Nucleotide and deduced amino acid sequences of the nominal nonstructural phosphoprotein of the ERA, PM and CVS-11 strains of rabies virus

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The nominal nonstructural (NS) phosphoprotein of rabies virus is an integral component of the viral ribonucleoprotein complex. By analogy, to the NS protein of the vesicular stomatitis virus, the prototype of the Rhabdoviridae family which includes the rabies virus, the NS protein of the rabies virus is required for the transcription and replication of the single-stranded RNA genome (1). The nucleotide sequence and deduced amino acid sequence of the NS gene of the Pasteur strain of rabies virus has been reported previously (2). We have sequenced the NS genes of three additional laboratory-adapted strains of rabies virus: EvelynRokitnicki-Abelseth (ERA) strain, Pitman-Moore (PM) strain, and challenge virus standard-11 (CVS-11) strain. The NS gene of the ERA strain has been cloned (3), and the cDNA was sequenced in its entirety by the dideoxy chain termination method (4) and intermittently by the chemical cleavage method (5). The nucleotide sequence was confirmed by direct sequencing of the single-stranded RNA genome of ERA using NS-specific oligonucleotide primers to processively sequence through the region of the genome containing the NS gene. Nucleotide sequences from the PM and CVS-11 strains were also obtained by directly sequencing the genomic RNA of the viruses (6). The advantage of using genomic RNA as the template for dideoxy sequencing lies in the ability to obtain accurate data from a homogeneous population rather than from a cDNA clone which may contain a misincorporated nucleotide(s).

The sequences in this report are presented in the mRNA sense, which is the complement of the negative-sense RNA genome, and encompass all nucleotides between the NS mRNA transcriptional start site (5'-AACA-3') and the presumptive viral polyadenylation signal (5'-TGAAAAAA-3'). An open reading frame coding for 297 amino acid residues is located between the initiation codon (ATG) starting at nucleotide 30 and a termination codon (TAA) ending at nucleotide 923. The nucleotide and deduced amino acid sequences of the ERA and PM strains are 100% homologous throughout this region. The previously reported NS sequence of the Pasteur strain (2) displays 99% homology at the nucleotide level and 98% homology at the amino acid level to the ERA and PM sequences. The nucleotide sequence of the CVS-11 strain is 88% homologous to the ERA and PM strains, but displays 92% homology at the amino acid level

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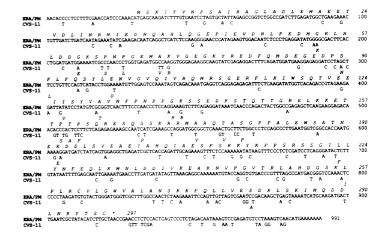


Figure 1. The nucleotide and deduced amino acid sequences of the ERA and PM strains of the rabies virus are presented on the second and first lines, respectively. The CVS-11 nucleotide and deduced amino acid sequences are presented on the third and fourth lines, respectively, which display only the differences between the two strains.

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