# Supplementary Materials: Molecular Characterization of a Trisegmented Mycovirus from the Plant Pathogenic Fungus *Colletotrichum gloeosporioides*

**Jie Zhong, Xi Dan Pang, Hong Jian Zhu, Bi Da Gao, Wen Kun Huang, and Qian Zhou**

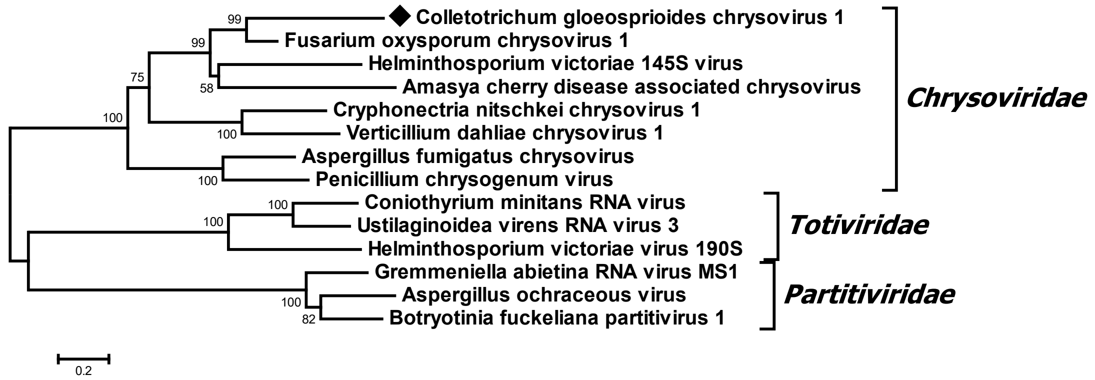

**Figure S1.** Phylogenetic analysis of the viral capsid protein (CP) amino acid sequences of Colletotrichum gloeosprioides chrysovirus 1 (CgCV1). The phylogenetic tree was generated using the neighbor-joining method in MEGA6 [24] (with a 1000-replicate bootstrap search). The values on the nodes refer to the percentage of bootstrap replicates supporting the branch. Respective GenBank accession numbers of these analyzed viruses are shown as follows: Amasya cherry disease-associated chrysovirus (YP_001531162.1), Aspergillus fumigatus chrysovirus (CAX48751.2), Aspergillus ochraceous virus (ABV30676.1), Botryotinia fuckeliana partitivirus 1 (CAM33267.1), Coniothyrium minitans RNA virus (YP_392466.1), Cryphonectria nitschkei chrysovirus 1 (ACT79252.1), Fusarium oxysporum chrysovirus 1 (ABQ58816.1), Gremmeniella abietina RNA virus MS1 (NP_659028.1), Helminthosporium victoriae 145S virus (YP_052859.1), Helminthosporium victoriae virus 190S (NP_619669.2), Penicillium chrysogenum virus (YP_392483.1), Raphanus sativas chrysovirus 1 (AFE83591.1), Ustilaginoidea virens RNA virus 3 (YP_009004155.1), and Verticillium dahliae chrysovirus 1 (ADG21214.1).

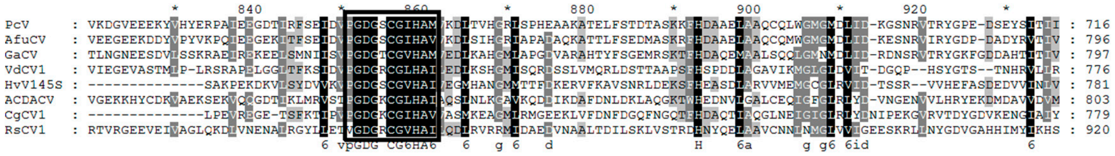

**Figure S2.** Multiple alignment of the amino acid sequences in the C-terminal region between the dsRNA3 of CgCV1 and other comparable regions of similar chrysoviruses. The alignment was made using CLUSTAL X [23]. The conserved motif is indicated by the black box. The full names and GenBank accession numbers of these viruses are listed as follows: PcV, Penicillium chrysogenum virus (FN178515); AfuCV, Aspergillus fumigatus chrysovirus (FN178515); GaCV, Grapevine chrysovirus (AFX73020.1); VdCV1, Verticillium dahliae chrysovirus 1 (HM004070); HvV145S, Helminothosporium victoriae 145S virus (NC005980); ACDACV, Amasya cherry disease-associated chrysovirus (AJ781164); and RsCV1, Raphanus sativas chrysovirus 1 (AFE83592.1).

