaggcctactgtcagctatttggaatacactttctagaactaactcttgatg**atg**ttggcctcacgactttgtagcttgcacctagcaccactcggaaggacatctattatccgagtggtgcaaaacagtaagctgccttcgacaaaaagcacaagcaatgaactgtttcgactctacagcaaccagggcagaggatcatggtctagggcatctcctcgtagacgtaccatcaaggaaatcgccatgcaaccagcatctggcacagctttcaacgttggcacagcagcagtggcgggcggagcagctgtcggaatcggtgcgttgtgcttctacggattgggcttggcatccaaacctggcgccatggatcagtcaatgatgtggcccgagtatgtgaaggaaagaatcagatcaacctatatgtattttggatcatcagtggctctcacagcagccagtgcttacgcttgcttcaattcaccagtcatggtcaaattgatgatgaagaactctttaatggcaattgcattgagtttggctgcgatgattggtacatcggttattgctaggagcattccttacacagaaggctttggattgaagcaggccgcctgggctctgcacaccagtgtcataggagcagtcatcgcgcccatctgtttcgtaggaggccccatcctagttagagctgcttggtacacggccggcgtagtgggtgggctgtcgttggtggctgcttgcgcacccagcgaacagttcctgaacatggcggggccgctcagcatgggcctggcggtagtgtttgccgcctccctcggctctgtctttatcgcccccaccaccgcactcggctccggactctactccatcagcctttacggcggcctgctcctattctccggatttctgctttacgacacgcagaagatcatcaagagtgccgaaactcattcgccttacgccatggagaaatacgatccgatcaacatgtctatgggcatctacatggatacaatcaacatcttcataagaattgctacaattttgaacaatggtggctcatcaaaaaggaga**taa**gtcaatttagaactgattatcctagaaaattaatgtaaactataagaattcatcattttcatctgccaatttcgtcaaaatatttattttagttctgatcatggttgacataaagcaatgtattatactcctttcaacaaaaatttgtaagcttattaatcaaatgatttgatggaaaaattgtattatacttaatttttcacaataaattgtaagattaaaatagtttgaaatacgaattactgttccaaattattgtaaaaacttcatccacaataaatcagttcatttgaaccgaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
Nascent polypeptide-associated complex subunit alpha 5' untranslated region [24 bp] CDS (25 bp-666 bp) [642 bp] 3' untranslated region [1517 bp] Poly (A) tail [30 bp] Total [2213 bp]	ctgaaatcttccattttcataaaa**atg**ccagaagcaacagaacttgataaaccagcccccactttgacggaagttaaaaatgatgcatcagggacggagtcagattccgacgactcaattcctgagctggaggagggaccaaaaggagcctccgatggtccaggatcatccattgcgtttggggaaggagctcctattgatatggtcagcaaagccaaacaatctcgtggagaaaagaaggctcgaaaaattatgttgaagctgggcctcaaaccgatcccaggagtctcaagagtgacaatccgcaaatccaagaatattctcttcgtaatcaacaaaccagacgttttcgaaaatcctgcatccgatacctacattgttttcggtgaagccaagattgaagatcttggacaacaagcgcaagttgctgcagccgaaaaattcaaagcccctgaaatttccgcagctgcagaggctggaggtagtgctgcgttggtgacacctatacaagaggaaagcgacgaagaagtcgatgagaccggcgttgaagacaaggatgttgatttggtgatgtctcaggcgaacgtcagtcgaggaaaagcaatcaaggctcttcgaaacaataagaacgacatcgttaatgcaatcatggaactcaccata**tga**agtgtttggatccgagtcgaagtgtcggtatcagggttttcaattttatcgagtgtttttcatctttacttatgatgtttgatttatttctgttgtgtaaaagacttctatcgtaatactatttcacttaattctctcatcaaagaaaaatcttacgaattttaaaagcgtgtaccaagaaatagttttgctgtttttgttgaataatagaacatgttatcggtgtagccaatatactaaaacacgtattacatctgaggtat

