

Nucleotide sequence of the phosphoprotein (P) gene of Newcastle disease virus (strain Beaudette C)

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The phosphoprotein, or P protein, of Newcastle disease virus is required for transcription of the viral genome (1) and is the major product of the P gene (2). The cDNA for the complete P gene of Newcastle disease virus (strain Beaudette C) was cloned and sequenced in both directions by using Bal-31 and restriction endonuclease subcloning. The largest open reading frame of the P gene codes for a protein of 395 amino acids with a calculated molecular weight of 42,241. The Beaudette C strain is mesogenic, or moderately virulent. When compared to the published sequences for the strain D26 (3), a lentogenic strain with little or no virulence, and for the strain AV (4), a velogenic or highly virulent strain, the Beaudette C strain showed 72% homology in the non-coding region and 89% homology in the coding region with the former and a 71% and 88% homology respectively with the later. The amino acid percent homology was 91.5% and 90% with the D26 and AV strains, respectively.

The P gene of other paramyxoviruses is bicistronic (5). For example, the Sendai virus P mRNA is translated into five proteins from two overlapping reading frames from different start codons (5). Ribosomal initiation for one of the proteins is from an ACG codon (6, 7). The number of translation products of the Newcastle disease virus P mRNA is not known. In addition to the long open reading frame for the P protein, the P gene from the Beaudette C strain contains four other open reading frames which could code for proteins of calculated molecular weights of 6,660, 7,151, 10,510, and 11,216. Two of these frames are +1 relative to the P protein and both have AUG codons for initiation. Two additional open reading frames are −1 relative to the P protein and one of these has an ACG codon with purines at −3 and +4.

Furthermore, paramyxoviruses transcribe more than one mRNA from the P gene (5). These mRNAs differ by G insertions and evidence suggests that the G residues are added by a stuttering mechanism during transcription (8, 9). The P gene of the Beaudette C strain contains a genomic sequence 3′-UUUUUCCC-5′ (nucleotides 467−474) which is identical to the stuttering site in Sendai virus and measles virus (9). We propose that this site is used by Newcastle disease virus to insert one G residue. This edited mRNA would encode a 239 amino acid protein with a predicted molecular weight of 25,485. The protein derives its amino terminus from the P protein yet contains a unique carboxy terminus. The carboxy terminus is cysteine-rich and the cysteine pattern resembles a zinc finger motif. The product of this proposed edited mRNA may have been detected recently (10). A monoclonal antibody raised against the P protein reacted with a cysteine-rich 36K protein from virus-infected cells.

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