

Supporting Information

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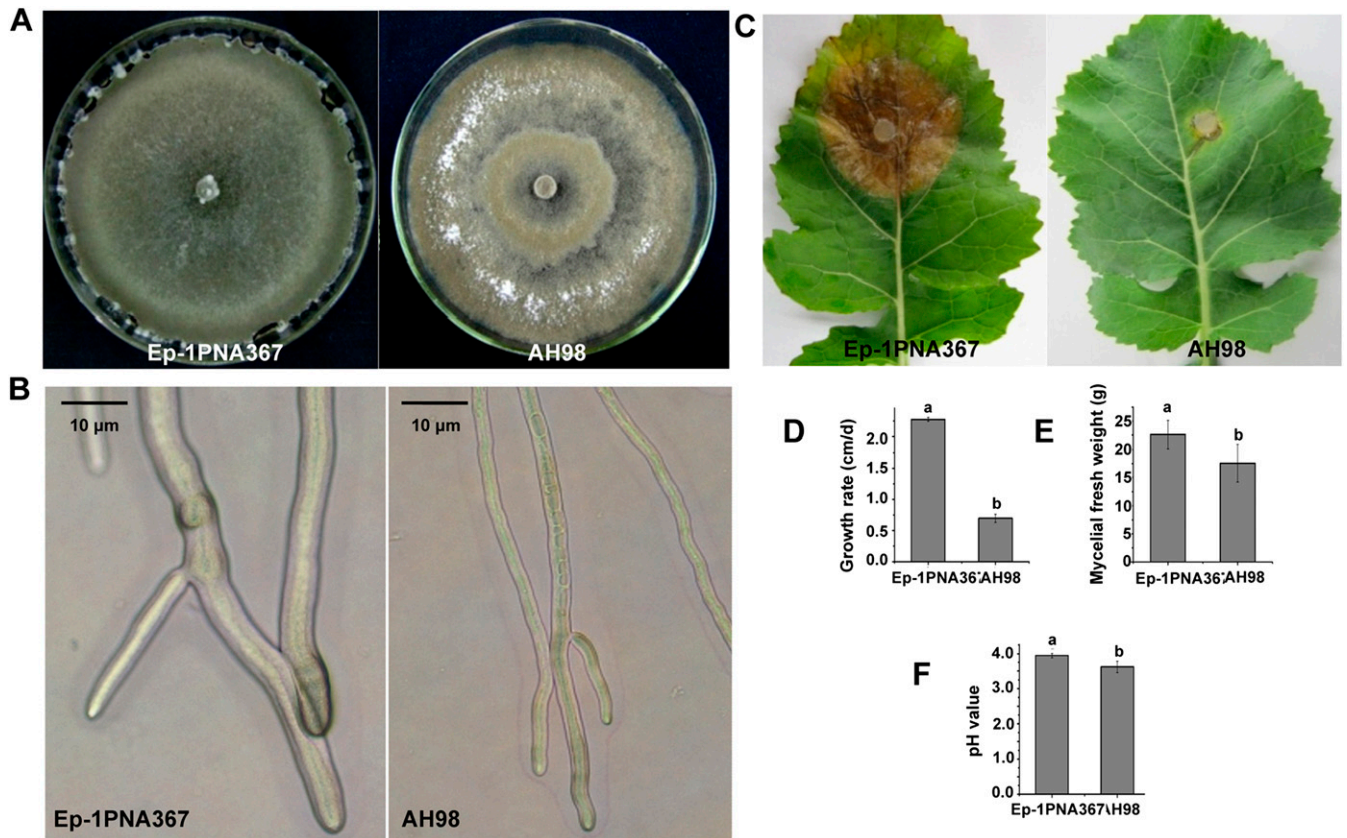


Fig. S1. Biological characterization of *Sclerotinia sclerotiorum* strain AH98. (A) Colony morphology of strain AH98 grown on potato dextrose agar (PDA) at 20 °C for 10 d. (B) Hyphal tips of strain AH98. (C) AH98 lost virulence on detached leaves of rapeseed. Photos were taken at 3 d postinoculation. (D) Growth rate of AH98 on PDA at 20 °C. (E) Fresh biomass of strain AH98 grown in 100 mL potato dextrose broth (PDB) in a 250-mL flask for 6 d. (F) pH values of filtrates of strain AH98 grown in 100 mL PDB in a 250-mL flask for 6 d. Error bars indicate the SD from five sample means. Means followed by the different letters on the top of each column are significantly different at the $P < 0.05$ level of confidence according to Duncan's multiple range test.

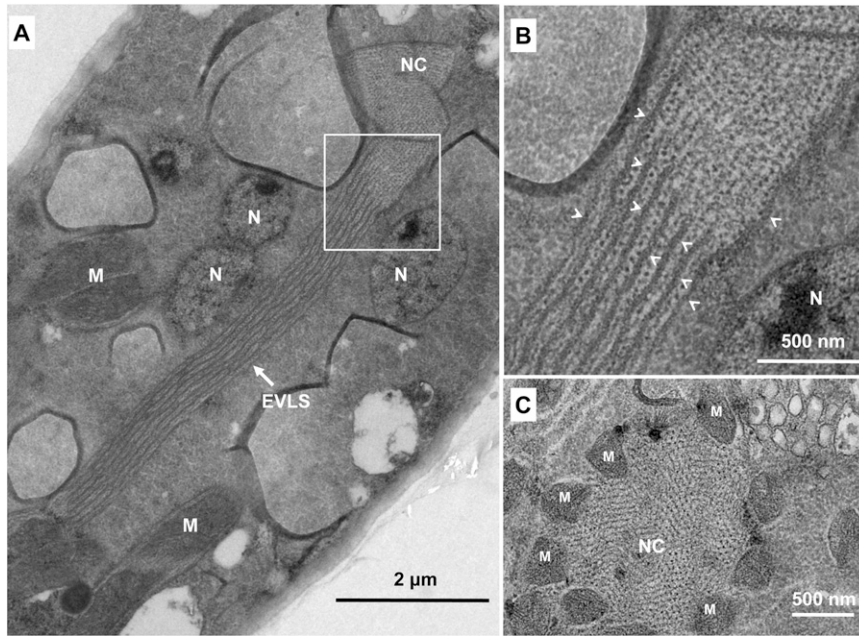


Fig. 52. Nucleocapsids and membrane EVLSs of SsNSRV-1 in ultrathin hyphal sections of virus-infected strain. (A) Intact EVLS (arrow) in original strain AH98. (B) Membranes of EVLS (white arrowheads). (C) Nucleocapsids in *Sclerotinia sclerotiorum* negative-stranded RNA virus 1 (SsNSRV-1)-infected strain Ep-1PNA367-PT2. EVLS, enveloped virion-like structures; M, mitochondrion; N, nucleus; NC, nucleocapsids.

