Volume 17 Number 16 1989 Nucleic Acids Research

Nucleotide sequence of the gene coding for the peplomer protein (=spike protein) of infectious bronchitis virus, strain D274

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Submitted July 26, 1989 EMBL accession no. X15832

The sequence of the peplomer protein of strain D274 of avian coronavirus IBV has been determined by sequencing overlapping cDNA-clones against the genomic RNA of the virus. Initial cDNA-clones were isolated from a library using a clone containing the peplomer gene of IBV strain M41 as a probe (1). The underlined R (=A or T) at position 2349 indicates a difference in nucleotide sequence between two cDNA clones resulting in an uncertainty in the amino acid sequence of the peplomer protein. The peplomer protein of IBV is a transmembrane glycoprotein which is proteolytically processed into two noncovalently bound subunits, S1 (coding region bp 67-1680) and S2 (coding region bp 1681-3528). The start of each subunit is underlined.

The sequence of the peplomer gene was compared with sequences of several other IBV strains (2, 3). The peplomer gene appeared to be most similar to those of strains H6/82 and D207; at only 13 or 14 positions (depending on which amino acid is coded at position 2347-2349) a different amino acid was encoded.

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TGAAAACTGAACAAAAGACCGACTTAGTAGTTAATTTACTAAGGAACGGTAAATTATTGGTTAGAGATGTTGGAGAGGTCACTGTTATTAGCGACTCTTTTGTCTGCACTATGTAGTGCC- 120
AATCTGTTTGGTAATAATTCTTACGTGTACTACTACCAAAGTGCCTTCAGACCACCTGATGGTTGGCATTTACATGGTGGTGCTTATGAAGTAGTAAATGTTTTTACGGAATCTAGTAAT- 240
GCAGGCACGACTGGGTGTACTGTCGGTGCTATTTATTGGAGTAAGAATTTCAGTGCTGCTTCCGTGGCTATGACAGCACCTCAAAATGGTATGTCATGGTCTACTGAGCAATTTTGTACG- 360
GCTCACTGCAATTTTACTGATTTTGTAGTATTTGTTACACATTGCTATAAAAGTAGTCATGGTTCATGTCCTTTAACAGGTCTGATTCCACAGAATCATATTCGTATTTCTGCTATGAAA- 480
AATAGCAGTTTGTTTTATAACTTAACAGTTGCTGTGACTAAATATCCTAGATTTAAGTCGCTTCAGTGTGTTAATAATATGACATCTGTATACCTAAATGGCGATCTCGTTTTTACTTCT- 600
AACGAGACTAAAGATGTTAGTGCTGCAGGTGTTCATTTTAAAGCTGGTGGCCCTATAACTTATAAAGTTATGCGGGAAGTTAAAGCATTGGCTTATTTTGTTAATGGCACCGCACAAGAT- 720
GTGATTCTTTGTGACGGTTCACCTACAGGTTTATTAGCATGTCAGTATAATACTGGTAATTTTTCAGATGGCTTTTATCCTTTTACTAATAGTAGTTTAGTTAAGGAAAAGTTTATTGTT- 840
TATCGTGAAAGTAGTGTTAACACTACTTTGGAGTTAACTAATTTCACTTTTTCTAATGTAAGTAATGCTACCCCTAACACAGGGGGTGTCCAGACCATACAATTATATCAAACCAGCACG- 960
GCTCAGAGTGGTTATTATAATCTTAATTTCTCCTTTCTGAGTAGTTTTATTTATAAGGCGTCTGATTATATGTATGGGTCTTACCACCCAAGTTGTAAGTTTAGACTAGAAACTATTAAT-1080
AATGGTTTGTGGTTTAACTCACTTTCCGTCTCTCTTGGTTACGGACCTATCCAAGGTGGTTGTAAGCAATCTGTGTTCGCAAATAGGGCAACTTGTTGTTACGCCTACTCGTATAATGGA-1200
