



Current Topics in Microbiology and Immunology / Ergebnisse der Mikrobiologie und Immunitätsforschung

W. Arber, W. Henle, P. H. Hofschneider, J. H. Humphrey, N. K. Jerne, P. Koldovský, H. Koprowski, O. Maaløe, R. Rott, H. G. Schweiger, M. Sela, L. Syru?ek, P. K. Vogt

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The processes involved in herpesvirus replication, latency, and oncogenic transformation, have, in general, been rather poorly defined. A primary reason for this is the size and complexity of the herpesvirus genome. Undoubtedly, a better understanding of the functions of the viral genome in infected and transformed cells will be achieved through studies with temperature-sensitive (ts) mutants of herpesviruses since, theoretically, any essential gene function can be affected by mutants of this type.

A. The Herpesviruses

A consideration of the genetic analysis of members of the herpesvirus group necessitates a description, albeit brief, of the properties of the group and, most importantly, of their genetic material. The herpesviruses comprise a group of relatively large (100-150 nm), enveloped viruses. The envelope surrounds an icosahedral capsid enclosing a core which contains double stranded DNA (ROIZMAN, 1969). The group is thus defined on the basis of a common virion morphology. In addition to a common structure, members of the group share a number of biological properties such as a similar replicative cycle, the ability to cause latent and chronic infections, and the ability to induce antigenic modifications of infected cell membranes. Several herpes viruses have been associated recently with malignancies in man and animals (KLEIN, 1972). Herpesviruses are ubiquitous and have been described in over 30 different species (HUNT and MELENDEZ, 1969; WILDY, 1971; FARLEY et al. , 1972; KAZAMA and SCHORNSTEIN, 1972; NAHMIAS et al. , 1972; ROIZMAN et al. , 1973). Their widespread occurrence in nature suggests a common ancestor.

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