**Table S1.** CgCV1-like sequences in the NCBI database.

| Database | Species | Contig/Singleton | dsRNA1 | | | dsRNA2 | | | dsRNA3 | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | | | **Coverage (%)** | **Identity (%)** | **E-Value** | **Coverage (%)** | **Identity (%)** | **E-Value** | **Coverage (%)** | **Identity (%)** | **E-value** |
| TSA | *Noccaea caerulescens* | isotig06317_isogroup02885 (GASZ01006339.1) | 67 | 37 | $7 \times 10^{-155}$ | | | | | | |
| | *Noccaea caerulescens* | Nc_isotig05844_isogroup02412 (GASZ01005866.1) | | | | 53 | 26 | $1 \times 10^{-44}$ | | | |
| | *Noccaea caerulescens* | Nc_isotig05933_isogroup02501 (GASZ01005955.1) | | | | | | | 57 | 30 | $7 \times 10^{-47}$ |
| | *Camellia taliensis* | CtaTrans37938 (GCRZ01034361.1) | 65 | 29 | $7 \times 10^{-83}$ | | | | | | |
| | *Camellia taliensis* | CtaTrans13937 (GCRZ01012637.1) | 19 | 28 | $2 \times 10^{-15}$ | | | | | | |
| | *Camellia taliensis* | CtaTrans29091 (GCRZ01026355.1) | | | | | | | 38 | 27 | $5 \times 10^{-10}$ |
| | *Artemisia annua* | Artemis Contig26286 (EZ166880.1) | | | | | | | 73 | 25 | $4 \times 10^{-39}$ |
| | *Artemisia annua* | Artemis Contig6582. Aml (EZ193025.1) | | | | | | | 59 | 25 | $2 \times 10^{-25}$ |
| | *Artemisia annua* | Artemis Contig3687. Aylt (EZ206676.1) | | | | | | | 47 | 25 | $8 \times 10^{-24}$ |
| | *Artemisia annua* | Madagascar Contig12667. Blt (EZ326121.1) | | | | | | | 57 | 24 | $2 \times 10^{-23}$ |
| | *Artemisia annua* | Madagascar Contig9777. Mt (EZ283390.1) | | | | 8 | 33 | $1 \times 10^{-4}$ | | | |
| | *Artemisia annua* | Artemis Contig7017. Aylt (EZ210006.1) | | | | 6 | 36 | $4 \times 10^{-4}$ | | | |
| | *Artemisia annua* | Artemis Contig11776. Aml (EZ198219.1) | | | | 16 | 27 | $6 \times 10^{-10}$ | | | |
| | *Artemisia annua* | Artemis Contig24510 (EZ165104.1) | | | | 9 | 35 | $6 \times 10^{-7}$ | | | |
| | *Artemisia annua* | Uganda Contig20290 (EZ403795.1) | | | | 7 | 35 | $7 \times 10^{-7}$ | | | |
| | *Artemisia annua* | ArtemisContig3870. Aml (EZ190313.1) | 39 | 43 | $6 \times 10^{-11}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig25044 (EZ165638.1) | 23 | 50 | $6 \times 10^{-71}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig4906. Aylt (EZ207895.1) | 22 | 36 | $2 \times 10^{-41}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig4484. Amlt (EZ237814.1) | 16 | 43 | $8 \times 10^{-38}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig24942 (EZ165536.1) | 17 | 36 | $1 \times 10^{-34}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig 9161. Aml (EZ195604.1) | 18 | 37 | $1 \times 10^{-28}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig7563. Aylt (EZ210552.1) | 18 | 37 | $4 \times 10^{-28}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig1636. Amlt (EZ234966.1) | 18 | 36 | $5 \times 10^{-27}$ | | | | | | |
| | *Artemisia annua* | Uganda Contig17865 (EZ401370.1) | 9 | 52 | $1 \times 10^{-25}$ | | | | | | |
| | *Artemisia annua* | Contig1233. Amlt (EZ234563.1) | 16 | 37 | $2 \times 10^{-24}$ | | | | | | |
| | *Artemisia annua* | Contig1198. Amlt (EZ234528.1) | 7 | 58 | $1 \times 10^{-22}$ | | | | | | |
| | *Artemisia annua* | Contig2871. Aml (EZ189314.1) | 15 | 33 | $1 \times 10^{-22}$ | | | | | | |
| | *Artemisia annua* | Madagascar Contig18240. Mt (EZ29185 3.1) | 10 | 42 | $2 \times 10^{-20}$ | | | | | | |
| | *Artemisia annua* | Uganda Contig5658. Uht (EZ358497.1) | 7 | 49 | $5 \times 10^{-19}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig10169 (EZ150763.1) | 14 | 31 | $9 \times 10^{-19}$ | | | | | | |
| | *Artemisia annua* | Madagascar Contig6103 (EZ263000.1) | 5 | 63 | $7 \times 10^{-18}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig6641 (EZ147235.1) | 10 | 44 | $3 \times 10^{-17}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig6413. Aylt (EZ209402.1) | 6 | 54 | $5 \times 10^{-17}$ | | | | | | |
| | *Artemisia annua* | MadagascarContig19552. Mt (EZ293165.1) | 12 | 35 | $1 \times 10^{-15}$ | | | | | | |
| | *Artemisia annua* | Contig7536 (EZ148130.1) | 15 | 31 | $2 \times 10^{-14}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig5462. Amlt (EZ238792.1) | 10 | 32 | $1 \times 10^{-13}$ | | | | | | |
| | *Artemisia annua* | Uganda Contig21105 (EZ404610.1) | 12 | 36 | $1 \times 10^{-12}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig2500. Ac (EZ179024.1) | 11 | 32 | $3 \times 10^{-12}$ | | | | | | |

| | | | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|
| | *Artemisia annua* | Artemis Contig947. Ac (EZ177471.1) | 6 | 55 | $5 \times 10^{-12}$ | | | | | | |
| | *Artemisia annua* | Madagascar Contig7630. Mt (EZ281243.1) | 9 | 34 | $7 \times 10^{-11}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig6864. Aylt (EZ209853.1) | 5 | 48 | $4 \times 10^{-10}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig1606. Amlt (EZ234936.1) | 10 | 32 | $1 \times 10^{-7}$ | | | | | | |
| | *Artemisia annua* | Uganda Contig3311. Ulm (EZ369860.1) | 7 | 37 | $2 \times 10^{-7}$ | | | | | | |
| | *Artemisia annua* | Uganda Contig2972. Ulm (EZ369521.1) | 6 | 42 | $4 \times 10^{-7}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig1982. Aylt (EZ204971.1) | 7 | 36 | $1 \times 10^{-6}$ | | | | | | |
| | *Artemisia annua* | Artemis Contig1184 (EZ141778.1) | 5 | 40 | $2 \times 10^{-6}$ | | | | | | |
| | *Allium fistulosum* | contig: AFU_22548 (FX576273.1) | 17 | 31 | $1 \times 10^{-21}$ | | | | | | |
| | *Allium fistulosum* | contig: AFU_01016 (FX554741.1) | | | | 52 | 26 | $5 \times 10^{-38}$ | | | |
| | *Allium fistulosum* | contig: AFU_00430 (FX554155.1) | | | | | | | 48 | 31 | $2 \times 10^{-43}$ |
| | *Bemisia tabaci* | comp13683_c0_seq1 (GARP01025880.1) | 39 | 21 | $3 \times 10^{-5}$ | | | | | | |
| | *Caligus rogercresseyi* | tsa-crog-ngs-11124173 (GAZX01040384.1) | 47 | 23 | $2 \times 10^{-10}$ | | | | | | |
| | *Caligus rogercresseyi* | tsa-crog-ngs-11124172 (GAZX01040383.1) | 47 | 23 | $2 \times 10^{-10}$ | | | | | | |
| | *Caligus rogercresseyi* | tsa-crog-ngs-11124002 (GAZX01040226.1) | 45 | 23 | $3 \times 10^{-8}$ | | | | | | |
| | *Humulus lupulus var* | contig: comp13164 2_c0_seq1 (LA332420.1) | 27 | 26 | $3 \times 10^{-10}$ | | | | | | |
| | *Grylloblatta bifratrilecta* | s13623_L_120298_0 (GAWP01013600.1) | 15 | 31 | $4 \times 10^{-10}$ | | | | | | |
| | *Grylloblatta bifratrilecta* | s17247_L_150202_0 (GAWP01017218.1) | 32 | 24 | $2 \times 10^{-7}$ | | | | | | |
| | *Grylloblatta bifratrilecta* | s7948_L_90492_0 (GAWP01007931.1) | 14 | 30 | $4 \times 10^{-8}$ | | | | | | |
| | *Phakopsora pachyrhizi* | Thai1Pp_contig01637 (GACM01002541.1) | 25 | 24 | $1 \times 10^{-7}$ | | | | | | |
| | *Phakopsora pachyrhizi* | Thai1Pp_contig04037 (GACM01003506.) | 28 | 25 | $4 \times 10^{-6}$ | | | | | | |
| | *Uromyces appendiculatus* | Ua_contig01686 (GACI01004215.1) | 19 | 28 | $9 \times 10^{-7}$ | | | | | | |
| | *Teleopsis dalmanni* | Td_comp6756_c0_seq1 (GBBP01176362.1) | 20 | 26 | $1 \times 10^{-6}$ | | | | | | |
| | *Lepeophtheirus salmonis* | lsal-pac-6261972 (JP332015.1) | 18 | 25 | $7 \times 10^{-6}$ | | | | | | |
| | *Mengenilla moldrzyki* | contig03151 (JP089782.1) | 27 | 22 | $8 \times 10^{-06}$ | | | | | | |
| | *Acanthosoma haemorrhoidale* | C369386 (GAUV01086077.1) | 6 | 38 | $1 \times 10^{-5}$ | | | | | | |
| | *Vigna radiata* | Vr16063_c0 (GBXO01026945.1) | | | | 21 | 33 | $8 \times 10^{-18}$ | | | |
| | *Colobanthus quitensis* | Colobanthus_quitensis_contig_31970_1 (GCIB01032448.1) | | | | 18 | 30 | $8 \times 10^{-12}$ | | | |
| EST | *Zinnia violacea* | AU307126 cDNA cloneZ16843 (AU307126.1) | 16 | 49 | $4 \times 10^{-45}$ | | | | | | |
| | *Zinnia violacea* | FM881064 SSHSTS0 cDNA clone SSHSTS0 6xxxA02F2 (FM881064.1) | | | | | | | 12 | 31 | $5 \times 10^{-5}$ |
| | *Zinnia violacea* | FM881063 SSHSTS0 cDNA clone SSHSTS06 xxxA02F1 (FM881063.1) | | | | | | | 12 | 31 | $5 \times 10^{-5}$ |
| | *Zinnia violacea* | AU307096 cDNA clone Z16810 (AU 307096.1) | | | | | | | 28 | 23 | $2 \times 10^{-8}$ |
| | *Dactylis glomerata* | BG04060A1C03.f1 BG04- primary and normalized libraries (HO148595.1) | 11 | 46 | $1 \times 10^{-30}$ | | | | | | |
| | *Dactylis glomerata* | BG04058A1B02.r1 BG04-cDNA (HO1476 84.1) | | | | | | | 16 | 29 | $2 \times 10^{-7}$ |
| | *Lepeophtheirus salmonis* | EST_lsal_af_785797 lsalaf whole Lepeophtheirus salmonis (Pacific) cDNA clone lsal_af_1_85_rev 5′ | 18 | 25 | $5 \times 10^{-6}$ | | | | | | |
| | *Artemisia annua* | CATA453.fwd CATA A Tanzanian, cDNA cloneCATA453 5′ (EY047151.1) | | | | | | | 17 | 29 | $2 \times 10^{-6}$ |

