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3′-Terminal sequence of human parainfluenza virus 3 genomic RNA

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SEQUENCE: The 3'-terminal nucleotide sequence of the human parainfluenza virus 3 genome.

3'- UGGUUUGUUC UCUUCUUUGA ACAAACCUUU AUAUUUAAAU UUAAUUUUAA
UUGAAUCCUA AUUUCUGUAA CUGAUCUUCC AGUUCUUUUC CCUUGAGAUA
UUAAAGUUUU UACAACUCGG

The transcriptional initiation site (*) and the triplet complementary to the translational initiation codon (underlined) of the HPIV3 nucleoprotein (NP) mRNA (1) are indicated.

METHODS: Genomic RNA of human parainfluenza virus 3 (HPIV3) strain 47885 was isolated (2) and purified on sucrose gradients(3). The 3' end of the genomic RNA was labeled with ^{32}pCp and T_4 RNA ligase and chemically sequenced (4). HPIV3 3'-terminal sequences cloned into M13mp10 following polyadenylation and oligo(dT)-primed cDNA synthesis (5,6) were also sequenced.

COMMENTS: Only 2 of the 3'-terminal 29 nucleotides of HPIV3 genomic RNA (positions 20 and 24) are consistently different from those in the genomic RNA of three Sendai virus strains (7,8,9). In addition, nucleotides 54-65 show strong homology with the R1 sequence of Sendai virus. This conserved sequence is considered to be a recognition site for RNA polymerase (9). The first 9 nucleotides from the 3'-terminus of HPIV3 genomic RNA are also identical to those of measles virus genomic RNA (6). From nucleotide 56 onwards our sequence (including unpublished data) is identical to that reported for the HPIV3 NP mRNA untranslated and coding regions (1). However, the complement of the 5'-end of the viral replicative RNA (1) does not correspond to the sequence we have identified by direct sequencing of HPIV3 genomic RNA.

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