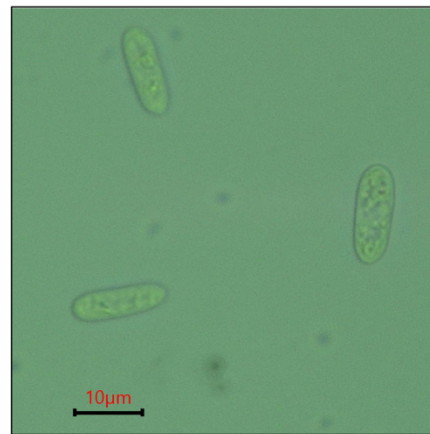


Table S1. List of primers used in this study.

Primer name	Sequences (5'-->3')	Note
ITS1	TCCGTAGGTGAACCTGCGG	ITS region of fungal strain
ITS4	TCCTCCGCTTATTGATATGC	
5RACE_545-P1	TCTATCAAGGTTCCGAGC	5' RACE
5RACE_398-P2	GACTTCTGTGCGATTCCTAAC	
3RACE_2213-P1	CTCAATGGCTTATCTGGTGTT	3' RACE
3RACE_2335-P2	AGACCTTGAGGGAAATGG	
ORF1-357-F	CAAGATTACGGTTGACGATG	RT-PCR of ORF 1
ORF1-866-R	AGTAGTTGGGTTCTCCGCA	
ORF2-1374-F	CGATTAGTCAACAGGATGGTG	RT-PCR of ORF 2
ORF2-2179-R	CACTTCTCTGGCTTGAGCA	

A



B

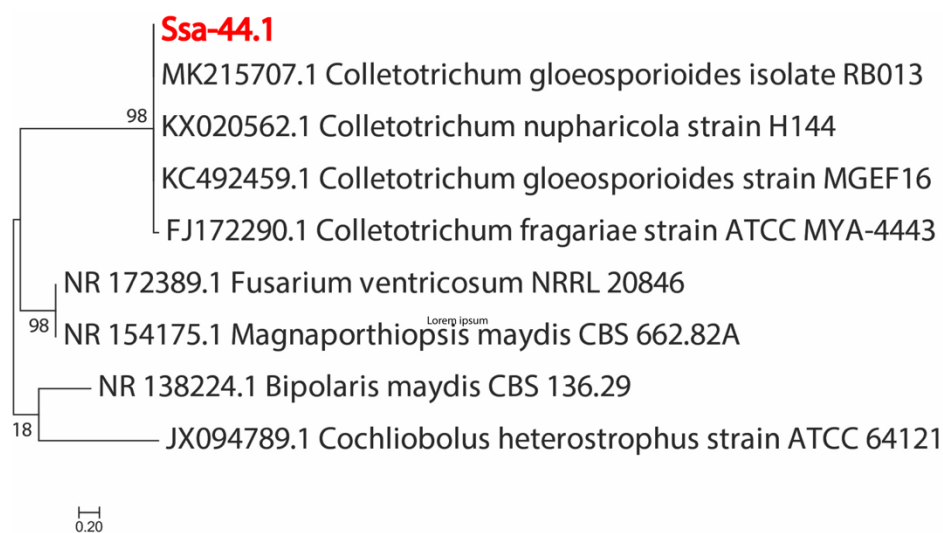


Fig. S1. Conidia morphology and Phylogenetic tree. (A) microscopic views of individual spores of *C. gloeosporioides* strain Ssa-44.1. Spore was observed under light microscope (40X). (B) Phylogenetic tree of isolated phytopathogenic fungal strain Ssa-44.1 and other related species, based on ITS gene partial sequences. Branch length values were shown, the tree was reconstructed using the Maximum Likelihood method and tested by bootstrapping (1,000 replicates). In the phylogenetic tree, strain Ssa-44.1 is represented by a red letter and substitutions per position are displayed by scale bars.