| | | | | | |
|---|---|---|---|---|---|
| NR | *Solanum tuberosum* | Solanum tuberosum uncharacterized LOC102579694 (LOC102579694) (XM_006340898.1) | 73 | 24 | $5 \times 10^{-37}$ |
| | *Medicago truncatula* | Medicago truncatula hypothetical protein (MTR_5g084970) (XM_003616807.1) | 63 | 25 | $5 \times 10^{-28}$ |
| | *Medicago truncatula* | Medicago truncatula chromosome 5 clone mth2-75o19 (CT573055.2) | 66 | 25 | $9 \times 10^{-27}$ |
| | *Medicago truncatula* | Medicago truncatula chromosome 5 clone mte1-85h10 (CR936947.2) | 66 | 25 | $9 \times 10^{-27}$ |
| | *Medicago truncatula* | Medicago truncatula hypothetical protein (MTR_5g084940) (XM_003616804.1) | 48 | 24 | $2 \times 10^{-19}$ |
| | *Trifolium pratense* | Trifolium pratense genome assembly redclover, chromos ome:chr4 (LN846352.1) | 39 | 28 | $1 \times 10^{-21}$ |
| HTGS | *Solanum tuberosum* | Solanum tuberosum strain Diploid genotype RH89-039-16 chromosome 9 clone RH204J10, (AC239340.1) | 73 | 24 | $2 \times 10^{-37}$ |
| chromosome | *Solanum tuberosum* | Solanum tuberosum cultivar DM 1-3 516 R44 unplaced genomic scaffold, SolTub_3.0 scf00020, whole genome shotgun sequence (NW_006238946.1) | 73 | 24 | $3 \times 10^{-36}$ |
| | *Medicago truncatula* | Medicago truncatula chromosome 5 (NC_016411.1) | 66 | 25 | $3 \times 10^{-26}$ |

Note: these similar sequences were collected by tBLASTn searches against the NCBI databases including nucleotide collection [nr/nt], high-throughput genomic sequences [HTGS], non-human, non-mouse expressed sequence tags [EST], and transcriptome shotgun assembly [TSA].

