

Involvement of cysteine in Semliki Forest virus (SFV) induced fusion of *Aedes albopictus* cells

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Aedes cells infected with SFV fuse when exposed to pH 6. We have previously shown that 1) this process is a 'fusion from within', 2) a conformational change occurs at the plasma membrane, presumably of the viral spike proteins and 3) the new conformation is stable. The conformation of proteins may be stabilized by disulfide bonds. To examine this, sodium thiosulfate and sodium sulfite at 1 mM concentrations were added to the cells 16 h after infection. Application before lowering the pH had no effect on the fusion. However, application after lowering the pH completely inhibits fusion. This result substantiated that the known conformational change on the cell surface leads to exposition of disulfide bonds which are essential for maintaining the fusogenic conformation. Incorporating the results obtained with dithiothreitol and tetrathionate we conclude that at least three cysteines are involved in fusion.

In vitro protein synthesis by cells infected with different types of bovine herpesvirus 1

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Based on present knowledge strains of bovine herpesvirus 1 (BHV-1) can be assigned to one out of three major virus types, i.e. BHV-1/type 1, BHV-1/type 2 (with subtypes 2a and 2b), and BHV-1/type 3 (with subtypes 3a and 3b). Comparison of the various virus types and subtypes revealed that BHV-1/subtype 3b viruses were consistently difficult to grow to satisfactory infectivity titers. This was paralleled by delayed appearance of virus-induced cytopathology, concomitant with the production of smaller plaques.

The present study shows that the protein synthesis rate at various times after infection (as determined by measuring incorporation of (³⁵S)methionine into translational products) was more efficiently reduced by subtype 3b strains, when compared with the other viruses. This reduction was followed by a low virus-induced protein synthesis rate. The results imply that some non-impaired host cell functions could be of importance in determining the efficiency of viral growth.

Bovine herpesvirus 1 and caprine herpesvirus 1: viral polypeptides exhibiting shared and unique antigenic determinants

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It is established that strains of bovine herpesvirus 1 (BHV-1) are immunologically closely related, whereas strains of BHV-1 and CapHV-1 (caprine herpesvirus 1) display a non-reciprocal immunological relationship. In order to identify viral polypeptides exhibiting shared or unique antigenic determinants a panel of 11 monoclonal antibodies (McAb's) was used to immune precipitate infected cell proteins of three strains of BHV-1 (representing the three established virus types) and one strain of CapHV-1. The McAb's had been generated with a BHV-1/type 1 virus. With the homologous virus the following 13 proteins (p) and glycoproteins (gp) could be identified (mol. wt $\times 10^{-3}$ in parentheses): p3 (153), gp7 (126), gp10 (102), p11 (96), p11A (95), gp12 (87), p16 (76), gp17 (73), gp17A (74), p18 (69), p19 (68), p20 (67), and gp23 (55). The same panel of McAb's precipitated a reduced number of proteins from infected cell extracts obtained with the other virus strains. Taken together, our data implied the following antigenic relationship: BHV-1/type 1 > BHV-1/type 2 >> BHV-1/type 3 >>> CapHV-1.

Restriction site maps of a new type of bovine herpesvirus 1

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Bovine herpesvirus 1 (BHV-1) isolates can be divided into three types based on DNA restriction patterns, protein profiles and monoclonal antibodies. Type 1 and 2 were characterized before, whereas the clearly differing third type was recognized only recently. Most isolates of the third type stemmed from brains of calves suffering from meningoencephalitis.

In order to compare type 3 DNA with type 1 and 2 DNA we examined their structure by electron microscopy of self-annealed double stranded molecules and constructed various restriction site maps by conventional methods. The genome structure corresponded to that of BHV-1, whereas the physical maps differed apparently. Nevertheless, cross-hybridization experiments showed a complete base sequence homology between the three types. This is indicative of mutations concerning only limited regions of the genome and confirms the close relationship between BHV-1 types. More detailed analysis will be necessary to enlighten the significance of these findings.

Regulation of the promoters in SV40 chromosomes and construction of a substituted SV40 containing a *Drosophila* hsp70 promoter

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We have studied the chromosome structural elements and transacting factors which together regulate the late and early promoters of SV40. Isolated SV40 chromosomes were bound to hydroxylapatite and the chromosomal proteins recovered by washing with increasing concentrations of salt and urea. A protein fraction was obtained which, when added to in vitro transcription reactions with naked SV40 DNA templates, markedly stimulated the late promoter. Experiments using an electrophoretic band-shift assay suggested that protein(s) in the active fraction bound specifically to an SV40 DNA fragment containing the late promoter giving rise to DNA-protein complexes of distinct electrophoretic mobility.

To study the role of chromatin structure in regulating the *Drosophila* hsp70 promoter we are inserting a DNA fragment containing this promoter into SV40. The hsp70 sequences replace a similarly sized stretch from the SV40 early region, giving a defective virus able to replicate in T-antigen-containing COS cells.

Detection of viruses by electron microscopy in fecal samples from patients with gastroenteritis in the canton of Vaud

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During the period January 1982 to December 1984, 757 stool samples obtained from 531 patients with diarrhoea, were examined by electron microscopy. The specimens were resuspended in distilled water, negatively stained with 2% phosphotungstic acid before being spread on a formvar-carbon coated copper grid.

In 30.51% of the cases rotavirus was present while in 2.64% there were adenovirus particles out of which 50% could not be isolated in cell cultures. Norwalk-like viruses were seen in only 0.85% and in 3.58% bacteriophages were present. Coronavirus particles were not observed in any of the fecal samples.

Electrophoretic studies made on the genome of the rotaviruses revealed at least seven electropherotypes which were distributed as follows: two in 1982, three in 1983 and two in 1984. The samples were sent in from various parts of the canton.