Molecular Biological Analysis of Measles Virus Gene Expression in the CNS of Acutely and Persistently Infected Rat Brain Cells

SCHNEIDER-SCHAULIES, SIBYLLE, U. G. LIEBERT, K. BACZKO, and V. TER MEULEN

Inst. f. Virologie u. Immunbiologie, Univ., D-8700 Würzburg

In order to characterize parameters leading to the establishment and the maintenance of persistent measles virus (MV) CNS-infection we analysed viral gene expression in our animal model of MV-induced acute and subacute encephalomyelitis (AE and SAME) in Lewis rats and primary astrocyte cultures. The expression of the M, F and H proteins was found to be reduced in vivo early in infection. Analysis of the corresponding mRNAs revealed that the synthesis of the F and H mRNAs is restricted in brain cells of the Lewis rats one week following infection and the primary astrocytes as soon as 24 hours after infection. The synthesis of the M-protein is obviously restricted on translational levels because the corresponding mRNA is transcribed efficiently in all systems tested. — The results indicate that persistence of MV in brain cells is accomplished by a restriction of viral gene expression on both transcriptional and translational level very soon after infection probably as the result of intrinsic properties of the infected host cells.

Organization of Repetitive DNA Sequences of the Genome of Fish Lymphocystis Disease Virus and their Evolutionary and Regulatory Role

SCHNITZLER, P., J. SCHOLZ, and G. DARAI

Inst. f. Med. Virologie, Univ., D-6900 Heidelberg

The genome structure of the Fish Lymphocystis Disease Virus (FLDV) was found to be circularly permuted and terminally redundant. The FLDV genome was screened for presence of repetitive DNA sequences using the defined and complete gene library of the viral genome (98 kbp) by DNA-DNA hybridization, heteroduplex analysis, and restriction fine mapping. A repetitive DNA sequence was detected at the coordinates 0.034 to 0.057 and 0.718 to 0.736 map units of the FLDV genome. The complete DNA nucleotide sequence of both regions was determined. The size of these repetitive DNA elements was founded to be 1397 bp and 1416 bp, respectively. The degree of DNA nucleotide homology was greater than 90%. For the evaluation of the evolutionary role of this DNA element the DNA sequences of the repetitive DNA elements of other types of FLDV isolated from other fish species (dab) were determined and compared to each other. This analysis revealed that these repetitive elements are conserved in the genome of different strains and types of FLDV, indicating the importance of these DNA elements for virus progeny, e.g. virus replication and encapsidation. – DFG Da 142/2–2.