**Genome sequences of Colletotrichum gloeosprioides chrysovirus 1 (CgCV1):**

>dsRNA1
TGATAAAAATAGAAATTAATATTTTCGTTTTTATCCTAGTGAAGTTGCCACGTTAAACAACTCT
GAACAAAATGTCGGGACGAATGACTAGAATGAGTCAAACTTCAAAGAAGAAAGTGGAGCA
AGCAGCGGCAAATATACAAGCGAGAGTGCAGTATTTTGGATCTGACAAAGGTAGGATAGAC
TTTACTGCTGAAGTTCTGTCTTCGATGGAAAGATACGAAAAGAGGAGGAGAGATAACTTCTT
TGCGATCGTTATGCCGTCAGGTTCTGGTAAAACTCAACTTTGTGACAAGTATGGATTTATCGA
CGTTGACAGATTGTGCACAATAGCGGAACACGAGTACCTGAATGACCTAAGGCTGGATGCT
ATCAACGGGAAAGATACCTGGGATGAGCACAACAAAGTGTGGTTCGAGTTGTTGAACGAA
ACTCTGGACCTGATGGAGTTCAAGGAGGACACGGTTATCATGGTGCAGAGTGAGGTAATAG
CGTTGGGCATAGGGGCACTGCCTCTGGCTGGGTTCATCTTAGATGATAAGACATATCAGATG
GTGTATAACCAGAAAGTCGAAAGAGGGAATAGAGCAGGTGCTCTGCTAATGGCTGAGAAC
AGAGCCCAGTTTCTGAGCAACACGAACATAGTGATGAAAACAAAGAAGATGGTGAGAGGA
TTTGAGATGATGGAAGCAAAGGTGATAGAGACTCTGAATGTGAATGAAATACCATGCGCTTG
CCCGCTAAAATTCTCATTGCGATATCCGGGATACGGTTACGGCCCTTCTGTTCCTGATTGGGTT
ACGAAAGGGGAGCGAAAGTACATGAATGTTGTGGAATTGTTGGACCTGCATAGGTCAGGGA
TGGTGCCCAAACAGTGCATGGATTACTTCATGAGGGACCCAGAAATTCCTGCTTCTTACGGA
TTCGGCGTGAGAGACAATGAGTGGTCACAGTTCTTCGCAAACATGAGGGCTTCTATTGGCTC
ACCTCAGAACTTCGACCCAAGGGATGATCTGGGGAAGGTGTTCCCATACAAATACGAAAAG
AACTTGACGAGGGCGAACATGACAGTGAGTAGATTACAGAAAGGCATGGAACTGCTTGAC
GATGAGGAGGCTTATGAGATAGCGTCACATCATGTGGGCAAGCCAAACAATTTTGTGACAG
CAATATTGTGTTACTGGCAAGGGGCAGGTAGATTCTCAAAGTTCAGAGAGTTCATCAAGAA
GGCAATGTGTGTAAACTTTAGATTCTGGGGACAGGTGTTCAAAGAGTTCCACAATTTAATAA
GAGTATCAGACTATTTCTTTGGAGAAAAAGTGRGCGAAGAGGAAAGGCATAGAATGATGTA
CTTCGACCAGATGTTGGGGAAGGAAGTGGAGGATGCGGACTGGAAGCAGGAGATTGAGGA
TAGAACTTGGGCATATGAATTGCCAGACCACAAGTCTTACAACGATGATATACAAATGTGGA
CACAAGAACAATACATGGTCGATTTCGACAGAGCACTATCTTTTGCGTATTCTAGGCTGGGA
AATAGGTGGAATGCGGAAGTGAGATCGTTTGCTGACTTCTACGAAAGGAGAGGGTCTTGGC
TAACAAAGGGGAGTACGGTGTTCACACAATTGGATAGCACAATGCGGAAGTACACAATAGA
CTTAATCAATGAGGTGGGCGAGATAGTGGACAAACTGACAGCCAGGCACAACAAGAAGTC
GCTGTTCGAAGTGATGCATGCCATACCAGAATTGGGTGCAGACTTTGAATTGTTCAACGCGA
CCAAGATTGTTACCAAGTTGGACGAAAACGGTCACAAGAAAAGGGCCCTCTTACCGGGCA
CGCTGATGCACTACCTGGTGTTTTCATATGTGTTGTTTTTTGTGGAGTCCGATGCTCAAATAGG
GTCGGTGAGGTTGAATGCACCACCTGATGATGACTGGGTATATTTCGAGCAAAAGCTGGCTG
CAATTCCCAGATTGCTATTCGACTGGTCCAACTTCAATCTGTACCACTCAACCTGGGAAATG
GAGAGGGTGATAAAGAAATTGGAGGGCAGTGTTTATGCACCTGAGGATTATGGTGTATTTGT
GACTGCGATAGCGGAGGCTATGCACCACATGGTGATAATAGATCCTGAAGGGCAGAGGCAT
AAGGCAGGGAGAGGGTTGTACTCGGGTTGGAGAGGAACAACTTTCATCAACACTGTGCTAA
ATGAGGTGTACACCCAATGTGCAGAGATGAGTTTTCAGAGATTGTTCGGAAGGGAGGCCTA
CCGATATAAAGATGGCGGTGGCGACGATCACGACGGTGGGTTGAACAGAGCAGACGATGG
GTACAGGATGTTGGCAATAATGAGGAAAATGAATTTCAAATCAAATTCCATAAAGCAGATGG
TTGCAATGAAAAGTGAGTTCTTTAGAAACACTGTGACATCGACAGGTGCTTACGCTAGTCCA
ATTAGGGCTCTAGTAACATTTGTGAATGGTAGGTGGGAAGGAACAGGACAGGTGCCGATAG
CCGAGAGAGTAGGAGCGATATTGGATCAAGTTGCGAAGGTACAAAGAAGAGGGGTGGACG
CACACTTCTGCAATACAATGGCAGTGTTGTCTCTTAGTCACTGGTGCAAGGTGAACGAGGAC
GGCGAGTKGTTAGACTTGCCCGGTTATGTAATACATGGCCATCCGGATGACGGAGGCTTTGG
AGTACCGGATAACATGGGACTGGTCTGGAGACTGAGGGACAGGGTGCCTGAGCCTAAGGTG
ATTGGGGAAGCGAGAGAAGTGCCGGGAACATTGGCAACTAGGGATTGGTTGTCAGTGCTTT
GCAGAGAAGTGAGGTCTTTGAACATTGATGTGGACATAGATGAAAAGAAAGTGATAGATAC
AGCGAAAAGCTCATTCGAGGCTTACAGTAGGTATGATTATACAGAAGTGTTGAAGTTCAGAA
CAGAAATAGTGGGCAAGGCGCCGGCTGTGGAACCTCGAAACAACGAGTCGGCCTGGGAAT

