

Sequence of an avian adenovirus (CELO) DNA fragment (0–11.2%)

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The nucleotide sequence of a DNA fragment (0–11.2%) from avian adenovirus serotype FAV-1 (CELO; chicken embryo lethal orphan virus, strain Phelps) genome has been determined. The leftmost 63 nucleotides of the sequence represent an inverted terminal repeat which coincides with the repeat sequence published previously [1]. A region of the sequence positioned at 3777 to 4216 including the VA-RNA gene is exactly identical to the CELO DNA sequence reported in [2]. Open reading frames of E1A and E1B transforming regions characteristic of analogous (left terminal 0–11%) fragments in mammalian adenovirus genomes were not identified in the CELO genome fragment

sequenced, at least in the same polarity. According to our data the 0–11.2% fragment fails to transform primary cells unlike the 0–18% fragment which has transforming activity. Thus the location of the transforming region in CELO DNA may be shifted rightwards from the genome leftmost part.

REFERENCES

1. Aleström, P., Stenlund, A., Li, P. and Pettersson, U. (1982) *Gene* 18, 193–197.
2. Larsson, S., Bellet, A. and Akusjarvi, G. (1986) *J. Virol.* 58, 600.

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1  GATGATGAT AATAACCTCA AAACTAACG CAGTCATAAC CCGCCATAAC CGCAGCGTGT CGCTATACGC AAAATAGTTT TATGACGCAT AATAAAACCA
101  CACCCATAAA TATGAATGAT ATCATAAATT AGTTTATTGA TTTATTTGTT TTCTAACCAA TACGAATACG AATCTTGACA GGAACAGACA AATAGCTTCT
201  GGGATCACA GTAGGCTGAC GTCACCTGGT CTCCATTTAA ATACAGCGAG TCTCCGCTC CCCGANTTTC ATACCTGTAT GCAAAATTAAC AGGTTACTTC
301  CGGGTTTTCA CTCCCGGTTG AACTTCCGCA TACGTACAT CCCGGATGTG ACGTATAACA TGACTCACCA TGGTACGTAA TCATCGTACG ATGCATCCAC
401  CCAATCAGCT CCGTCTTCG ACTTCCTGGT TACGCCAGC CAGTTAGTTC CTGTCCGCA TTGGCCGAGA AGGAACTCCT GTAAGGGGTC TCCGTTAATT
501  TTTGTATTTT TCGGGGAATT AGGAGTTTCC TGGAAATTTAA CTTTTTACCT TTTCTCTTC GGAACGCGGA ACTGCTAGCT CCGCCCTTGG CTGTCTACAA
601  AATTTTTCGG CTTCACTCCA ATTGGACTCT GACTCCGAAA AGTAGTAGCA CTTGCTTTGA AATCCGATCC AGTCTCGCGG GCATACACG TCAAACTCCG
701  GAAAGCGGTC GCAACCTATC GGGGGCAGCA TTATGGTGGG TGACCCTTTT TTTAGACATG CCTTTTCTTA CGTCACAATA CTTACGCCCA ATGATTGCTA
801  TGGTATGGT GGCGGTTATG ACACAGCATA TTATGCAAT GACTGGAATC CAGATCCACC TATGGGAGGG CTCCTTTAAG ATGATTCITT TTTTGTTCCT
901  TCTGGTGCCT TCCGGTATTC CGTCTTCTAT ACTGACGTCA CAGAAATGTC CGAGAAGCTT TTCTAATTGG TCGGTTATTC TCTGCCGAC TFCAGGGGTA
1001  TTTGCATATA GGTAAATGAA CAATATGCAA AGCACTCCTA AGATTATAAT GCCCACAATG TATCCTGTAT ATGCGCACTC CGTCCCTATA AATAATTACA
1101  GAGGTTTCTT AATGTGTTCA GTTATATTCT ATATAATGTC TATAGAGGGC GCTACTTACT CTCTGATGGT TCGGCGGTGT CCATACTTAT TGCACGGAG
1201  TTTTTGAGA CTTGATTGGA TGCCGTACAT GAATACATTA CCCCTAAGG TCCAAAGAGC ATGCTCTGAT TTTCTGACCC GACTATGATT GGGTGGTAT
1301  AATTCCAATG CCAGGAGACA TTGCCGTAGG AACCGGCCGG TAGATGGCAG GATATATTGG TGAAGTTTT CCCGTTGATT TGCATAGTGG TTCCCTTGAC
1401  TTCAGGGCGT GGAATCGGGT CTGGATAATT AATGCTCTAT TAGATAGGTG ATATTAATGC ATATTGTAAG TATGTATATA ATGACATACC TTGAACAATC
1501  ACTTTGAAAT TGTCCGTTGT TTCCGTGCCA TCATTTTCTT CCTGGTGGAG TGAGTAGGTT CCGCTGTCTT CGTAGCTGGC ATTATGAATG GTTAAGTTAT
1601  GTTTGGTGGG GTTAAACTCG GATCGATTTT GGAACCGGTT ATCGGGAAAT TTGATTTCTA ATTGGTTAGT GATGACATT TCGGCTATCA CAATTTTTAG
1701  ATTTCCAAAC CGCATTCAA ATTTGTATTG CCTTTCTGT TTAGCCCCCA CACCAATTC TACTGCCC CCTTTCCGAG CGTATAGAT AGGATGCTCC
1801  GCAGCGAGGG TGACCCCCAC CAACAGAACT ACTGTGAGAA GTAGCATTGT TCCGGTGTGG GTATCTGTCT AATTTTCCAT TCCCTATATA TACCTGTGTG
1901  AATGAGGAGG CACCTGAGAA AAGTTTCCAT GACGCACT GCTTTATTGT TTTATATCAT TTCGAAATTT CCCCGCCCGT TTACATTGAG CTGACGTAGG
2001  CAACACAAGA CCGCAATTAC CCGGATAAGC AAACAGCTAC AAATGGCAAT TGTCTAGAA ATAGTTTTAT GATATCCAG GTGTGCTACG ATTGGTGGAT
2101  TCTCGGAGAC TGTAAGGTTT ATGGTGAAGG TTAGGTTTGT TTGCTGATCA ATGACGCATT GGAATATCCC GGCATCTGTT ATCAGCAGAG GGTGGAGAGT
2201  GAGGGTGTGG TTTCCGGGAT CAAAGTCCAT GTTTGCAATA TAGCCGGGTC CTTTGTATT TGTCTGTGG GACAATGCC AGCTGATAAT GAGTTTCCGT
2301  TCCGATTCTT CCAGCCGAC CCATCGTGA TAATTACCCT GTTCAATAC CTGTCTTGT AAGGTAAGG TATTTCCAGC CCAAGTGAAG GCTGTGGTGA
2401  TCGATTGTCC CAGCGGTTGT ACAGTTATCA GATAGGTTGG GTTGTGTCCT GTTTCGGAGA TCACAGTGA CAGGTTAGTT CCCGATTCT TCTTGGTGGT

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