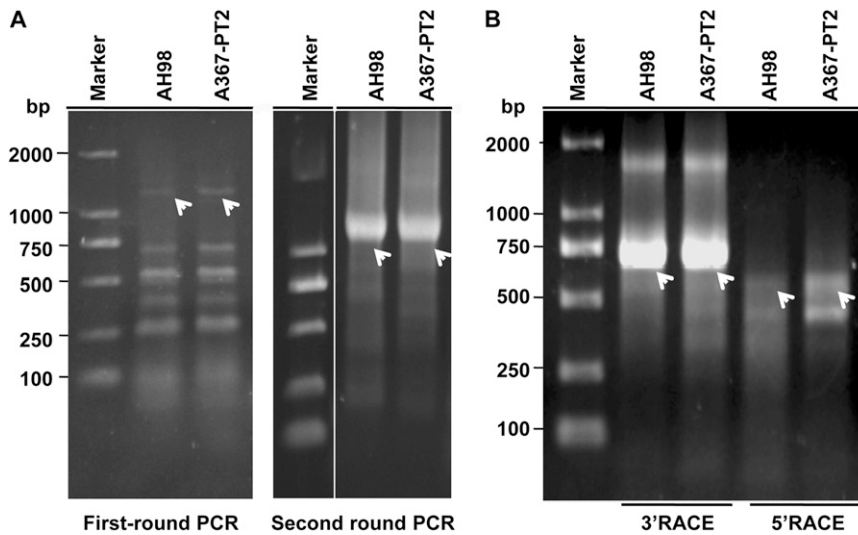


Fig. 53. (A) Viral genomic RNA of SsNSRV-1 was circularized and RT-PCR amplified with specific primers. (B) Viral genomic RNA of SsNSRV-1 was ligated to an oligonucleotide and 5' and 3' rapid amplification of cDNA ends analyzed. The primers and other oligonucleotides used for cDNA cloning are listed in Table S3. Both circularization and oligonucleotide ligation were catalyzed by T4 RNA ligase. The arrows indicate the specific DNA band of SsNSRV-1 amplified by PCR.

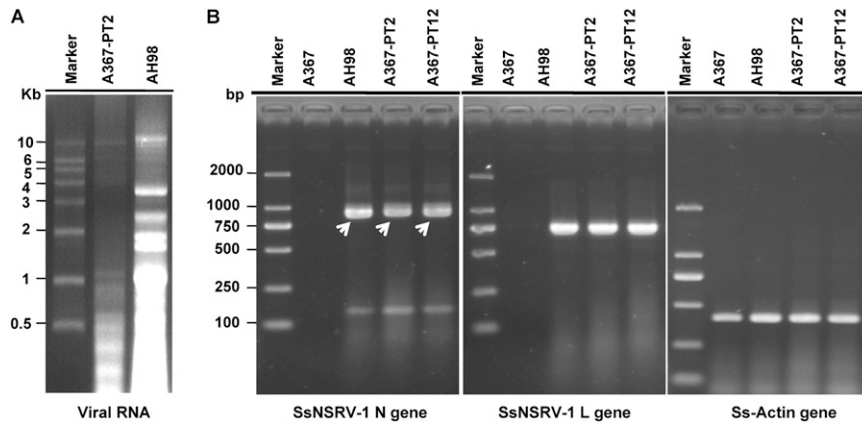


Fig. 54. (A) Viral RNA samples extracted from transfected strain Ep-1PNA367-PT2 and original strain AH98. RNAs were electrophoresed in 1.2% agarose gel containing 1% formaldehyde in 1× Mops buffer (pH 7.0). (B) RT-PCR detection of myxovirus SsNSRV-1 in transfected isolates (Ep-1PNA367-PT2 and Ep-1PNA367-PT12) using total RNA. The actin gene was used as an internal control. The sizes of the RT-PCR products for SsNSRV-1 are 721 and 921 nt, respectively.

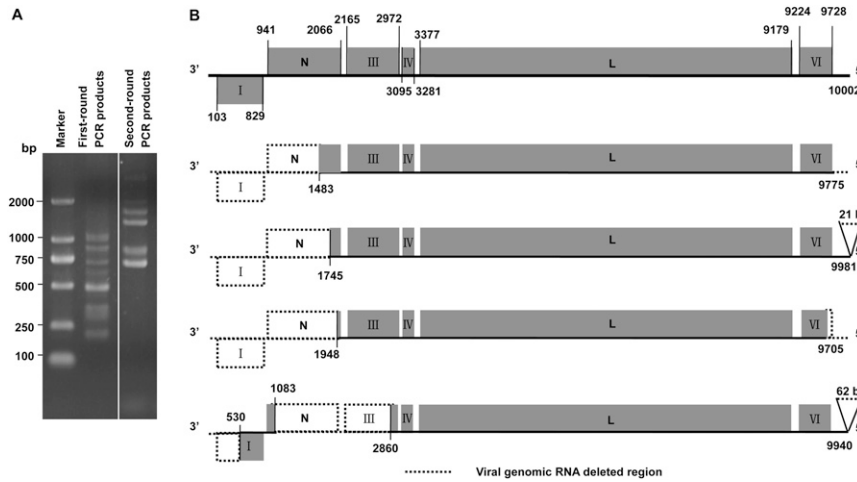


Fig. 55. (A) RT-PCR amplification of 5' and 3' terminus of defective viral RNAs. (B) Genome organization of defective viral RNAs of SsNSRV-1. A diagram of the genomic organization of SsNSRV-1 is shown in the first line.