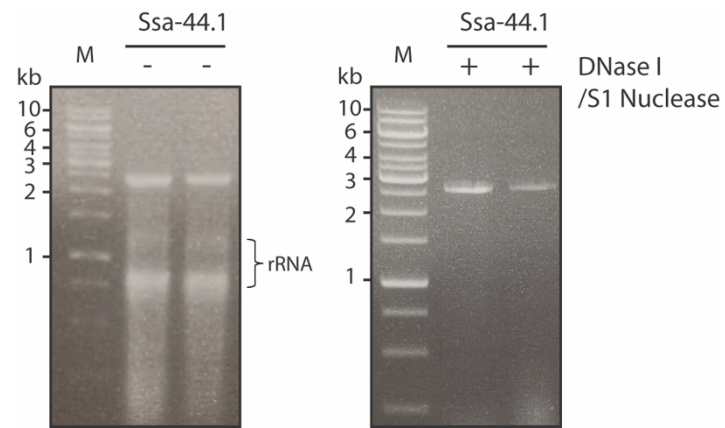


Fig. S2. Analysis of the CgRV1-Ssa-44.1 dsRNA segments. Electrophoretic profiles on a 1% aga-rose gel of dsRNA preparations from total RNA of strain Ssa-44.1 before (–) and after (+) digestion with DNase I and S1 nuclease.

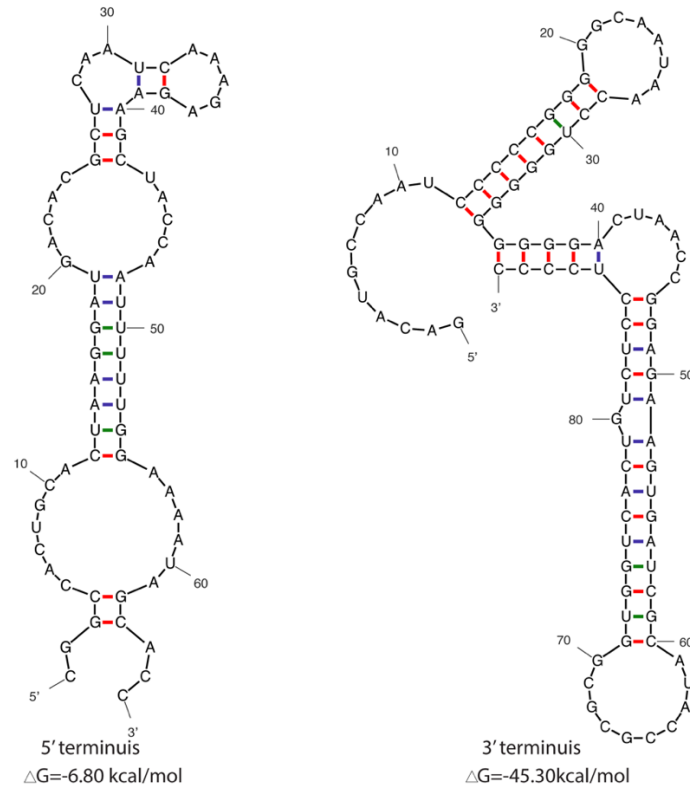


Fig. S3. Predicted secondary structure of the 5'- and 3'-untranslated regions (UTRs) of CgRV2 with a complete genome sequence identified in *C. gloeosporioides*. (A) Predicted secondary structure of the 5'-UTRs. (B) Predicted secondary structure of the 3'-UTRs. The RNAs were folded and the free energy (ΔG) was estimated using the Mfold web server (<http://mfold.rna.albany.edu/?q=mfold/download-mfold>) (accessed on 17 May 2022).