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ATP synthase lipid-binding protein 5' untranslated region [46 bp] CDS (47-469 bp) [423 bp] 3' untranslated region [598 bp] Poly (A) tail [30 bp] Total [1097 bp]	ggagttcgtcgctgctgtgcaagaaaacccaactccaaactccaaa**atg**tactcaaacattgcaagaattgttggcccagctgcccgatctgctttggtatcaggatcaagagcctacgtgaggccactgagcagttcagtgtgcacacccaccgctttcaactcacagaatacacagagcactccaaccgttagtttgttacccgccgtaaggaacttccaaacctcagctgtgtcgcgcgatattgactcagctgccaaattcatcggtgccggagccgccaccgttggagtcgctggctcaggagccggaatcggaacagtgttcggttcgctgatcatcggctacgccaggaatccatcgctcaagcagcagctgttctcttacgccattctgggattcgccctgtccgaggccatgggtctcttctgtcttatgatggccttcctgctcttgttcgctttc**taa**acagcatttctacatttagttgattacaaaaataagataattataaattgaaaaacagaacaggactacactgccacttggggtgatttaaaaccaggtcgcgatcattttcatttaaaaagggttgttggtagcgaggagtggttacggcgaacgatcgaggctcgatattcatcgactatcgatatttatcgactagtgttggggcttgcacattagtggttgaatatcgaacgatgtttggtttaattggggcaaaccttccatcgaaactcttacaccaaaacatcggctcaccacggtgtaaacactcctagattttaagtttcatccctccttcagcaataataagcttacaagctagatgaagaaacaattcaccatcaatgtttatttatgttactagttgtacttctcaaaaaatttaaataattgtaatttttcatccatctatccgggatgagttgttgacattacaatgctattgaacttcaatttttgttataaaaaatcggctttattatcgtcttaattgtttcttttgaaacttggatgatatgtcagcgagagacatttccattgtgtacagtgttagagtaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

Supplemental Table S2: Primers used in this study

Primer name	Primer sequence
Yeast two-hybrid	
SRBSDV-P10-F:	5'- ATTAACAAGGCCATTACGGCCATGGCTGACATAAGACTTGA-3'
SRBSDV-P10-R:	5'-AACTGATTGGCCGAGGCGGCCCCTCTGGTGACTTTATTTAA-3'
pPR3N-F	5'-GTCGAAAATTCAAGACAAGG3'
pPR3N-R	5'-AAGCGTGACATAACTAATTAC3'
M13-F	5'-CGCCAGGGTTTTCCCAGTCACGAC-3'
M13-R	5'-AGCGGATAACAATTTCACACAGGA-3'
Full-length gene sequence amplification	
Vesicle-associated membrane protein 7	
GSP-1	5'-AACCGTACAGGTGATT-3'
GSP-2	5'-TAGTTGCTCGGAATGTGA-3'
GSP-3	5'-ATCCAATTCGCCATGTAC-3'
Vesicle transport V-SNARE protein Vti1a	
GSP-1	5'- ATCACGACCACAAGG-3'
GSP-2	5'-GATTTCTGTATCGTTTCCCTCT-3'
GSP-3	5'-GATAGCCAGCAGTCAATTTCTT-3'
Growth hormone-inducible transmembrane protein	
GSP-1	5'-TAAAGGCTGATGGAGTA-3'
GSP-2	5'-CAACGACAGCCCACCCACTA-3'
GSP-3	5'-CCAATCATCGCAGCCAAACT-3'

Nascent polypeptide-associated complex subunit alpha	
GSP-1	5'-TTCTTCGTCGCTTTCC-3'
GSP-2	5'-ATCTTCAATCTTGGCTTCACC-3'
GSP-3	5'-ATTCTTGGATTTGCGGATTG-3'
ATP synthase lipid-binding protein	
GSP-1	5'-GCTTGAGCGATGGATT-3'
GSP-2	5'- TACGGCGGGTAACAAACT-3'
GSP-3	5'-GGCGGGTAACAAACTAACG-3'
GST Pull-down assay	
pGEX+P10–F	5'-CGCGGATCCATGGCTGACATAAGACTTGA-3'
pGEX+P10–R	5'-CCGCTCGAGCATCTGGTGACTTTATTTAA-3'
pCold+VAMP7-F	5'-CGCGGATCCATGCTTATCCTATACAGTGTA -3'
pCold+VAMP7-R	5'-CCCAAGCTTTCAGCAACTGGACAAAGTCGA-3'
pCold+Vti1a-F	5'-CGCGGATCCATGGCTGCTTTAATTGATGTTTA-3'
pCold+Vti1a-R	5'-CCCAAGCTTTTATCGAGAGCGAGTAGCTGATA-3'
pCold+Ghitm-F	5'-CGCGGATCCATGTTGGCCTCACGACTTTGTA-3'
pCold+Ghitm-R	5'-CCCAAGCTTTTATCTCCTTTTTGATGAGCCA-3'
pCold+ Nascent-F	5'-CGCGGATCCATGCCAGAAGCAACAGAACTTGA-3'
pCold+ Nascent-R	5'-CCCAAGCTTTCATATGGTGAGTTCCATGA-3'
pCold+ ATPase-F	5' -CGCGGATCCATGTACTCAAACATTGCAAG-3'
pCold+ATPase-R	5'-CCCAAGCTTTAGAAAGCGAACAAGAGCAG-3'
Gene expression analysis (RT-qPCR)	
qVAMP-7-F	5'-ACAGAACAAATCCTGGCGAAAA-3'
qVAMP-7-R	5'-CAAACTCATCATCCGCAATACA-3'
q Vti1a-F	5'-CGCAGAGGGAAACGATACA-3'

q Vti1a-R	5'-ACCACAAGGCAGAACACGA-3'
q Ghitm-F	5'-GTAGTGGGTGGGCTGTCGTT-3'
q Ghitm-R	5'-GCCGTAAAGGCTGATGGAGT-3'