Table S1. Sequencing analysis of the mRNAs of each viral gene of SsNRV-1

| Viral gene | 5'RACE sequence* | 3'RACE sequence† |
|------------|--|--|
| ORF I | TCGAGGGGGCGGACATGTTTTGTTTTTTTTTCTTTTTTTTTTCTTTTTTTTTTTTCAGGGAGTATTAAATTC ACCTTCCGTAGTTGTTCTTACTCTCGTGACCTACCTCCAGAAAATCTATTAACTTTAAATTC CCATAAAATACATAAAGTATCAAT ATCTC AGCACAACCTGTTGACATTAAGRAAAGAGG- AAGACATTTTCGAGAACCTCGAATTTGATATAAAGGACTCGGAAGTGTCTATAGAGAAC- GATCAGGAATTAAGAACCTCTATTGCTGCACTAACCTGCGAACCTTACCTGGAAATATGAGA- GAGATTCCCGTGGAAACAAGACACTACAGCGTAAATTCCTCTGGTGAATATTTAGA- TGAACCTATTATGCAATCTACTCTCTCACAICGTCTGTAAGAACTCTCCCTCA- GCGCGAATCAAGAACATTTTCC CTTCGAGTGCAGCTCTTTTTAAAC | GAAGCATTTAGTTCTCCAGAGGTC AACRAAATTTCTGACTTACAAGATCAGAAATTTCTGCATCCGAGT- TGAARAATCAGGCATGCCACTCGCTGTCTCCTCCATTAAGCAACAACACAGCTGATGCCATTAGCGCA- GCTTCTGCTGATACCGGACAGAAATTCGACGCACTGTCATTATAAAGAGACTCCAGGATTA- GTTACAGGACTGACAGCAGTACCBAATAATATTATCCATGATCCGAGGAAATTAARAACAGG- TTTGAAAGAAGGTAGAAATTTGACGAAGACTGATCAAGTATTTGATCCAAAATACACTACTAACCTCA- CTTTACTAAGGTTAAGCTTTCCGAAAGACTCTCAGAAAGTAGACTCTCAATCTATATCTCGGAAGCT GT ATGATTTATATATATATATAAAAAAAAAAAAAAAAAAACAACAATGTCGGCCGGCTCTCG |
| ORF II | CGAGGGGGCGCGACATGTTTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTTT TGAGGAGA- TTTCAATATAGTCTCATCTGTCTTACTCATCTACTCTACTATACTCATTTCTCG- TTTATTACC ATCTC TCTGACTCTCGAAGAACCTATCCAGATGTCTTTAAAGACAAGGATAC- CTATGGAGTGAATTTGAGGCTAACCGGATTCGACTCCTACTACTCGAATTTGACCAGAAA- TTGTGAATACTCGGAGATTTTGTGTAGTGAATGATCTTCCCGTCCGTTATGTCCTTTGGCT- GGAAATCAACATGCAGAGATTTCTGACGACATTTGCCAACTGTTATCCGTTGGGATGATTT- CTGCAAGCGGTGTTAAATTTACTCTGCTGATTTGGCTAAATGTATTCAAAAGATACCTTCAG- CTGAAATCAAGAAATTTGGTTATAT CTCGATTTAGTCATGTCGGCTGTGA | GTTATGTTTCGCTTACTTTTTGG GGAATCTTAAGTCTCTGTC CTGATTTACCAATGCAAGAAAAGT- ATCTTCAATTTTTTCAGAGAAATTCAGCGGATCTCGAAACCGAATAATTTCCGCTGCCATCCCA- ACGTTTTCTAGATACATCCACTAAACGCAATGATCTGAAAGTGATTTTTGGAAAGTGCATACAT - CCAAATTGATCTGATAATTAATTAAGAACTTTCTCGGATGAGAGTTTTCGCTCTACTCTCAAACAGGAG- TTCCACTTTGGAACAAATACCGAGGAACTCTTAGTGTCAACACAGAGAAAAATTTGATCGCTCTT- CTCAACATCCGAGAGGCTCTGAGGAACTGTCCCGAGGCTCCAGCCAAATAAGTTCTATTCTCAT - CTGATATGCACAAATCTTTGAA AGTAAAGATCTCTTGATAATTTAATTAATAAAAAAAAAAGAAAAA- AAC AAACATGTCGGCCGCTCC |
