

Nucleotide sequence of infectious bursal disease virus genome segment A delineates two major open reading frames

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The genome of infectious bursal disease virus (IBDV) consists of two segments of double stranded RNA. We have determined the sequence of the larger segment A, encoding 3 structural polypeptides, of IBDV strain Cu-1 (1). Sequencing of overlapping cDNA clones revealed the presence of two major open reading frames (ORFs): in addition to a large ORF (nucleotides 96 to 3132), we found a small ORF (nucleotides 62 to 497), overlapping the large ORF. Another start codon, at position 30, lies between a perfect Kozak consensus sequence; this ORF is terminated at position 60, prior to the start codons of the major ORFs. Only one ORF has been described recently in genome segment A of IBDV strain 002-73 (2). Two ORFs have also been described for segment A of infectious pancreatic necrosis virus, a serologically unrelated other member of the birnavirus family (3).

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GGGACAGCG CGTCAAGGCT TGTCCAGGA TGGGACTCCT CCTTCTACAA CGCTATCATT GATGGTTAGT AGAGATCAGA CAAACGATCG CAGCGATGAC AAACCTGCAA GATCAACACC 120
AACAGATTGT TCCGTCATA CGGAGCCTTC TGAATGCCAC AACCCGGACCG CCGTCCATTC CGGACGACAC CCGTGGAGAAG CACACTCTCA GGTCAGAGAC CTCGACCTAC AATTTGACTG 240
TGGGGACAC AGGGTCAGGG CTAATTGTCT TTTTCCCTGG ATTTCCCTGGC TCAATTGTGG GTGCTCACTA CACACTGCAG AGCAATGGGA ACTACAGATT CGATCAGATG CTCCTGACTG 360
CCCAAGACCT ACCGECAGT TACAACACT GCAGGCTAGT GAGTGGAGT CTCACAGTGA GGTCAAGCAC ACTTCTGTGT GCGCTTATGT CACTAAACCG CACCATAAAC CCGCTGACCT 480
TCCAAGGAAG CCGTAGGAA CTGACAGATG TTAGTACAA TGGGTTGATG TCTGCAACAG CCAACATCAA CGACAAAAT TGGGAAGCTC TAGTAGGGA AGGGTCCACC GTCTCAGCT 600
TACCACATC ATATGATCTT GGTATGTGA GGTCTGGTGA CCCCATTCCC GCAATAGGGC TTGACCCAAA AATGTTAGCC ACATGTAGCA CAGTGCAGAC GCCCAGAGTC TACACATAA 720
CTGCAAGCGA TGATTACCAA TTCTCATGAC AGTACCAACC AGGTGGGGTA ACAATCAGAC TGTCTCAGC CAACATTGAT GCCATCACAA GCCTCAGCGT TGGGGAGAG CTCGCTTTTC 840
AAACAGCGT CCACGGCCTT TACTGGGCG CCACCATCTA CCTCATAGGC TTTGATGGGA CAACGGTAAT CACCGGGCT GTGGCTGCAA ACAATGGCT GACGACGGC ACCCAACCC 960
TTATGCCATT CAATCTGTG ATTTCAACAA ACGAGATAAC CCAGGCAATC ACATCCATCA AACTGGAGAT AGTGACCTCC AAAAGTGTG GTGAGGCGAG GGATCAGATG TCATGTGCG 1080
CAAAAGGAG CCGTAGCAGT ACGATCCATG GTGGCACTA TCCAGGGGCG CTCCTCCCGC TCACGCTAGT GGCCTAGSAA AGAGTGGCAA CAGATGTCGT GGTACGGTC GCTGGGGTGA 1200