TCATGGTGGAATTCATGGCAATAGAAAAACACGATCTTAAAATTGGCAAACTC
ATGAGGTACCAGGAATTGATACCTTATATGACAGTTGGCGGAAAACCGATGACAAGACAGC
AACTGGGCGAAGCTATGGAGTTGGGTGTGAATACAGAAGTCGTAGACTTCAAAGGAGACGT
GTATTATAGGAGACTGATATCAGAGCCATTAGCAAAGGTAGTAACTGAGTTCTGCATGGAAG
CAATAGCCAGGGAGATATATAGTCTAAAAGAAGGCGAAGAAACCTTCAAAGATCTGTGTTT
CATGATGTTCATGAACACAGAGTTCAAGATCTAAGTGCGGGGACTAGATCG
AGAACGGTGAGAAAATCACGCTATTCGGGCGTAGATTAGCGC

>dsRNA2

TGATAAAAATAGAAGTTCAATTCTAATTTTTATCCTAGTGAAGTTGCCACGTTAAACAACTCT
GAGACAAAATGGACAAGTGGAATCCGAAGAAGTATCAAAAAGTGGAGGAGACTTTCCAGC
TGCTAAGGTCGAGATCTCGATATGTGCAGCAGTTGCAAAAGGATGAAAAAGAGAAGAGAG
TGTGGAATCCATCTCGCTATGACAATTCAAAGGATTACGCAGGAGGAAGAGGATCTATAGGC
CAGGTGATATCGCACATGCAAGACTACTTGTCAAAGTATAGTGTTGGCGCTATGGAAGTGCT
GTCTGAGGAGAACATAGATGTGTGGTATATGATAATGGGTGATCTTGAAAGAAAAGCGAATC
TGGGAGAAAACACATGTGGCATAAGAGCGGATTTCGAGTGGACACAGATGGCGTGCAGTGT
GGTGACGCACGCCGGGCAGAACACTGAATTGGCATTTAGTGCGACGACAGCTGAGGTGATA
AACAAAAACATGAATGACAGGGCGAAGATACAAAAAGCAACGGGATTTGAGATGCCAGAC
GTCCACAATATGAGGAGTGGAGATGCCGAAGATTTGAAGCGGTTGATACTTGCAGCTGCCG
GAGGTCAAAACAAATTCACGAGACTTGTGAAGGGTATGAGTCTGTATATAGATATGCTAATA
TATGGGAACCAAAGGTTTGAAGGCCAGATCAAGAACKCTGCCGAATACAATCTGCAGAACG
TTCTAGCTGCATTTAGGGCCAAGGACAGATCGCATTCATATTGCTCAACCGAACATTCTGACC
CGTACTTCGTGTTGATGTACTTGATAGGGCTGGAGTACCCTTTCAATGGGAACAACATGAAG
TGCAGAGGCGCCACGAGGATTCCAGCCGATGCTGATGACCATTGGGTAATGGTACGCGGGA
CTCCTAACAAATCGGAGTTAAAGACTGGTCTGACCGCTAATGCGGTGTGGGCGGGTATGGTG
AGCTACGCATCAGAAATGGAGGTGTCTGATCAGCTAAGCAGTGCACTCATTGTAGCGGCTAG
CCTATACCAGAATCGATACCTGAGGGAAGTGTCTTTACCCAAGGTTGGAAGTACAATTGACA
TAATAAGGCCGGCGTTCCATGAAGTTAGCACTGACGATGCARAGAAACCTTATCTTGACGCG
AGCGCAGTAGTAGCGTTGGGTAGGGTTCATCAGTTGAATTGTTTCTTAGTGGCAAAGGATCT