| ORF III | CGAGGGGGCGGACATGTTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTCGAGGGAGTAAACATAA- ATCTTTATCGACCAAT ATCTC CTACTCTATCGAATAACTGCCAAGCTCTGCTCATCTTTGTG- TAAATTTGTAGTCCGACTAGTGTGACGTCACACAGCTFAGCAATCTGCTGGACCTTC- AATCAAAAATTAATGCTACCAAATCTCATCTGAACTTTGAGAAATAAAATAGGATTC- TTTCAAAAATGCTTTGATCTTGACAAATGAGATAAACTGAACTCTCTCTGGGATATCTT- AGCTCAACTTTGATCGAAAACTAAGTTGAAAAATTTGCAATGTCGCCCTGCACAAAAGGATA- TTAATCTTTCCTGATCAAAAAGCTCTCTTTTTTCGGTAACTCTAGTTGATCAAGCTAA- AACCAACAATGTCGGGTTTTGATGATTTTTGAATGATGAT ATGGACTACATAATGTCAG- ACTCGG | ATGTCAACT CGGATCAATGGATCGGGAATAACTAATCACT GTAAACAGATGTTATCAT - TTCCGAAATTCGAAATCGCGCCATCCGATCATCTCCATACTCGAATTTCTCTAGAT - CTCAAGTCAAGATGATGACCACTCTCTATCGAGACAGACTTTCCAGTGGGAAAAAT - TTAACCTGGAGAAAGATTTGATTAATACTAACTCCAGTATCTTCTGAGTCTATCATCTGCGAT - CAGCCGATTCATTCGCGGAGATTTTGTTCGCTCCGACGGAATACTCGAATACTCGCATTC- GTCACACTCGCTACGCATCAGATGACAGCAATTTGCTGCAGCTAAATACTGCAATTTCCGAA- TACTCTTAATTACTACATAATAATGACCAAGTACTGTCAGGATGAACAACAGACAACAGTGCATCTC- ATAACA ATTTTCGCTCACAAACA CTCACCTCAGATA TTTAT ATAATAAAAAAAAAAGAAAAA- AAAAAACA AAACATGTCGGCCGCTCCGGTCTC |
| ORF IV | TCGAGGGGGCGGACATGTTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTCGAGAAACCACTACTTACA- TCGCATACGAACTTAGATTTACAAATAATGGACGTTCTCGAAAAATCAACCTCAATTTGA- TTTTACTCGTTTTGTCTGGCACTAGTTTTGCTAGAAATCTAACTAAGAGAGCTGTTGG- GAATCGAAATCTATAGAAAACCTCAAGTGAHTTTCTACTAGTTACGGAAAT ATGGTGAAT TCGAGAAGATTTGAAGTC | CTCGTTTTGCTGGGACATAGTTTTGCTAGAAATCTAATAAGAGACTCGGAATCGAAATCTATAG- AAAACCTCAAATGAGATTTTTTCACTAGTTACGGAAAGATGGTGAATTCGAAAGAAATTTGAAGTCAAT - CTGGTTCGAACTTAGTAATAACGAAAGGCTTAAGAAATTTGATCAATTAATCTCGAATTCACGTG ATA- ATAATAATATA GTAAAAAATAAARAAGAAACAACAACATGTCGGCCGGCTCC |
| ORF V | TCGAGGGGGCGGACATGTTTTGTTTTTTTTTTTTTTTTTTTTTTTTTTTCGAGAAATCAACAAAACCT- TCACTC ATG ATAATTCAGCGAAACGTTTTCGAGTTCGATTCGATTCGATTCGGGAAACGTCCTCGCTG- CTCGGCAGAGAAGACTCTTTCGAAGTCCAATCTTCTTTGATGGATAGGATGAG- GTTCCCTCTATAACGAAGATTAACACTCAAAGAAAACTAGATTTCCCTCAAAAGCAA - TTCCCTTATATAAATTCGATGTTCCACAAATAGTAAAGCAATTTGTAAGCAATAACTAA - TTCCTCCTTATCTGTTCTGAAAGCGGTGCAACGCTTTGTTATTCGATTTAAATAGAA- CATACTCTCCGCTATAATGTCACGGCGGACCAATACTCTGAGCTATTACTCTGTACTCCT- TGATATCGAGAAAGACTCTCAAAAATATCCCTAGCTGATCACTCAGGCTTTACGCTCG- GAATTTCTGCG | TCAGAAATCAAGTATCAGATGTCGTCCTC TACACCCAGATTTAGGTTCCGCTCGGAAATGGTAATTA - TCAGAGCATCGAGTTTAAACAAAAGAAATGAGATCAATTAATTCATATGCTCCACACAGAGTTAGTA - TCCCAATTTCTGGAAATGGAAACGAAATCTCTAGACATTTTCAATTAAGTAACTAATCTGTTCT- TCTCTCAGCCTTAGTATAAAATCTTTATAGTATGCCACGACGAAAGATTTCCGGAAGTATAATA - TTCACTTATGGGATATAATGATGCAATGCAAGTTTTGAATGCAATCAACAGGTTAACGATCTTCGATG - TCGGGCAATTT AGATAATAATTTTCAAGTAAGATGCTATGATA ATGACATTTGCTTGAACCTACTAAT ATAA- AAAAAAGAAAAAACA AAACATGTCGGCCGGCTCC |