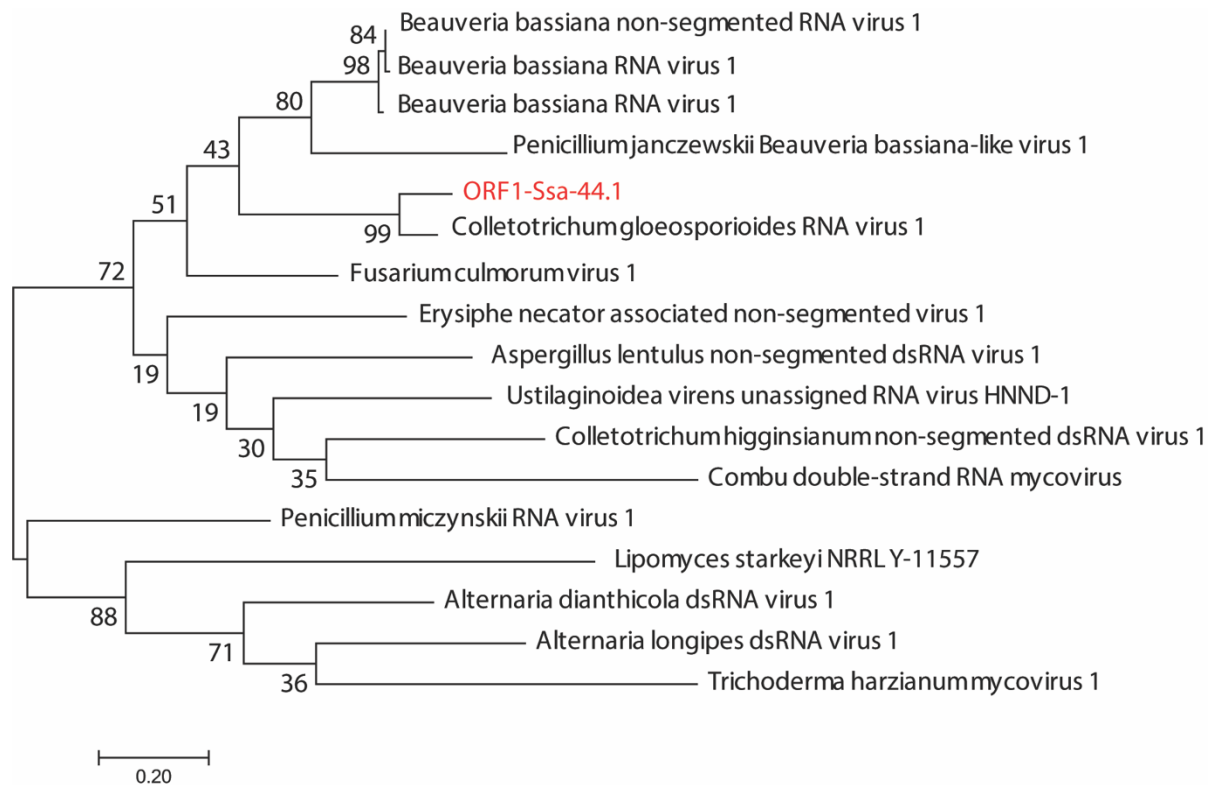


Fig. S4. Phylogenetic analysis of ORF 1 encoded hypothetical protein. The Maximum Likelihood method was used to create a phylogenetic tree based on the alignment of hypothetical protein complete aa sequence along with the previously reported members of other genera. The percentage of trees in which the associated taxa clustered together is shown next to the branches. In the phylogenetic tree, ORF 1 of strain Ssa-44.1 encodes a hypothetical capsid protein is represented by a red letter and genetic distance substitutions are displayed by scale bars.