CCTTCTCTTTGCAAAGGTGTTTATAGAGGTGAGTTAACAAAAAGCTTTGAATGTGGATTGCTGGTTTTTGTGACTAAGACTGATGGTTCCCGTATACAAACTAGAAATGAACCATTTACG-1320
TTAACCCAGCACAATTATAATAATATTACTTTAGATAGATGTGTTGAGTATAATATATATGGTAGAGTTGGACAAGGTTTTATTACTAATGTAACTAACTATGCCATTAATTATAATTAT-1440
CTAGCTGATGGTGGTATGGCTATTTTAGATACATCTGGCGCCATAGACATCTTCGTTGTACAAGGTGAATATGGTCTTAATTATTACAAAGTTAACCCTTGTGAGGATGTTAATCAGCAG-1560
TTTGTAGTTTCTGGTGGTAAATTAGTAGGTATTCTTACGTCACGTAATGAGACTGGCTCGCAGCCTCTTGAAAACCAGTTCTATATCAAAATCATTAATGGAACTCGTCGTTCTAGACGC-1680
TCTATTACTGGGAATGTTACAAATTGTCCTTATGTTACTTATGGCAAGTTTTGTATAAAACCTGATGGTTCAATTTCCACAATAGTACCAAAAGAATTGGAACATTTTGTGGCACCTTTA-1800
CTTAATGTAACTGAAAATGTGCTCATACCTGACAGTTTTAATTTAACAGTCACTGATGAGTACATACAAACGCGTATGGATAAGGTCCAAATTAATTGCCTTCAGTATGTTTGCGGCAAT-1920
TCTTTGGAGTGTAGAAAGTTGTTTCAACAATATGGGCCTGTTTGTGACAACATATTGTCTGTAGTAAATAGTGTTGGTCAAAAAGAAGATATGGAACTTTTACACTTCTACTCTTCTACT-2040
AAACCATCTGGTTTTAATACACCAGTTCTTAGTAATGTTAGTACTGGTGAGTTTAATATCTCTCTTTTGTTAACACCTCCTAGTAGTGCTAGTGGGCGTTCTTTTATTGAAGATCTTTTA-2160
TTCACAAGTGTTGAATCTGTTGGATTACCAACAGATGACGCATACAAGAAGTGCACTGCAGGACCTTTAGGCTTTCTTAAGGACCTAGCGTGTGCTCGTGAATATAATGGTTTGCTTGTG-2280
TTGCCTCCTATTATAACAGCAGAAATGCAAACCTTGTATACTAGTTCTCTAGTAGCTTCTATGGCTTTRGGTGGTATTACTTCAGTTGGTGCTATACCTTTCGCCACACAATTGCAGGCT-2400
AGAATTAATCATTTGGGTATCACCCAGTCACTCTTGTTGAAGAATCAAGAAAAAATTGCTGCTTCCTTTAATAAGGCCATCGGCCATATGCAGGAAGGTTTTAGAAGTACGTCTCTAGCA-2520
TTACAACAAATTCAAGATGTTGTTAATAAGCAGAGTTCTATCCTCACTGAGACCATGGCGTCACTTAATAAAAATTTTGGTGCCATTTCTTCTGTACTTCAAGATATTTACCAGCAACTT-2640
GATTCTATTCAAGCAGATGCTCAGGTTGATCGTATTATTACAGGTAGACTTTCTTCATTATCTGTTTTAGCTTCTGCAAAACAGGCAGAGTATTACAGAGTTTCACAACAGCGTGAGTTA-2760
GCCACTCAGAAAATTAATGAGTGTGTTAAATCTCAATCTATTAGGTATTCATTTTGTGGTAATGGAAGACATGTTCTAACCATACCACAAAATGCTCCTAATGGCATAGTGTTTATACAC-2880
TTTACATACACGCCAGAGAGTTTTGTCAATGTGACGGCAATAGTAGGGTTTTGTGTAAACCCAGCTAATGCTAGCCAGTATGCAATAGTGCCTGCTAATGGCAGAGGTATTTTTATACAA-3000
GTTAATGGTAGTTACTACATCACTGCAAGAGATATGTATATGCCAAGAGATATTACTGCAGGAGATATAGTTACGCTTACTTCGTGTCAAGCAAATTATGTAAGTGTAAATAAGACCGTC-3120
ATTACTACATTTGTAGACAATGATGATTTTGATTTTGATGACGAGTTGTCAAAATGGTGGAATGATACTAAGCATGAGCTACCAGACTTTGACGAATTCAATTATACAGTACCTATACTT-3240
GATATTGGTAGTGAAATTGATCGTATTCAAGGCGTTATACAGGGCCTTAATGACTCTCTAATAGACCTTGAAACCCTTTCAATACTTAAAACTTATATTAAGTGGCCTTGGTATGTTTGG-3360
TTAGCCATAGCATTTGCCACTATTATTTTTATCCTAATATTAGGATGGTTGTTTTTTATGACAGGTTGCTGTGGTTGTTGTTGTGGATGCTTTGGCATTATTCCTTTAATGAGTAAGTGT-3480
GGTAAGAAATCTTCTTACTACACGACTTTTGATAATGATGTGGTAACTTAACAATACAGACCTAAAAAGTCGTTTAATGATTCAAAGTC-3570
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The R at position 2349 is T or A

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