Table S2. Peptide mass fingerprinting analysis of virions crude preparations, 20% and 25% sugrose gradient components, and p43 and p41 proteins

| Amino acid sequence | Mass | | $\pm\Delta$ | Putative ORF | Position | Ion score | Frequency |
|---|-------------------|-------------------|----------------|--------------|----------------|--------------|-----------|
| | Observed | Calculated | | | | | |
| Virion crude preparations | | | | | | | |
| DRLPTIDLTR | 1,198.6617 | 1,198.667 | -0.0053 | ORF II | 27-36 | 21.69 | 1 |
| VIFGSAYIPIDR | 1,349.7277 | 1,349.7343 | -0.0066 | ORF II | 319-306 | 40.78 | 2 |
| NAISQFMPSGELK | 1,420.6941 | 1,420.702 | -0.008 | ORF II | 183-195 | 31.48 | 2 |
| QSPENLDAFNLK | 1,454.6971 | 1,454.7041 | -0.007 | ORF II | 168-180 | 58.88 | 3 |
| LTFGASLSPLLLITK | 1,572.9415 | 1,572.9491 | -0.0076 | ORF II | 251-265 | 59.31 | 1 |
| VFTDNSPYLASHAVLSK | 1,776.8962 | 1,776.9046 | -0.0084 | ORF II | 196-211 | 79.74 | 2 |
| LVIGAMISASGVNYSTAR | 1,808.926 | 1,808.9454 | -0.0194 | ORF II | 71-88 | 43.27 | 2 |
| EFSDLETEYFAAAHALQR | 2,096.9693 | 2,096.9803 | -0.011 | ORF II | 276-293 | 109.06 | 3 |
| ALVMSSIVDKDDPMVSGTQR | 2,148.0433 | 2,148.0555 | -0.0122 | ORF II | 224-243 | 73.21 | 5 |
| FSHVPSDASEAELPALPNSCVPK | 2,580.1969 | 2,580.2166 | -0.0197 | ORF II | 108-131 | 14.73 | 2 |
| QTTADAIASAADLR | 1,489.7315 | 1,489.7372 | -0.0057 | ORF I | 156-170 | 68.9 | 1 |
| NIFPSSAALLTESTK | 1,577.8209 | 1,577.8301 | -0.0092 | ORF I | 93-107 | 55.58 | 2 |
| VEIQACHSSVSLHK | 1,593.7866 | 1,593.7933 | -0.0067 | ORF I | 142-155 | 38.08 | 2 |
| LTAATNNILSMYPPELK | 1,906.9647 | 1,906.971 | -0.0063 | ORF I | 190-206 | 59.01 | 1 |
| INALEALVHSQGQQISDLQDQNSALR | 2,847.4275 | 2,847.4475 | -0.02 | ORF I | 116-141 | 3.09 | 1 |
| Sugrose gradient components, 20% | | | | | | | |
| DRLPTIDLTR | 1,198.661 | 1,198.667 | -0.006 | ORF II | 27-36 | 12.61 | 2 |
| VIFGSAYIPIDR | 1,349.726 | 1,349.7343 | -0.0083 | ORF II | 319-306 | 28.55 | 1 |
| NAISQFMPSGELK | 1,420.6931 | 1,420.702 | -0.0089 | ORF II | 183-195 | 66.14 | 2 |
| QSPENLDAFNLK | 1,454.6958 | 1,454.7041 | -0.0084 | ORF II | 168-180 | 14.12 | 4 |
| DKDTYGVNIEANR | 1,493.7044 | 1,493.711 | -0.0066 | ORF II | 14-26 | 25.06 | 1 |
| LTFGASLSPLLLITK | 1,572.9414 | 1,572.9491 | -0.0077 | ORF II | 251-265 | 90.24 | 1 |
| QSPENLDAFNLR | 1,610.7975 | 1,610.8053 | -0.0078 | ORF II | 168-181 | 47.07 | 1 |
| VFTDNSPYLASHAVLSK | 1,776.8925 | 1,776.9046 | -0.0121 | ORF II | 196-211 | 72.36 | 3 |
| LVIGAMISASGVNYSTAR | 1,808.9345 | 1,808.9454 | -0.0109 | ORF II | 71-88 | 28.04 | 5 |
| EFSDLETEYFAAAHALQR | 2,096.969 | 2,096.9803 | -0.0113 | ORF II | 276-293 | 46.81 | 4 |
| ALVMSSIVDKDDPMVSGTQR | 2,148.0401 | 2,148.0555 | -0.0154 | ORF II | 224-243 | 50.1 | 6 |
| FSHVPSDASEAELPALPNSCVPK | 2,580.2023 | 2,580.2166 | -0.0143 | ORF II | 108-131 | 29.94 | 2 |
| Sugrose gradient components, 25% | | | | | | | |
| DRLPTIDLTR | 1,198.6611 | 1,198.667 | -0.0059 | ORF II | 27-36 | 2.69 | 1 |
| VIFGSAYIPIDR | 1,349.7308 | 1,349.7343 | -0.0035 | ORF II | 319-306 | 48.55 | 1 |
| NAISQFMPSGELK | 1,420.6941 | 1,420.702 | -0.008 | ORF II | 183-195 | 54.25 | 1 |
| QSPENLDAFNLK | 1,454.6974 | 1,454.7041 | -0.0068 | ORF II | 168-180 | 10.42 | 3 |
| LTFGASLSPLLLITK | 1,572.9391 | 1,572.9491 | -0.01 | ORF II | 251-265 | 73.49 | 1 |
| LVIGAMISASGVNYSTAR | 1,808.9336 | 1,808.9454 | -0.0119 | ORF II | 71-88 | 43.11 | 3 |
| EFSDLETEYFAAAHALQR | 2,096.9696 | 2,096.9803 | -0.0107 | ORF II | 276-293 | 68.86 | 2 |
| ALVMSSIVDKDDPMVSGTQR | 2,148.0365 | 2,148.0555 | -0.019 | ORF II | 224-243 | 47.55 | 1 |
| FSHVPSDASEAELPALPNSCVPK | 2,580.1942 | 2,580.2166 | -0.0224 | ORF II | 108-131 | 13.23 | 3 |
| p43 protein | | | | | | | |
| ALVMSSIVDK | 1,077.57 | 1,077.57 | -0.0023 | ORF II | 224-233 | 78.65 | 18 |
| ALVMSSIVDKDDPMVSGTQR | 2,164.05 | 2,164.05 | -0.004 | ORF II | 224-243 | 115.46 | 16 |
| DKDTYGVNIEANR | 1,493.71 | 1,493.71 | -0.0036 | ORF II | 14-26 | 107.32 | 8 |
| DRLPTIDLTR | 1,198.66 | 1,198.67 | -0.0049 | ORF II | 27-36 | 80.87 | 9 |
| D TSAEIK | 762.38 | 762.38 | 0.001 | ORF II | 95-101 | 43.18 | 2 |
| D TSAEIKNWVISR | 1,517.79 | 1,517.78 | 0.0014 | ORF II | 95-107 | 66.63 | 1 |
| D TYGVNIEANR | 1,250.58 | 1,250.59 | -0.0051 | ORF II | 16-26 | 83.24 | 12 |
| EAAEETVPEAPAQ | 1,340.61 | 1,340.61 | -0.0016 | ORF II | 363-375 | 104.85 | 11 |
| EFSDLETEYFAAAHALQR | 2,096.98 | 2,096.98 | -0.0038 | ORF II | 276-293 | 81.54 | 6 |
| EKLIALLNIR | 1,181.75 | 1,181.75 | 0.0047 | ORF II | 353-362 | 47.28 | 4 |
| FLDTSTK | 810.41 | 810.41 | -0.0026 | ORF II | 294-300 | 37.37 | 4 |
| FSHVPSDASEAELPALPNSCVPK | 2,580.21 | 2,580.22 | -0.0101 | ORF II | 108-131 | 58.75 | 1 |
| INKTFNSIIR | 1,205.69 | 1,205.68 | 0.012 | ORF II | 212-221 | 30.67 | 1 |
| LANVFKD TSAEIK | 1,434.76 | 1,434.77 | -0.0113 | ORF II | 89-101 | 53 | 1 |
| LPTIDLTR | 927.54 | 927.54 | -0.0002 | ORF II | 29-36 | 55.25 | 34 |
| LTFGASLSPLLLITK | 1,572.94 | 1,572.95 | -0.0057 | ORF II | 251-265 | 69.61 | 16 |
| LVIGAMISASGVNYSTAR | 1,808.94 | 1,808.95 | -0.0008 | ORF II | 71-88 | 141.13 | 9 |
| MFYVMFR | 1,008.45 | 1,008.46 | -0.0029 | ORF II | 244-250 | 42.49 | 16 |
| NAISQFMPSGELK | 1,420.7 | 1,420.7 | -0.0042 | ORF II | 183-195 | 86.58 | 42 |
| NWVISR | 773.42 | 773.42 | -0.0025 | ORF II | 102-107 | 30.34 | 13 |

