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      1        10        20        30        40        50        60        70        80        90       100       110       120
DaV   MATIVTTTKRISNNSGNNFSTRNRRTPKVTVQSVSSRQIVGKNCPMVQGPRRRGRNRPRKSGSQVAYSAMPKTTLSGVDIIGVIEVQPQRAVGASLFAQAICPTAMSDSRLQQQSKLYSR
RYMV  ............TNSNQGQQGKRKSRRPRGRSAEPQLQRA----PVAQASRISGTVGPLSSNT---------WPLHSVEFLADFKRS---STSADATTYDCVPFNLP--RVWSLARCYSM
CoMV  ..................................................................DWFDTGMITYLGGFQRTAGTTD...SQVFIVSPAALD..RVGTIAKAYAL
CarMV ......AVKLVTRGWASLSTNQKRRAEMLAGYTPAILAFTPRRPRMTNPPPRTSRNSPGQAGKSM........TMSKTELLS..TVKGTTGVIPSFEDWVVSPRNVA.PQLSLLATNFNK
TBSV  ........GLGKKALNKVRNRRKQGNQQIITHVGGVGGSI--MAPVAVSRQLVGS-KPKFTGR----TSGGVTVTSHREYLTQVGFVVNGGIVGNSL-QLNPSNGTLFSWLPALASNFDQ
SBMV  ........AQAIQNTLPNPPRRKRRAKRRAAQVPKPTQAGVSMAPIAQGTMVKLR.PPMLR......SSMDVTILSHCELSTELAV....TVTIVVTSELVMPFTVG.TWLRGVAQNWSK
TNV   EANGIFVEQRWNGKRWVTEASWRAGQAPNKERAATVTKSIARKVRGGVSRAGGFVTAPVIGAMVTRPTVPRFGMRGNSTVVSNSELILNLTPIALAYTVQSLPLIAT.AWLGTIADNYSK

               130       140       150       160       170       180       190       200       210       220       230       240
DaV   WRPKKLRVLVVGSGSANTFGSLAIGWSPDPANNISGNDTQNLNRVMACRPSSMNRMNQTTVLNIPVATTRKWYLTKGNPDDANHGFINVVVASTTGGYTGSTTFTVTLEWVIEFEGAELG
RYMV  WKPTRWDVVYLPEVSATVAGSIEMCFLYDYADTIPRYTGKMSRGAEGCHLLSGGSARNAVVASMDCSRVGWKRVTSSIPSSVDPNVVNLAVRSSIKPTVSDTPGKLYVIASMVL......
CoMV  WRPKHWEIVYLPRCSTQTDGSIEMGFLLDYADSVPTNTRTMASDGSSLLHTSMKSMGNAVTSALPDEFSNKWFKLSWSTPEESENPARFVVRSDFPVVTADQPGHLWLRSRILLPSTNL.
CarMV YRITALTVKYSPACSFETNGRVALGFNDDASDTPPTTKVG....FYDLGKHVETAAQTAKDLVIPVDGKTRFIRDSASDDAKLVDF GRIVLSTYGFDKADTVVGELFIQYTIV......
TBSV  YSFNSVVLDYVPLCGTTEVGRVALYFDKDSQDPEPADRVE----LANFGVLKETAPWAEAMLRIPTDKV-KRYCNDSATVDQKLIDLGQLGIATYGGAGADAVGELFLARSVTLYFPQPT
SBMV  YAWVAIRYTYLPSCPTTTSGAIHMGFQYDMADTLPVSVNQLSNLKGYVTGPVWEGQSLCFVNNTKCPDTSRAITIALDTNEVSEKRYPLVTAMEGGSSKTAVNTRLYASYTIRLIEPIAA
TNV   WRWVSLRIIYSPKCPTTTSGTVAMCLSYDRNDVAPGSRVQLSQTYKAINFPPYAGYDGAAILNTDVTPTSAIYVDVDVTRFDKAWY.TVHIGSDGGPAVAVPPGDIFFKYVIELIEPINP

      250       260       270       280       290       300       310       320       330       340       350       360       370       380
DAV   AVSIDEDITPDTGFQDLFTTSDGSWNSEYLTMKMHHGGQMVPFSAAHQAYVYTNAPGTNVTYYLEDKTTLKTANFFAVIQGYSIPGFVMFASYTDAKDYIRTGDTGKCLKYYTQGPVISPPIPKFRVADEAVQTVETNL
RYMV  ..................................................................................................................................
CoMV  ..................................................................................................................................
CarMV ................LSDPTKTAKISQASNDKVSDGPTYVVPSVNGNELQLRVAAGK...WCIIVRGTVEGGFTKPTLIGPGISGDVDYES.....................................
TBSV  NTLLSSKRLDLTG.................SLADATGPGYLVLTRTPTVLTHTRATGTFNLSGGLRCLTSLT.....................................................
SBMV  ALNL..............................................................................................................................
TNV   TMNV..............................................................................................................................
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Supplementary Figure 1. Alignment of deduced capsid protein sequence of DAV with that of other RNA viruses; rice yellow mottle virus (RYMV), cocksfoot mottle virus (CoMV), carnation mottle virus (CarMV), tomato bushy stunt virus (TBSV), Southern bean mosaic virus (SBMV), tobacco necrosis virus (TNV). The alignment is based on structural motifs that are conserved between the viruses. The sequence of the DAV capsid is shown in the top line. For all other sequences amino acids shown in red represent alpha-helices, blue represent beta-strands, and black represents an insertion. Each grey dash represents a gap inserted into the sequence for better alignment, and a dot represents residues that are ignored in the alignment due to low homology.