A Survey of Mycoviral Infection in *Fusarium spp.* isolated From Maize and Sorghum in Argentina Identifies the First Mycovirus from *Fusarium verticillioides*

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1. Supplementary Data

1.1. Complete genomic sequence of Fusarium verticillioides mitovirus 1 (NCBI-GenBank accession numbers MT506024):

>FvMV1

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CCATTAGTTAATAATAATCTTGGGAATTTAGTCATTTGACTAAATTGTCCCATAGGACTAAT
GATAATTTCTGTATTATCATTACCATTAAAGAATCGGTTAGAACCCGTATCTCTATGGTTTTA
TCCTGTCTGAGTGGTTAGTCAGAATCTGACTAATTTAATCAGGTTGCAGGATAGGGCTTATA
CACCCTAAAGTATAGTTTTAATATACCAATATGAAGAAAAATTATACCAAAATTCTTTGAA
GAATAATGGTTTTAATCTTTCCGTCTATTGATACATCAAAATACCTCCGTCCATTATTCAAA
ATCATCTTTAAAATGATAAAGAATCATGGAACTATTTATACCATCAAGTATTTAAAAAGAG
TAAGACTCCACTGTACAAGGTACATTTGTGGAGATCCTCTTTTTACAAATACTATGATGATA
GGAATAGATAAGGAGGGTTGACCAAAAGTTTTCTCATTCCTTAAACCATTAGTTAATAATA
ATCTTGAATCATTAAAATTCCTTTTTACCATTCTTAACTTCACAAGAAGTTGAGATTTGTCTA
AAAAGGAATGAGACAAGATAAAACCTGATTATAATAGTATAACAGACAAATCTAAAATGT
CTATTACTATTCCTTCAGGTATTATTAACAAATTTGTTAAGGAATACAGGTTAAAGTCTAAC
CATCCTGAATTTGATAAATTGAAAGATGTTTATCTTTCAACAAAAGCAGGACCAAATGGTC
CAGCTACTTTATCATCTCAGGAAGATCTGTTAAATTTTAATTATCCAATGATGGATAAAATA
TTTAAAATTACAGATCAAAATGGTATAGATTTCTTCTGTAAAAATTATACTCAAGCATTTAA
CAAAAATATTACTCCAAGTAAAATTAGAACACTTGGAAAAATATCTTTTGTTAAGGACCCT
GAATGTAAATTAAGAATAATTGCTATATCTGATTATTATAGCCAATTATATCTTAAACCTAT
ACATAATATTATCATGAATAAACTTCATAATATTACTATGGATAGAACTTATACTCAGGATC
CTCATCATGTTTGAGAAATAAATAATGAGAAATTTTGATCTCTAGACCTTAGTTCAGCAACA
GATAGATTTCCTGTAGAATTACAGAAAGACTTTTAGCTAGAATATTCCATATGGAATTAGC
TCAAAGTTGACAATCTATTCTGAATTCAAGAGAGTTCACGACTCCAGAAGGTTACCAGTTA
AAATATGCAACTGGACAACCCATGGGAACGTATTCCTCTTGAAGTGTTTTCACCTTGACTCA
CCATTTAGTTGTATATTATTGTGCAACTATAAATGGCTACAAGAACTTTGACCAATATATAA
TTCTTGGTGACGATATCGTTATAAAAAATGATAAAGTTGCTAAGACTTATAAAAAGGTCATT
AAAGCTCTTGGAGTCGAATTATCTGAAAGTAAAACACATGTATCATCAAATACATATGAAT
TTGCTAAAAGATGAATTCAATGAAGTCAAAACCGTGAGATAACTGGACTTCCTCTTGGAGG
TATTCTTCGTAATATAAATAATCCTAATATAGTTTTCACTGTATTATACGATTATTTTAAAAT
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ATAAATTATTATTAAAAAATAAAAAGATTAAAACTAAAAATAATAAAATTATTTTTAGAAA
ATCTTTTTATAAGCTTAATGATAAAATGGTATCATCTCTAGAGTCATTCTCCTTGATGTTAGA
TATAGTCTTTGATTATAAGTCTTACGATAAGTTAAGAAACTTATTCGTTAAGAATATTACAA
CCTTAGACTATAATATTCCAAGTGAAAGTACAATCCTTTCCGAATTGAAAGGATACTTTCT
CATGGACTATCATCAAGAATTTTACAGATGAATAGTAATATAATAAATTCACCTAAAGTCC
TAATATCTAAATTTGATATTGAGGACAAGAATTTATTAAATACTAACCCTGTGTTCCTTTCC
ATCTATAACACAATCTCCCGATTTAAAGATATTAAATTTGAAGATCTAGACGATCTTCATAA
TATCTCTAAGGAGATATGTGAAATCAATATTGAAAATATTTTTAATAAGGATAGGAACAAG
ATCCAATCATTATTAGAAATAGGTAAAATATTGAAAGATGGGTTTAAATATGTCAACAATA
CAACTGAAGTGTATTATGGGTCAGCTACATTAAGCGACTCATTTACACTTGGTGGTATTGGT
AAAATTCTGATGAATAATTTAAAATCATCAGAATTAGACGACATAATTAAAGGAACTTACA
CTGAGCCACAGCCACAAGGTGGTTATGCTTCAATGTGAGAAAACTTTAAGATGTAATCCCT
AGACAATGATTGATTAAAATCATTATCTCCACTAACCATAGTGGGGAATCTAGTCAGAAAT
GAC