Table S2. Cont.

| Amino acid sequence | Mass | | $\pm\Delta$ | Putative ORF | Position | Ion score | Frequency |
|---------------------|-----------------|-----------------|----------------|--------------|----------------|--------------|-----------|
| | Observed | Calculated | | | | | |
| QSPENLDAFNLK | 1,471.73 | 1,471.73 | -0.0056 | ORF II | 168-180 | 117.68 | 51 |
| QSPENLDAFNLKR | 1,628.83 | 1,628.82 | 0.0166 | ORF II | 168-181 | 86.47 | 2 |
| RNAISQFMPSGELK | 1,593.78 | 1,593.78 | 0.0002 | ORF II | 182-195 | 51.77 | 4 |
| RTIPDVK | 974.55 | 974.55 | -0.0045 | ORF II | 6.0-13 | 24.69 | 1 |
| TFNSIIR | 849.47 | 849.47 | -0.0018 | ORF II | 215-221 | 46.64 | 21 |
| TFNSIIRDR | 1,120.62 | 1,120.6 | 0.0224 | ORF II | 215-223 | 33.65 | 2 |
| TIPDVK | 818.45 | 818.45 | 0.0008 | ORF II | 7.0-13 | 40.01 | 28 |
| TIPDVKDK | 1,061.57 | 1,061.58 | -0.0037 | ORF II | 7.0-15 | 35.37 | 1 |
| VFTDNSPYLASHAVLSK | 1,776.91 | 1,776.9 | 0.0009 | ORF II | 196-211 | 114.85 | 18 |
| VIFGSAYIPIDR | 1,349.74 | 1,349.73 | 0.0011 | ORF II | 307-318 | 100.69 | 39 |
| YPQFFR | 856.42 | 856.42 | -0.0002 | ORF II | 270-275 | 38.32 | 8 |
| IVELTQKER | 1,114.59 | 1,114.63 | -0.0406 | ORF V | 539-547 | 14.12 | 1 |
| p41 protein | | | | | | | |
| ALVMSIVDK | 1,061.57 | 1,061.58 | -0.0089 | ORF II | 224-233 | 57.34 | 4 |
| ALVMSIVDKDDPMVSGTQR | 2,180.03 | 2,180.05 | -0.0121 | ORF II | 224-243 | 97.35 | 4 |
| DKDTYGVNIEANR | 1,493.71 | 1,493.71 | -0.0051 | ORF II | 14-26 | 44.44 | 3 |
| DRLPTIDLTR | 1,198.66 | 1,198.67 | -0.0082 | ORF II | 27-36 | 21.95 | 3 |
| DTYGVNIEANR | 1,250.58 | 1,250.59 | -0.0087 | ORF II | 16-26 | 60.88 | 3 |
| EAAEETVPEAPAQ | 1,340.6 | 1,340.61 | -0.008 | ORF II | 363-375 | 29.56 | 7 |
| EFSDLETEYFAAAHALQR | 2,096.97 | 2,096.98 | -0.0089 | ORF II | 276-293 | 66.41 | 1 |
| EKLIALLNIR | 1,181.74 | 1,181.75 | -0.0117 | ORF II | 353-362 | 37.07 | 1 |
| FLDTSTK | 810.42 | 810.41 | 0.004 | ORF II | 294-300 | 15.99 | 2 |
| LIALLNIR | 924.61 | 924.61 | -0.0047 | ORF II | 355-362 | 48.51 | 1 |
| LPTIDLTR | 927.53 | 927.54 | -0.0061 | ORF II | 29-36 | 29.12 | 7 |
| LTFGASLPLLLITK | 1,572.94 | 1,572.95 | -0.0076 | ORF II | 251-265 | 85.58 | 3 |
| MFYVMFR | 1,024.44 | 1,024.45 | -0.0081 | ORF II | 244-250 | 19.79 | 4 |
| NAISQFMPSGELK | 1,436.69 | 1,436.7 | -0.0117 | ORF II | 183-195 | 66.55 | 14 |
| NWVISR | 773.41 | 773.42 | -0.0038 | ORF II | 102-107 | 24.69 | 6 |
| QSPENLDAFNLK | 1,471.72 | 1,471.73 | -0.0115 | ORF II | 168-180 | 114.4 | 10 |
| RNAISQFMPSGELK | 1,593.78 | 1,593.78 | 0.001 | ORF II | 182-195 | 18.58 | 1 |
| TFNSIIR | 849.47 | 849.47 | -0.0051 | ORF II | 215-221 | 28.07 | 11 |
| TIPDVK | 818.45 | 818.45 | -0.0029 | ORF II | 7.0-13 | 24.35 | 7 |
| VFTDNSPYLASHAVLSK | 1,776.89 | 1,776.9 | -0.012 | ORF II | 196-211 | 44.13 | 5 |
| VIFGSAYIPIDR | 1,349.72 | 1,349.73 | -0.0097 | ORF II | 307-318 | 57.38 | 5 |
| YPQFFR | 856.42 | 856.42 | -0.0053 | ORF II | 270-275 | 17.06 | 3 |
| LLESLIK | 814.48 | 814.52 | -0.035 | ORF V | 509-515 | 20.24 | 1 |

The peptide sequences in bold are identified from virion crude preparations and from the mixture of p43 and p41 sample.