AATAGTGTCAGCGCAACATTCAAGTGAGAATGGGCTGAACTACGAGGAGGTGGTGATGCAG
TACTTGAAGCAGGATGAAACTGTTATGAGTAGGATGGCTGAATGGTCATCAGGATTATCGCY
GCWAGRSSCCACGAAGCAGATGAGGTGGATGGGGTGTCTTGACAGAGAAGATATACAGGAT
CTGAGTGCTATATCAATCTTTGAAGCACTATGGCTGTGTGATTCCACAACAAAGAGTGTAGA
GAGAGGAGCCATTGACTGTCTGGTGAGGGGAAGGAAAGACATGATGCCGAGGAACGGATA
TATTGAGCTGTTGGACGAAGAAATGCGCAAATTTGGAGTGCGACTTGACAGGTCCAGGATA
CCATCTGGGGCCTTCTCAGTGCAACGAAGGAGTATATGCTCAATGAACAGGTGGGCTCCTAA
GAAAAAGAAATGGGTTGAGAGTGATAGCAGCATGGTACAGCCTTGTGACTACGGTAAGTCA
GGTAAGAAGGAGGAGGTGAGAAGAAAAAGATTTTCTGTTAACCCACAGTCAGGCGACCAC
GTTTGGGAAGTGCACTACAAGGCCTATGCAGAAAGAAAAGCGAAGGAAAGGACACCTACA
CCTTCTAGTTCGGATGTGGATGAAAGTCCAAAAAGGAGGTCTTTTGATGGGAAAAAGATTGT
AGGGCTAGAGTTGCCACGCTTTCCTGGCCAGGTAGAGAGGAATGTGACTATGGTTGAGGTA
AGAAGTAGTAAATTGGGAGCTTCGGAGTACGGTGAAATAAGTGACGCTGGGTCATCAGAAG
TTGAGAGGATAGAGGCAGAGAAGCAAATGTTCGAGGAAGAGGAAGCACAACAGGAAGTA
GAATTGGTGCAGATAGACAACGATGGAGCATTCGGAGAAGTGTTGAGAAAGAAGGGCAGC
AAACAGAAGAAGAAAGTGAGTTACGCAGAATTCATGAAAGAAGAGAATCCAATTAATGAT
GAGCAGCAGGCAATACACGAAGGGAAGGAATACCACGGGGTAATAGATTGGTCATGGGAC
CCAGACACATTGTGGAGGATAAGGAACAGCAAGTCGGTAGGTGAGTTCTTAGATGATAAGG
GCCTAAGCAGAGGGAGCACGATTCTTGGGCTCTCAAGAGAAGAATTCTTCGGAGAGGCAGT
TAGGCACAGTCTGATAATGAAGCACCTAGATGTTACGATAGTGACATTTAAGGAGAGTATGA
CTAGAGTGCCTATGTATGCACTAGAAATGGCATTCGTGTCAGAAGTGGTATTCGGACTGAAC
GCCAGAGAAAGGCAGAATGAAGATAGCTTTGAAAAAGGCAAGCTGGGATTAGGTGACGCG
TATGTGGCAGACCTTGTACACAAGAACGATATGGTGGCCGAGTCATTGTCTAAAGTTCAGAG
AGAGAGGATCAATAGGCAATACAAGGCAACCAAGAGAGAGATAGCAAGGCTGAAGGAATT

TAGTAGGCGATCTGTCTCAGGCTCTGATAGTTCTAGGGGTATTGTACAGTACTCAATAGAATC
AGATGCAAGGTCAATCTAGCATGTTTATGCTAGATTGATATCCTAAGTGCGATGTGGGAAGG
CTCGCATGAGGGACGGTGAGAAAATCACGCTATAGGGGCGTAGATTAGCGCA

