SECTION 12 INFECTIONS DUE TO DNA VIRUSES

216 Herpes Simplex Virus Infections

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DEFINITION

Herpes simplex viruses (HSV-1, HSV-2; *Herpesvirus hominis*) produce a variety of infections involving mucocutaneous surfaces, the central nervous system (CNS), and—on occasion—visceral organs. Prompt recognition and treatment reduce the morbidity and mortality rates associated with HSV infections.

ETIOLOGIC AGENT

The genome of HSV is a linear, double-strand DNA molecule (molecular weight, ~100 × 10^6) that encodes >90 transcription units with 84 identified proteins. The genomic structures of the two HSV subtypes are similar. The overall genomic sequence homology between HSV-1 and HSV-2 is ~50%, whereas the proteome homology is >80%. The homologous sequences are distributed over the entire genome map, and most of the polypeptides specified by one viral type are antigenically related to polypeptides of the other viral type. Many type-specific regions unique to HSV-1 and HSV-2 proteins do exist, however, and a number of them appear to be important in host immunity. These type-specific regions have been used to develop serologic assays that distinguish between the two viral subtypes. Either restriction endonuclease analysis or sequencing of viral DNA can be used to distinguish between the two subtypes and among strains of each subtype. The variability of nucleotide sequences from clinical strains of HSV-1 and HSV-2 is such that HSV isolates obtained from two individuals can be differentiated by restriction enzyme patterns or genomic sequences. Moreover, epidemiologically related sources, such as sexual partners, mother-infant pairs, or persons involved in a common-source outbreak, can be inferred from such patterns.

The viral genome is packaged in a regular icosahedral protein shell (capsid) composed of 162 capsomeres (see Fig. 214e-1). The outer covering of the virus is a lipid-containing membrane (envelope) acquired as the DNA-containing capsid buds through the inner nuclear membrane of the host cell. Between the capsid and lipid bilayer of the envelope is the tegument. Viral replication has both nuclear and cytoplasmic phases. Initial attachment to the cell membrane involves interactions of viral glycoproteins C and B with several cellular heparan sulfate–like surface receptors. Subsequently, viral glycoprotein D binds to cellular co-receptors that belong to the tumor necrosis factor receptor family of proteins, the immunoglobulin superfamily (nectin family), or both. The ubiquity of these receptors contributes to the wide host range of herpesviruses. HSV replication is highly regulated. After fusion and entry, the nucleocapsid enters the cytoplasm and several viral proteins are released from the virion. Some of these viral proteins shut off host protein synthesis (by increasing cellular RNA degradation), whereas others "turn on" the transcription of early genes of HSV replication. These early gene products, designated *α genes,* are required for synthesis of the subsequent polypeptide group, the β polypeptides, many of which are regulatory proteins and enzymes required for DNA replication. Most current antiviral drugs interfere with β proteins, such as viral DNA polymerase. The third (γ) class of HSV genes requires viral DNA replication for expression and encodes most structural proteins specified by the virus.

After viral genome replication and structural protein synthesis, nucleocapsids are assembled in the cell's nucleus. Envelopment occurs as the nucleocapsids bud through the inner nuclear membrane into the perinuclear space. In some cells, viral replication in the nucleus forms two types of inclusion bodies: type A basophilic Feulgen-positive bodies that contain viral DNA and eosinophilic inclusion bodies that are devoid of viral nucleic acid or protein and represent a "scar" of viral infection. Enveloped virions are then transported via the endoplasmic reticulum and the Golgi apparatus to the cell surface.

Viral genomes are maintained by some neuronal cells in a repressed state called *latency*. Latency, which is associated with transcription of only a limited number of virus-encoded RNAs, accounts for the presence of viral DNA and RNA in neural tissue at times when infectious virus cannot be isolated. Maintenance and growth of neural cells from latently infected ganglia in tissue culture result in production of infectious virions (*explantation*) and in subsequent permissive infection of susceptible cells (*co-cultivation*). Activation of the viral genome may then occur, resulting in *reactivation*—the normal pattern of regulated viral gene expression and replication and HSV release. The release of virions from the neuron follows a complex process of anterograde transport down the length of neuronal axons. In experimental animals, ultraviolet light, systemic and local immunosuppression, and trauma to the skin or ganglia are associated with reactivation.

Three noncoding RNA latency-associated transcripts (LATs) are found in the nuclei of latently infected neurons. Deletion mutants of the LAT region exhibit reduced efficiency in their later reactivation. Substitution of HSV-1 LATs for HSV-2 LATs induces an HSV-1 reactivation pattern. These data indicate that LATs apparently maintain—rather than establish—latency. HSV-1 LATs promote the survival of acutely infected neurons, perhaps by inhibiting apoptotic pathways. LAT transcript abundance and low genome-copy number correlate with subnuclear positioning of HSV genomes around the centromere. Indeed, chromatization of HSV DNA appears to play a vital role in silencing expression of lytic replication genes. Highly expressed during latency, LAT-derived micro-RNA appears to silence expression of the key neurovirulence factor infected-cell protein 34.5 (ICP34.5) and to bind in an antisense configuration to the immediate-early protein ICP0 messenger RNA to prevent expression, which is vital to HSV reactivation. Although certain viral transcripts are known to be necessary for reactivation from latency, the molecular mechanisms of HSV latency are not fully understood, and strategies to interrupt or maintain latency in neurons are in developmental stages.

While latency is the predominant state of virus on a per-neuron basis, the high frequency of oral and genital tract reactivation for HSV-1 and HSV-2 suggests that the viruses are rarely quiescent within the entire biomass of ganglionic tissue. Recent data indicate that HSV-2 antigen is often shed: most persons infected with HSV-2 have frequent subclinical bursts of reactivation lasting 2–4 h, and the host mucosal immune system can contain viral reactivation in the mucosa before the development of clinical reactivation. Supporting this clinical observation, recent work using microdissection plus real-time polymerase chain reaction (PCR) of individual neurons from cadaveric trigeminal ganglia explants revealed that many more neurons (2–10%) harbor HSV than would be predicted by in situ hybridization studies for LATs. Viral copy number is highly variable between neurons, with extremely high levels in certain neurons, and HSV DNA copy numbers are similar in LAT-positive and LAT-negative neurons; these findings add to the uncertainty about the role that LATs play in preventing reactivation.

PATHOGENESIS

Exposure to HSV at mucosal surfaces or abraded skin sites permits entry of the virus into cells of the epidermis and dermis and initiation of viral replication therein. HSV infections are usually acquired subclinically. Whether clinical or subclinical, HSV acquisition is associated with sufficient viral replication to permit infection of either sensory or autonomic nerve endings. On entry into the neuronal cell, the virus—or, more likely, the nucleocapsid—is transported intra-axonally to the nerve cell bodies in ganglia. In humans, the transit interval of spread to the ganglia after virus inoculation into peripheral tissue is unknown. During the initial phase of infection, viral replication occurs in ganglia