Table S3. Primers pairs used in this study

| Primer name | Primer sequence (5'–3') | Genomic location | Product size, bp | Application |
|-------------|------------------------------|------------------|------------------|--|
| AH98-p1-F | GGACTCGGAAGTGTACATAGAGAACG | 175–190 | 582 | (i) To make probe I; (ii) to detect the gene expression of ORF I; (iii) to detect the property of RNA–nucleoprotein complexes (RNPs) |
| AH98-p1-R | CGTCAATTCTACCTTCTTCAAACCTG | 721–747 | 839 | (i) To make probe II; (ii) to detect the gene expression of ORF II; (iii) to detect the property of viral RNA from AH98 |
| AH98-p2-F | TGCCAAACTGGTTATCGGTGC | 1143–1164 | | |
| AH98-p2-R | AGAGTTCTCTGCGTATTGTTCC | 1957–1981 | 721 | (i) To make probe III; (ii) to confirm transfectants that were infected by SsNERV-1; (iii) to detect the gene expression of ORF III; (iv) to detect the property of RNPs |
| AH98-p3-F | CTATCGAATAACTGCCAAGACCTCG | 2174–2199 | | |
| AH98-p3-R | GCATGTGATGTCGTAGCGAGTGTG | 2870–2894 | 176 | (i) To make probe IV; (ii) to detect the gene expression of ORF IV |
| 98-Gene4-R | AACCAGATGTGACTTCAACTTCTTCG | 3244–3270 | | |
| 98-Gene4-F | TTGATTTTACTCGTTTGTCTGCGC | 3122–3147 | 891 | To detect the property of RNPs |
| AH98-p5-F1 | GAACGTCGTTCTGCGGCTCC | 3415–3435 | | |
| AH98-p5-R1 | AAGATTTCTGTTACGGATTCTGGACC | 4280–4305 | 873 | (i) To make probe V; (ii) to detect the gene expression of ORF V; (iii) to detect the property of viral RNA from AH98 |
| AH98-p5-F2 | ATTTATGGGGCGGATTCTGG | 5103–5124 | | |
| AH98-p5-R2 | TCTGTGTTCTAAGGCATAAAGAGGGG | 5949–5971 | 940 | To detect the property of RNPs |
| AH98-p5-F3 | ATTCCTTACCACTTGC GGGAATGC | 6760–6783 | | |
| AH98-p5-R3 | TGTAACCGGATTCTCACCCACTCTC | 7674–7699 | 722 | To detect the distribution of SsNSRV-1 |
| AH98-p5-F4 | AAGCCAAACGACGCATCTCACC | 6244–6266 | | |
| AH98-p5-R4 | CGTCCACGGAGAACGAGCAG | 6945–6965 | 1,051 | To detect the distribution of SsNSRV-1 |
| AH98-P5-F5 | TTCAAATGGCGGGACAAGGA | 5552–5572 | | |
| AH98-P5-R5 | TCGTCCACCAGGCTTCTTTCG | 6581–6602 | 921 | To confirm transfectants that were infected by SsNERV-1 |
| AH98-p5-F6 | AGACCACGATACGAAGATAAGAAAGAGA | 8146–8174 | | |
| AH98-P5-R6 | CGGAAACTTCTGTTTCGTGTC | 9044–9066 | 358 | (i) To make probe VI; (ii) to detect the gene expression of ORF VI |
| 98-Gene6-R | CGAGGACGGTTTCTGCTTGGTTC | 9686–9709 | | |
| 98-Gene6-F | ATCGTTTAACTACAATGGAAGGGC | 9260–9285 | 682 | To detect the property of RNPs |
| AH98-p6-F | AGGAGGATGCCTTCGTATAAAGAGAAG | 9218–9245 | | |
| AH98-p6-R | CGTGTACCCGTAACCTTGTTCGTCT | 9875–9900 | 413 | 5' RACE of ORF I |
| 98-G1-RC5-1 | TGATTGCCTTAGTGCTCTCCGTT | 408–431 | | |
| 98-G1-RC5-2 | CCGTTAAAAGAGCTGCACTCGAAG | 389–413 | 340 | 5' RACE of ORF II |
| 98-G2-RC5-1 | CTCGGCTTCGCTGGCATCTT | 1281–1301 | | |
| 98-G2-RC5-2 | CAGACGGGACATGACTAAATCGAG | 1257–1281 | 414 | 5' RACE of ORF III |
| 98-G3-RC5-1 | CGATCCCATTGATCCCCGAGTC | 2561–2582 | | |
| 98-G3-RC5-2 | CCCGAGTCTGACATATGTAGTCCAT | 2544–2579 | 165 | (i) 5' RACE of ORF IV; (ii) to clone defective RNAs |
| 98-Gene4-R | AACCAGATGTGACTTCAACTTCTTCG | 3244–3270 | | |
| 98-G4-RC5-2 | GACTTCAACTTCTTCAATTCACCAT | 3234–3260 | 519 | (i) 5' RACE of ORF V; (ii) to clone defective RNAs |
| 98-G5-RC5-1 | GTTCCCCATTTCTTAAACGCACAT | 3793–3817 | | |
| 98-G5-RC5-2 | CGCACATAATCCGAGCGGT | 3780–3800 | 310 | 5' RACE of ORF VI |
| 98-G6-RC5-1 | GCATCCCTCAATAAAGATACCGC | 9515–9538 | | |
| 98-G6-RC5-2 | CCCTCAATAAAGATACCGCATTAAAT | 9508–9534 | 327 | 3' RACE of ORF I |
| 98-G1-RC3-1 | GAAGCATTAGTTCACTCCCAAGGTC | 459–484 | | |
| 98-G1-RC3-2 | CAAGATCAGAATTCGCACTCCG | 501–524 | 366 | 3' RACE of ORF II |
| 98-G2-RC3-1 | GTTATGTTTCGTCTTACTTTTGGGGC | 1678–1704 | | |
| 98-G2-RC3-2 | GGGCATCCCTAAGTCCCTCTCTTG | 1700–1723 | 398 | 3' RACE of ORF III |
| 98-G3-RC3-1 | ATGTCAGACTCGGGATCAATGGG | 2556–2577 | | |
| 98-G3-RC3-2 | GGGATCGGGAATACTAACATCAC | 2574–2598 | 149 | 3' RACE of ORF IV |
| 98-Gene4-F | TTGATTTTACTCGTTTGTCTGCGC | 3122–3147 | | |
| 98-G4-RC3-2 | CTCGTTTGTCTGCGCACTAGTTT | 3132–3155 | 367 | 3' RACE of ORF V |
| 98-G5-RC3-1 | GTCCCTACGCTGGTCTTTCTCTATGTG | 8780–8807 | | |