>dsRNA3

TGATAAAATTGGAAGTTATCAATCCGTTTTATCCTAGTGAAGTTGCCACGTAAAACAACTCTG
AAGATGGCCCAGTTCAAGACTGTGTATGATCTTATGGGCGATGCAGCGAAGGGGAAGTTCTT
TAGGGGTAAGAGCATGAGCGAAAGTGCAGTTGATGAGATGGAACATGTTGATTGTGAGTTT
GAAGAATTCAAGTCGTTGGGGTTGGTTGAGAAAAATATCCTTGCAGGAATAAGCATGCCTG
ACAATTTCACAGTTAAGAAGTCAGAGGGTAAGGTCGACATACTTGAGATTGGCATGACAAC
ACTGGCCAAGGCGGTGAGTGAGCACGGGGGTGTCACTGATCTAACGCACACAGCTGTCAA
GAAAATAGATCCTTTCCGAGTGTATGGAGACTGGAAATTGGAATATGAGCACGGCAGCATAA
TGTATCCTTGGCACAAAGGGATAAAGGCAGACAGGGACAAAGGAGTAATGGGCAGGATAT
CGGCACAATTCCCGCATTTGAACTCGACAGAGTCAAGCGGTTTTACAAGAACACTGCTCAC
ACATATGCTAGCGCAGAAAACGGACATGACACACGTGTTCATGAAGGGATATCTGATAATGA
TGGACTTGAACACGTCGGTTGTATTCAGACGCACCATAAGAAGAGCAACGGCAAAGAGAG
ACAACTTCTATCCAAACAAGAGTAATGATCATAGGATGGGACTGGTTGGCGCAGCTAGAATA
GTTGTGGACGCAGATGGATTCTCAGCTGAGGAGCTAGAATCTCTGGACATGATGTGCCAAG
AGTATCCGACAGTCAAGTACTGCGAAGATAACATATACAATACATGCAACATGGAGGCAGA
CAGGTTGGCCATAACAAGTAGCCGTGAGATACCTAGGGCACAGGGTAGAATTCCAACTCCA
CTGGAGTTTTACAGGTTGATGACCAGTATTGCATGTAAGCTGGACGCAGTGGAGGACATGTT
CACAGCCTTCAAATTGATGAGAGGACGGATGGCACACATAAGAGATGTTTACAGGTCATCA
GACGATAGGAAGTACTCCAGTGGCGTGCCACTTAGCACATGCTACTCAAGGTGCCTTGGAG
GAGGCACAGTGCACAAGAAAGTCTGTGCAACATACCCTGCTTACATGTGCTCTAGCGTGGG
ACTTGTCGCGGACGTACTGCTAGGTAGGTGCTATGAAGTCGCAGCGTCCATGCTTATAGAGA
ATTTGGGCGGACTGGGAGACATGATGTGCAGTGGAGGTGCGAGGGCAAGTGGACAATACA
ATGGGCTACTTAGAGAGTATGGCCTTTCCACAAAAGATGCAACAAAGAATGAGCTGATGTT
GGCGTGGGAAGGCATAGGCGCAATTGAGTACAAGTGGAGCCCAACTCTCACATGGAAGCC
ATACATAGTTAAGTTGACAGATGAAATAAGAGGAGGAAATGACGTAGAAATGCCACAACTG
TGCTATGAGATCGCGCACATGTTCCACGTAGACAACGCCTGGGGCGCAATACGGGGATATAA
AGGAATAACAGGAGCAGGTCTAGCAGAACACACCGACATAGGTGAAGGAGCAAGGAAGA
TGAAAGATGAAAGGCTACGGTATGCAGCAGCTTTCTCTTGGGCAATGGGAGTTAGGCGACA
GCGGCCCAAGATATTTGTAAATTCTTACGGAATGAAGGAAGTGGCAGTGTCAACTAATGAG
AGGAAATTTCTGAGGTCAGCAATAGGGGGGTACAAATTCACCAATTTGTCCTACACCCTGGA
AGAGGATTATGAAGGAAGAGAGGACTGGCTGGAGAACGCAGCAACTGAGCTGTTCAGGTC
AACTATAGATGGGACCAGGTGTTCGGTGATAATGTCAACGGCTGGAGAATGGCATTATTCAG
AGACCAAGGAGTCGAAGACTGAAGGAATCGCTGAGTCTCTGATGCAGAAACAAAAGTCTG
ACAATGTGGACGAGGAGATTCAGAGGATGACCACTGGCAAGTTAATAGAGCCAACAAGCA
ATGGAGCTGGAGATCTGTTCAGCAAGATGAGCAAGACAAGGTCTGTGGTCCACACACCCAA
AGTTAAGTTGTCAGGAGGATCGCTGCCAGAGGTGAGAGAGGGAGAGACGAGCTTCAAAAC
AATACCTGTTCCTGGTGATGGCAAGTGTGGTATACATGCAGTTGTTGCAAGCATGAAGGAGG
CAGGCATGCTTAGAATGGGTGAAGAGAAATTGGTATTCGACAATTTTGACGGCCAGT
TCAATGGGCAAACTTTCCACGATGCACAAACAATAGCACAGGGTCTGAACGAGATAGGGAT
CGGGCTTAGGCTGTATGATAATATACCAGAAAAGGGTGTGAGAGTAACGGA
CTATGGGGATGTGAAGGAGAATGGTATAGCAATATATAGGTCAGGCAACCAC
TTTGAGGGTGTAGTGGAGGGCCTGGGCGATACTAGAACAGTGATAGCTAAAGAA
GGAGGACAGCTGTCAAATGTTCAACAGGTAGACGCACTCAAAGAAATGAGGAG
ATTCTTTGAATAACACTGAAGCGTCTGCGGGGGTGACTCGACCTTGGTGTGT
ATCCTGAGGTGCGAGTTGCTGGAGAAAATTCTGAGTGGGGTCAGGGTTAGCGC