CGGCCACTGC	ACTAAGGATG	ACACGCTCAA	TCAAAGAGAA	GCTACCAATT	TTTGAAAAAT	60
AGCACCATGG	CCCCCAAACG	AAATGTTGGG	GATTTGGCGG	AAGCTAGCTC	TGGACGAGAT	120
CAGCCCCAGA	GCGCCCCCGG	TACCGCCCAA	AATACCGAGG	GAAGCCAGGC	TGGCACTAGC	180
GCAGAACCGG	CCCCGTGCGG	TAGTCGACGT	CCCGCCTTCA	GGGCCCCAGA	CCCTGAAGAG	240
TCACTCACCC	GTAACGCGTA	CCTAACTGGA	ACGTCTTCGG	GTCACGCAGC	AGCAGTTCTC	300
TATGTCATAA	GAGAATTCCCT	GGCGCAGCAA	GGGGTTACCG	ACCTGCCAGC	AGACCCATCC	360
TCGCTCTTCC	CGCAGGGATG	GAAAGTTGGC	AACACCCCTG	TTCCAGTCCG	CACTACTGGT	420
AACGACTTTC	CTTGGCTGAG	GGATGCCCTA	CCTCATCTAC	ATGGGTATGA	CGCTTCAGGC	480
CAAGAGGTGC	ACTGGATTGG	TGAGGGCAGA	GACATGTCCT	CTGTTGTCCG	TCTCACGGCG	540
AACTGGGATT	CCCCCGTGTC	CATTGTCTCC	TGCATCTTGT	CAGACACCAA	GAATGTCAAG	600
ATTACGGTTG	ACGATGTGTT	AGGAATCGCA	CAGAAAGTCG	CTCAGGCTCT	GGAGAAGCTT	660
AAGGCTTCCG	GGAAGGAGTT	TAAGGCCCAT	CTTCAGCGAT	TTCTCGACCC	GGTGGCGTTG	720
AGACGGAGCC	CCGAGTTTAA	TAGAGTCTCT	GCCGAGTACA	AGGCTAAGCT	CCGAACCTTG	780
ATTGATGCAC	AGCAGAAGGC	CATCATGGCC	GCTCGCCAGG	CGACAGCCGC	CGTCAACAAG	840
TGCCTTGGAG	AGAGGGATGA	TGCCTTATCG	TCCCCTTGATC	CTGGCTACGT	CGCTAAGCGA	900
GCCACCGCAC	GTAACGCATC	AGCTGCTTAC	GGCATTGATC	TCGGTGAAGA	TGCTGAGATG	960
GCAGATGCTG	AGGAGACTGC	GGCGCAGGCT	CCTCAGGACT	TGGATTTTTA	GTTTCCGCGG	1020
CCTCGATGCT	CGGCGGCGCG	GAGTTGGGTG	TAAGCGACAT	TAATGAGGAT	GTAATGGTCG	1080
ATTGGATTGC	GGAGAACCCA	ACTACTATGT	CGGAGGCTAG	CGGGAAGGGG	ACTAAGGATT	1140
GGCGTTATTT	TGTTTCGAAT	AAGCACTGGC	AGCGCCAGAT	TCCAGGAGTT	CAGGTTGTTG	1200
GATTTTCACC	GGCCGTCAGG	TATCGCTATG	TTACACCTGA	GACATCGGAT	TCCTGGTACT	1260
TTTCGTGCTT	TCTTGATGAG	AGCGGGATTG	AGCTGGGTGG	CATTGAAGGC	CCTGCCGCGG	1320
AGGTTATTAT	GTCAGAGTTC	GTTCCACCGT	CCCAAGAGGA	TCTTTATCAA	CACATTGCCG	1380
GCTTTGGGGC	CCCCGGTCTT	GACGGGTAC	ACCTATCGAC	TTACGATATC	GCGCGAGTCC	1440
TTAAGGACTT	ACATCGTGTC	GAAAGTTGGG	GTCTTCAGAT	CGAGGGCCTC	CTAGACGTGC	1500
AGCGTTTGCC	AAAGATAAAG	GTTCTTTCAC	GTACCAGTCC	TGGGATAAAG	TGGAAGCGTC	1560
TCGGCTATAA	GACCAAACGT	AGCGCCCTGG	TTCAGGCCGT	GGTCGAATCA	ACGCGATTAG	1620
TCAACAGGAT	GGTGGAGGAG	GGTCAGGAGT	ATGACGTCCC	CCCGTGTGGC	GTCGCCGGGA	1680
GGGGGAAGAG	GGTCGATATT	AATCGTGACT	TGACCGCGTC	CGACCGCAAG	GAGGGCAGAC	1740
TGATTGTCAT	GCCTGATCTA	GTGCGCCACT	TAATCGGCTC	GCTTGGATCA	TCCCCTTATA	1800
TGGCGAGATT	AAGGAACCTC	GATCACTCTC	TCGGTGGCGT	CCTCTTGGGC	ATGGGCCCAT	1860
TTCAAGAGCA	GTATCAGAGT	ATTGCTGAAT	GGGCTTCCGG	AGCGAACCAT	TTCTTGTTCA	1920
TCGATTTCAA	GAAGTTTGAT	CAGCGCATTC	CCCGCAGACT	TCTACAAGTA	GTCATGAAGT	1980
ATATTGCAGG	AAGGTTTACA	GCCGGCCCCG	GAACGCGAGC	GTATTGGAAG	TCTGAGTTTC	2040
GCCACCTGGT	CGAAACTGAG	ATCGCGATGC	CGGATGGATG	CGTGTACAAG	AAGAAGAGGG	2100
GCGTCGCCTC	CGGTGACCCA	TGGACTTCCC	TAGCGGACTC	ATATGCCAAT	TATATAATCC	2160
TCAAGATGGC	ATGTGATAAG	CTGGGGCTCA	AGGTTAAGAT	TTGGACGTTT	GGGGATGATA	2220
GCGTTTGTGC	TGTATGGGAT	TGGAAGTCCC	AGTACGACTT	GTTGGCTGAG	GTTTCGAGGA	2280
TTGCATGGGA	CATGTGGGGG	ATGGTAACCTA	GTAAGAAAAA	GAGCTACTCT	AGCTCACATC	2340
TAGTGGACAT	CGCAGAGAAT	CCCGAACCAC	GTAAGGGGGG	TTCTTTTCTG	TCGATGTATT	2400
TCCTACAAAC	AGAAATGGGG	GTTCGGCCGA	CTAGGCCCTT	CCAGGACATG	TATGAGCTCA	2460
TGCTCAAGCC	AGAGAAGTGC	AGAAACTCGC	TGGAGTGGGA	GGTCGTACGA	ACCTCAATGG	2520
CTTATCTGGT	GTCTACTTAC	AATAGCGACG	CCAGATTTCG	CCTTGAGGAG	TATTGGACCT	2580
GGCTCCACCG	CAAGTTTCAA	ATTCCCAGT	TGACTGGCAC	GGCAGAAGAC	TTGGAGACCT	2640
TGAGGGAAAT	GGACATTCCA	TGGTCCTCCT	TCAAGATGGA	ATGGCTGAAT	CGCCTACCTT	2700
TCAGTGGCGA	GGTAGAGCTG	ATGTATAAAT	ATGGCCACAC	AAAGTTCTTC	GCTCCTGTTT	2760
TGTGGGCAAC	GTGGTATCAT	GGAGACGGGG	ATGTGTTGGG	CAACCACCTC	GTTAATGATC	2820
CACGCCTGTA	CGTAGACCCA	CCAGATTAGG	ACATGCCAAT	CCCCCGGGGG	CAATAACCTG	2880
GGGGGGGGAC	TAACCGGAGA	AGTGATCGCA	TACCGCGCGG	TGGTCACTGT	CTCCTCCCC	2939