1.2. Complete genomic sequence of Fusarium andiyazi mitovirus 1 strain 162 (NCBI-GenBank accession numbers MT506025):

>FaMV1-162

TATCAATTAAGATAGACTCAATAGGTCCAAAGACCATTATACAGTTTAATTTCTGTATAATC
TAATGAAAGAAAGGTATAGCAAATCCTTTCTCTTTGGTCTTCCAAGAGTCCATATAATAATG
GGTTGCTCTTGGATAGCCGAGTGGCTTCTCGTTAAACAGTTAGACGGTAGGACTGCGAGTTA
AATACTCGAGTGAACATCCGCAACATTCAAATTTTATAATGTTAAGAAATTATATAAAAAT
AATCAAAAGATTAAGTTTTATATTTTTCCCTAACAAATACCATAAGGATGATTTTAATAAAA
TGCTGAAATTATATCAACATCTTATTAAACATCATAATATATCCGGTGCAATTAAATATATG
AAAAACATACGTTTAATTTGTACAAGATATATTTGTGGTAATCCATTATTAACTAATAATTTT
GGAATTGCCACAACCAATGGTTGACCAAATAAACTCTCATTCTTGAAGTCTAGGATTGATA
GTAATGAAGGTTTATCATACGTTCTTACTCTTCTAATATTTAATAGATCATTAGATCTAAATA
AATACGAAGTTAAGAAGAAATGAAAATCTTGATTATTCATCAATTACTTCTAAACAAAG
AATGAATTATACAATACCAACCGGTTTTATCAAAGAATTTGTAAAGAAGAATAATCTTTAC
ATTTCCAAAGATAAAATGGAGTTTTCCCTGAGTGACATTTATTTATCACAAAAAGGAGGAC
CACAAGGAAAAGCATCAAATACGGCTTTAGTAAATTTTAATAATTATAATTATTATAGTTTA
CAAAGACTATTTAATGTCCTTAGTGAGTCCGGTATTGATTTCATTTGTAAATCCTATAGTTAT
TTTGTGGAAAATTCTTCAAAATTTAAACCTAAACATAATGATTTAGGAAAGATTGAAGTTGT
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CTTTTACACAAAATCCACATCATAACTGAGAATCTAATCAACATAAGTTTTGATCATTAGAT
TTGAGTTCTGCTACGGATAGATTCCCAAGGAAACTACAAGCAAGATTACTATCAGAAATGA
TAGATATGCATTATGCATGATCTTGAAATAGAATCCTTGAGACAATAAGTTTCCATACAAA
GGATGGCAACTCCATTAGATATGAAGTTGGCCAACCTATGGGAACTTATTCCTCCTGAATTT
GTTTCACTTTAGCTCACCACCTAGTAGTTAACTATGCAGCTAAATTAGCTGGTATAGATAAT
TTCAACCAATATATCATTCTTGGTGACGATATAGTCATTAAGAATGATAAGGTTGCCTATTA

TTATATACGTATAATAAATAGACTAGGTGTTGATATATCTCTTACAAAAACACATGTATCAG
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CAGTGAGAGGGATTATCCATAATTTTAAAAATATAAATGTAGTATTTACAATACTATATTCA
CATTTTAAAATTAATGGTAATACCTATCTTTCAAAATACAGTTTAGTGGAATCCCTCCGTAG
ATTATATAAAGATTTCTATCTCATTAAAGGAAAGAAAAAATACTTTCCTATACGAAATATG
AAATCTTATATAAACAGACTTCAAACCTTTAGTAATATATTAGATATAACCTTTGGTTATTCT
AATGACCAAAGTATCAGACAAATATTCACTAAAAATATTATTAGTGATTATTATATGATAC
CAACGGCACTAGAGGATAGCCTTCTTGAAATCAAGAAGATCCTTAGTACTGGTCTTGGTAA
GTTACTAAGTTCCAATGTAGGTAAAGTTTCGTCGTGACAGACGAAAATAATTGAAAATTAT
GACGATGAAAATCGTAATAATTTAATATATTATCCAACATTTGTTGGGCTTTACAATTACAT
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ACAAGATCTTAATGTTATAGATGTTGATAAAGTTTTCAGTAAGGAAAGATCAAAATTTGAT
CATCTCCTTACTATAGGAAAAGTTTAGAAGTAGGTTTCACTAACATCAATAAAACTGATG
AGATCTATTATGGATCTGCAACAGTTGAATCATCACTGACACCGAAAGGTATGCAGTTATG
ATTCTCGAAATCTATAACAAAGATGTTATGGATTCAATTATTGAAGGTAAGTGAGAACCT
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ACTTGATGGTCTATGACCTCTTGAGCTTGTGTTAATTCACAG

