

The nucleotide sequence of the extreme 5' end of the avian coronavirus genome; implications for the discontinuous mRNA synthesis

P.J.Bredenbeek, J.F.A.Noten, J.A.Lenstra, M.C.Horzinek, B.A.M.van der Zeijst* and W.J.M.Spaan

Institute of Virology, PO Box 80.150 and Section Bacteriology*, PO Box 80.171, Veterinary Faculty, State University, 3508 TD Utrecht, The Netherlands

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Coronaviruses contain a positive stranded RNA genome of 18kb. After infection 5 to 6 subgenomic mRNAs are made consisting of a body and a 70 nucleotide leader sequence joined together by a sofar unknown mechanism of discontinuous transcription (1-3). For a murine coronavirus it has been proven that the leader corresponds to the 5' terminus of the genome (1,2). The addition of the leader is a transacting process (4). cDNA clones were made to genomic RNA of avian coronavirus IBV-M41; clones representing the 5' end of the genome were selected by hybridisation with a synthetic oligonucleotide complementary to the IBV mRNA A leader sequence (3). The following sequence was obtained:

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TATATATCTCATCACAAGCTAGCGCTAGATTTCCTAACTTAACAAACGGACTTAAA 60
TACCTACAGCTGGTCTCATAGGTGTTCATTGCAGTGCACCTTTAGTGCCTGGATGGC 120
ACCTGGCCACCTGTGAGGTTTTTGTATTAAAACTTTATTGTTGCTGGTATCACTGCTT 180
GTTTTGCCGTGTCTCACTTTATACATCCGTTGCTTGGGCTACCTAGTATCCAGCGTCTCT 240
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The sequence is identical to that of another isolate of IBV-M41 (7). The underlined stretch AACTTAACAA is very similar to the nucleotide sequence at the leader/body junctions (intergenic regions) of the IBV-M41 mRNAs E, D and C (5,6) indicating that base pairing between the leader/polymerase complex and the intergenic regions on the negative stranded template could be an important feature of the leader-primed viral mRNA synthesis.

Potential base pairing regions between the leader (bottom line) and the complement of these three intergenic regions on the negative strand (upperline) are:

D/C	ATACCATCTTTTGAATTGTTAGGC	E/D	TGCTACACCAATTGACTTGTTTTGT
	* * * * *		* * * * *
	CTAGATTTCCTAACTTAACAA		CTAGATTTCCTAACTTAACAA
F/E	AATTAACTTTTGAATTGTTTCT		
	** ** * * *		
	CTAGATTTCCTAACTTAACAA		

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