Table S3. Cont.

| Primer name | Primer sequence (5'–3') | Genomic location | Product size, bp | Application |
|-------------|--|------------------|------------------|---|
| 98-G5-RC3-2 | GAGAATCAAGTATCAGATGTCGTCCTC | 8812–8839 | | |
| 98-G6-RC3-1 | CTGCAAACTCAGTTAAATAATCCGC | 9337–9362 | 370 | 3' RACE of ORF VI |
| 98-G6-RC3-2 | CCGCAAAAAGAACTCGATGAATT | 9358–9381 | | |
| AH98-RC3-R1 | GGTAGCTGCTGTCAATCGCTC | 664–685 | >677 | To clone genome termini |
| AH98-RC3-R2 | CTGTCAATCGCTCAACTAATCCTG | 653–677 | | |
| AH98-RC5-F1 | CCTCAATTTCAATTACCCGCGC | 9433–9455 | >441 | (i) To clone genome termini; (ii) to clone defective RNAs |
| AH98-RC5-F2 | TTCGGACATTCATCCAAACCT | 9561–9583 | | |
| CDSIII-1 | TAGAGACCGAGGCGCCGACATGTTTTG- TTTTTTTTTCTTTTTTTTTVN | | | 5' and 3' RACE |
| CDSIII-2 | GACCGAGGCGCCGACATG | | | |
| CDSIII-3 | CGAGGCGCCGACATGTTT | | | |
| pC3-T7loop | GGATCCCGGAATTTCGGTAATACGACTC- ACTATATTTTTATAGTGAGTCGTATTA | | | Termini determination of genome |
| PC2-1 | CGTATTACCGAATTCCTCCGGG | | | |
| pC2-2 | CCGAATTCCTCCGGGATCC | | | |

Table S4. Viruses or virus-like sequences selected for phylogenetic analysis in this study

| Virus family | Genus | Virus name | Abbreviation | GenBank accession no. of L protein |
|---|-------------------------|--|--------------|------------------------------------|
| Mononegavirales | | | | |
| Filoviridae | | Zaire ebolavirus | ZeboV | NP_066251.1 |
| | | Marburg virus | MarV | YP_001531159.1 |
| Pneumoviridae | <i>Pneumovirus</i> | Human respiratory syncytial virus | HRSV | NP_056866.1 |
| | | Pneumonia virus of mice | PVM | YP_173335.1 |
| | <i>Metapneumovirus</i> | Avian metapneumovirus | AMPV | YP_443845.1 |
| | | Human metapneumovirus | HMPV | YP_012613.1 |
| | <i>Morbillivirus</i> | Canine distemper virus | CDV | NP_047207.1 |
| Paramyxoviridae | <i>Henipavirus</i> | Nipah virus | NiV | NP_112028.1 |
| | <i>Rubulavirus</i> | Mumps virus | MuV | NP_054714.1 |
| | | Avian parainfluenza virus type 4 | APMV4 | AFP89384.1 |
| | | Tioman virus | TioV | NP_665871.1 |
| | <i>Avulavirus</i> | Newcastle disease virus | NDV | AFH08721.1 |
| | Unassigned | Fer de Lance virus | FDLV | NP_899661.1 |
| | | J virus | JV | YP_338085.1 |
| Bornaviridae | <i>Bornavirus</i> | Borna disease virus | BDV | NP_042024.2 |
| | | Avian bornavirus | ABV2 | ADU05398.1 |
| Rhabdoviridae | <i>Novirhabdovirus</i> | Infectious hemorrhagic necrosis virus | IHNV | NP_042681.1 |
| | | Viral hemorrhagic septicemia virus | VHSV | NP_049550.1 |
| | <i>Lyssavirus</i> | Rabies virus | RabV | BAL49594.1 |
| | <i>Vesiculovirus</i> | Vesicular stomatitis Indiana virus | VSIV | NP_041716.1 |
| | <i>Ephemerovirus</i> | Bovine ephemeral fever virus | BEFV | NP_065409.1 |
| | <i>Cytorhabdovirus</i> | Lettuce necrotic yellows virus | LNyV | YP_425092.1 |
| Nyamiviridae | | Soybean cyst nematode midway virus1 | SbCNV1 | AEF56729.1 |
| | | Midway virus | MIDMV | YP_002905331.1 |
| | | Nyamanini virus | NYMV | YP_002905337.1 |
| Segmented negative-stranded RNA viruses | | | | |
| | <i>Dichorhabdovirus</i> | Orchid fleck virus (RNA2) | OFV | YP_001294929 |
| | <i>Varicosavirus</i> | Lettuce big-vein associated virus (RNA1) | LBVaV | YP_002308576 |
| | | Mononegavirus L protein-like sequences | | |
| | | <i>Sclerotinia homoeocarpa</i> TSA3-L | ShTSA3-L | JW828891 |
| | | <i>Sclerotinia homoeocarpa</i> TSA2-L | ShTSA2-L | JW826636 |
| | | <i>Sclerotinia homoeocarpa</i> TSA1-L | ShTSA1-L | JU091016 JU091017 |