2. Supplementary Figure
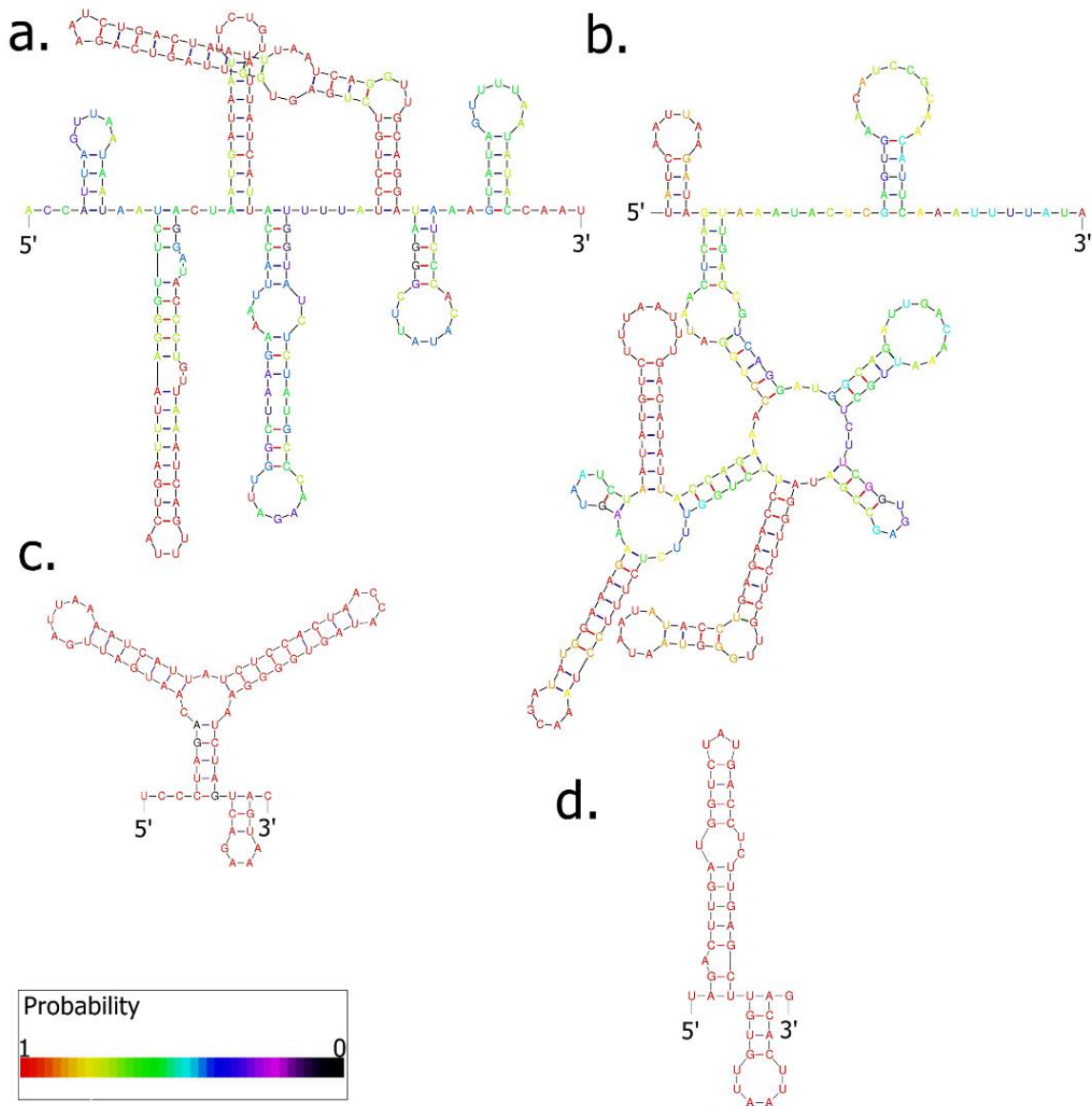
Figure S1. Predicted secondary structures (2-D representation of this self-folding) of the terminal untranslated regions (UTR) of FvMV1 and FaMV1-162. Schemes (a) and (c) represent the 5`-UTR and 3`-UTR of FvMV1 with dG = -82.52 and dG = -29.55, respectively. Schemes (b) and (d) represent the 5`-UTR and 3`-UTR of FaMV1-162 with dG = -73.96 and dG = -13.93, respectively. The +ssRNA molecules were folded, and the free energy was calculated with the RNA Folding Form V 2.3 Energies (MFOLD) program. For these calculations, the following conditions were sectioned: 25ºC, 1M NaCl and 0M divalent ions. The rendering of the structures has been defined with natural angles and annotated using colored base characters, based on p-num information. Colors are ranged from red to black representing the probability as well-determined (1) to poorly determined (0), respectively.