Fig. S5. Whole genome sequences of CgRV1-Ssa-44.1.

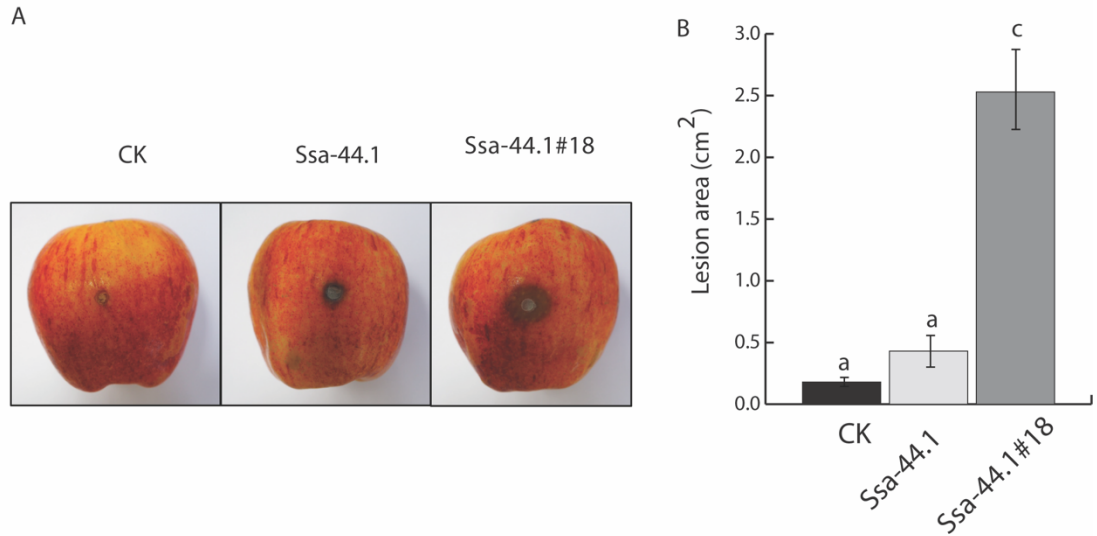


Fig. S6. Virulence assay of virus-infected and virus-free *C. gloeosporioides* on apple. (A) The images illustrate representative lesions elicited by the fungal strains 7 days after apple inoculation. (B) Graphical representation of lesion areas on apple measured in the experiment described in (A). The data from 5 replicates are means \pm SD with different letters are significantly different ($p < 0.05$) among treatments using one way ANOVA analysis. Control variable (CK) was inoculated with PDA (agar plugs) only.