GCAACTTCGA GCTGATCCCA AATCCTGAAC TAGCAAAAGAA CCTGGTTACA GAATAGGCCG GATTTGACCC AGAGGCTCAT AACTACACAA AATTGATACT GAGTGAAGG GACCTCTGTG 1320
GCATCAAGAC GCTCTGGCCA ACAAGGAGT ACACTGACTT TCGTGAATC TTGATGGAGG TGGCCGACCT CAACCTCCCG CTGAAGATTG CAGGAGCATT GCGCTTCAA SACATAATCA 1440
GGGCAATAAG GAGGATAGCT GTGCGGTGG TCCTCCACTT GTTCCCACTC GCGGCTCCCG TAGCCCATGC AATTTGGGAA GGTGTAGACT ACCTCTGGG CGATGAGCCA CAGGCTGCTT 1560
CAGGAAGTGC TCGAGCCGCG TCAGSAAAG CAAGAGCTGC CTCAGCCCGC ATAAGCAGC TGACTCTCGC GCGGACAAAG GGTGACGAG TAGTCCGAA TCTATCCAG GTGCCCAGA 1680
ATCCCGTAGT CGACGGGATT CTGCTCTCAC CTG666TACT CCGAGGTGCA CACAACCTCG ACTGCGTGTG AAGAGAGGCT GGCACGCTAT TCCCTGTGT TATTACGACA GTGGAGAGC 1800
CCATGACACC CAAAGCATGG AACAGCAAAA TGTTTTGCTGT CATTGAAGCG GTGCGAAGAG ACCTCCAACC TCCATCTCAA ABAGAGATCT TCATACGAAC TCTCTCTGGA CAGAGAGCT 1920
ATGGATATGC TCCAGATGGG GTACTTCCAC TGGAGACTGG GAGAGACTAC ACCGTTGTCC CAATAGATGA TGCTCTGGGAC CAGACAGATTA TGCTGTCCAA AGATCCCATTA CCTCTATTG 2040
TGGAAACAG TGGAATCTA GCCATAGCTT ACATGGATGT GTTTCGACCC AAGTCCCAA TCCATGTGGC TATGACGGGA GCGCTCAATG CTGTGGCCA GATTGAGAAA GTAACCTTTA 2160
GAGCAACDAA GCTCGCCACT GCACCCAGC TTGGCTTAA GTTGGCTGT CCGGAGCAT TCGATGTAAA CACC66GCC AACTGGGCAA GCTTCTCAA ACGTTCCCT CACAATCCAC 2280
GCGACTGGGA CAGGCTCCCG TACTCAAC TACCATACTT TCCACCAAT GCAGGACGCC AGTACCACCT TGCCATGGCT GCATCAGAG TCAAGAGAC CCCCAGACTC GAGAGTCCCG 2400
TCAGAGCAAT GGAAGCAGCA GCCACGCTGG ACCCACTATT CCAACTCTGA CTCAGTGTGT TCAATGTGGT GGAAGAGAA TGGATGTGTA CTGACATGGC CAACCTGCGA CTCACGACC 2520
CGAAGCCCAA TCGGATGCGA AATTTTCTG CAAAGCCACC ACAAGCAGCG ASCAAGTCCG AAAGGGCCAA GTGCGGGACA GCGAGCTAGC GAGTGGAGGC TCGGGCCGCC ACCACAGAGG 2640
AAGCAGAGG GAAAGAGAC ACACGATCT CAAAGAGAT GGAGACCATG GGCATCTACT TTGCAACACC AGAATGGGTA GCACTCAATG GGCACCGAG GCCAAGCCCC GGGCCACTAA 2760
AGTACTGGCA GAACACAGA GAAATACCG ACCCAAGCA GGACTATCTA GACTAGTGC ATGCAGAGAA GAGCCGTTG GCATCAGAG AACAAATCT AAGGACAGCT AGCTGATCT 2880
ACGGGCTCC AGGACAGCA GAGCCACCC AAGCTTTCT ATGACAGAGT GCGCAAGTCT ATGAAATCAA CATGAGAGT GCGCCAAACC AAGACAGAT AAGGACAGCT GCTCTGACT 3000
CGATGGAGT GAAGCATCC AATCCAGCG GGGCTCTACC AAAGCCCAAG CCAAAACCCA ATGCTCCAC ACAGAGACCC CDTGGTCCG TGGGCGCTG GATCAGGACC GTCTGTGAT 3120
AGGACCTTGA GTGAGGCTCC TGGGAGTCTC CCGCACCAC CCGGCGAGT GTGGACACCA ATTCGGCCTT ACAACATCCC AANTGGATC GCTT 3214

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