

The complete nucleotide sequence of the GDVII strain of Theiler's murine encephalomyelitis virus (TMEV)

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cDNA clones spanning the genome of the GDVII strain of TMEV were produced, and the complete nucleotide sequence determined (fig. 1).

Strains of TMEV cause a neurological disease in mice; the type of disease depends upon to which of the two subgroups of TMEV the strain used belongs. Sequence comparisons of strains representative of each subgroup e.g. GDVII and BeAn, are used to identify regions of the genome which may be involved in governing the different neurovirulence of members of the two subgroups. The genomes of GDVII and BeAn are, however, 90% identical (1): it is therefore important to consider the degree of divergence which may occur within a population of a given strain of virus.

The sequence of GDVII presented here was determined from virus kindly provided by Dr. H. Lipton (see ref. 1), but variations exist between it and that previously published (1). Briefly, this

sequence is 8101 bases in length rather than 8105. Both the 5' and 3' non-coding regions are shorter; consisting of 1067 not 1068, and 122 not 125 nucleotides, respectively. Of the seven changes detected in the nucleotides of the open reading frame, four result in amino acid substitutions, and it is interesting to note that three of these result in the amino acid present being identical to that found in the BeAn (2) rather than the GDVII (1) sequence of Pevear *et al.*

ACKNOWLEDGEMENT

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REFERENCES

1. Pevear, D.C. *et al.* (1988) *Virology* **165**, 1-12.
2. Pevear, D.C. *et al.* (1987) *J. Virol.* **61**, 1507-1516.

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Figure 1. Nucleotide sequence of GDVII. Lower case letters represent non-coding regions.