Supplementary Fig.1: GST Pull-down analysis of the interaction between SRBSDV-P10 and WBPH protein by Western blot

(A)

1: Protein Ladder

2: VAMP7-His (39.7 kDa) (Input)

3: VAMP7-His + GST (Pull-down = Negative control)

4: VAMP7-His + P10-GST (Pull-down)

(VAMP7-His = 39.7 kDa)

5: Protein Ladder

6: Vti1A-His (39.7 kDa) (Input)

7: Vti1A-His + GST (Pull-down = Negative control)

8: Vti1A-His + P10-GST (Pull-down)

(Vti1A -His = 40.4 kDa)

9: Protein Ladder

10: Ghitm-His (51 kDa) (Input)

11: Ghitm-His + GST (Pull-down = Negative control)

12: Ghitm-His + P-10-GST (Pull-down)

(Ghitm-His = 51 kDa)

(B)

Lane

1: Protein Ladder

2: Nascent polypeptide-associated complex subunit alpha-His (37.5 kDa) (Input)

3: Nascent polypeptide-associated complex subunit alpha-His + GST (Pull-down = Negative control)

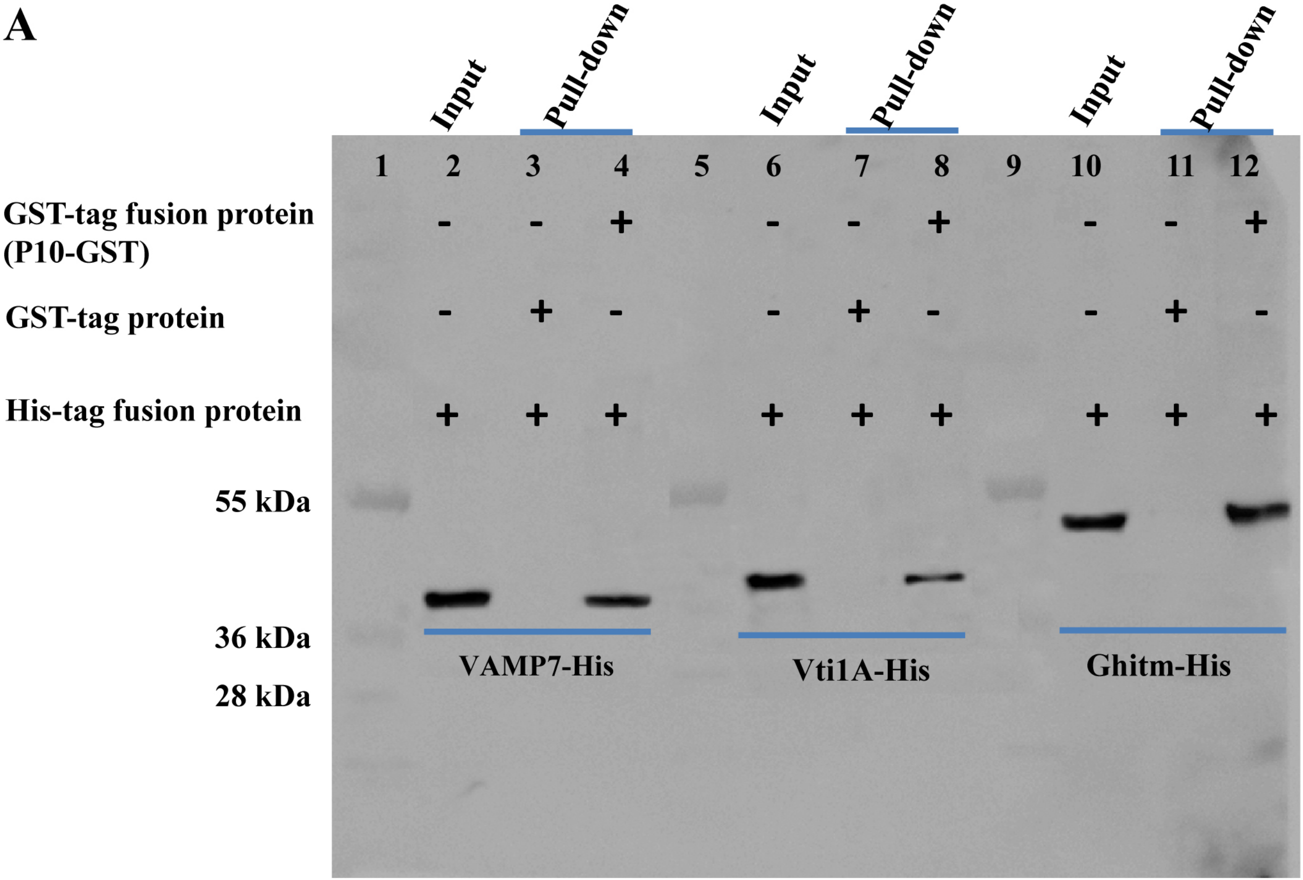
4: Nascent polypeptide-associated complex subunit alpha-His + P10-GST (Pull-down)

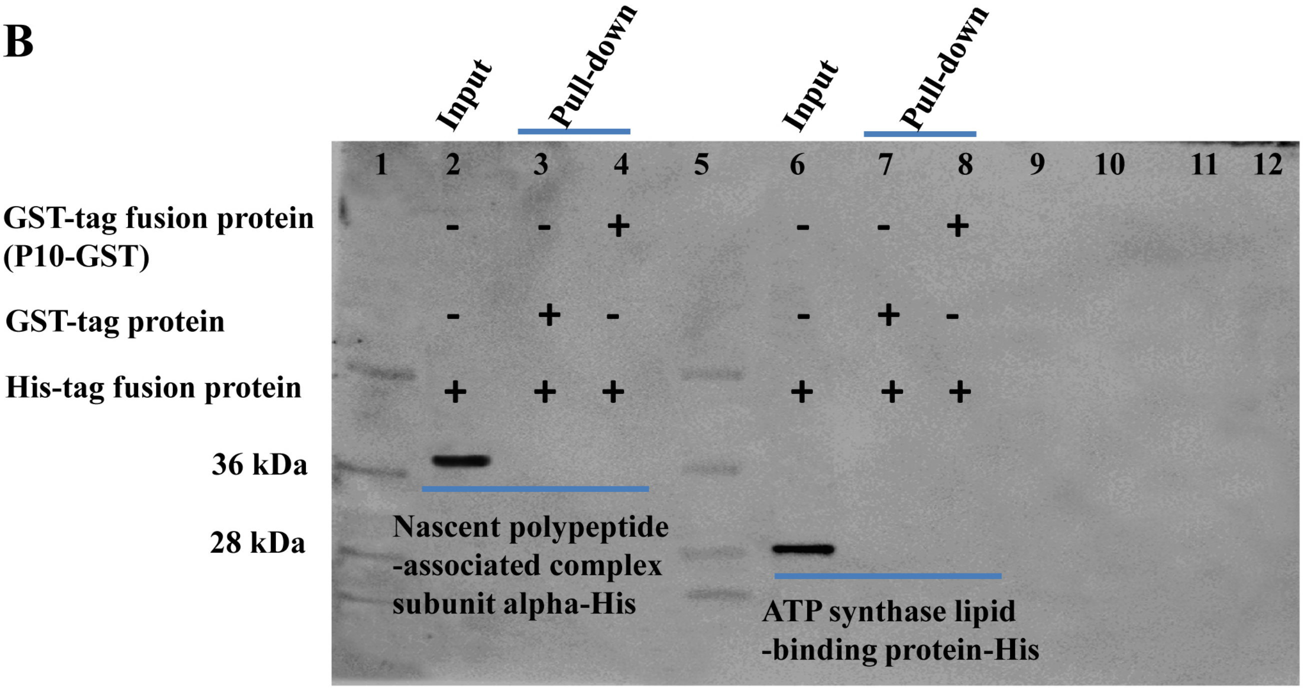
5: Protein Ladder

6: ATP synthase lipid-binding protein-His (29.4 kDa) (Input)

7: ATP synthase lipid-binding protein-His + GST (Pull-down = Negative control)

8: ATP synthase lipid-binding protein-His + P10-GST (Pull-down)


A
Input
Pull-down
Input
Pull-down
Input
Pull-down
1 2 3 4 5 6 7 8 9 10 11 12
GST-tag fusion protein (P10-GST)
- - + - - + - - +
GST-tag protein
- + - - + - - + -
His-tag fusion protein
+ + + + + + + + +
55 kDa
36 kDa
28 kDa
VAMP7-His
Vti1A-His
Ghitm-His


B
Input
Pull-down
Input
Pull-down
1
2
3
4
5
6
7
8
9
10
11
12
GST-tag fusion protein (P10-GST)
- - + - - +
GST-tag protein
- + - - + -
His-tag fusion protein
+ + + + + +
36 kDa
28 kDa
Nascent polypeptide -associated complex subunit alpha-His
ATP synthase lipid -binding protein-His