SECTION 14 INFECTIONS DUE TO HUMAN IMMUNODEFICIENCY VIRUS AND OTHER HUMAN RETROVIRUSES

225e The Human Retroviruses

Dan L. Longo, Anthony S. Fauci

The retroviruses, which make up a large family (Retroviridae), infect mainly vertebrates. These viruses have a unique replication cycle whereby their genetic information is encoded by RNA rather than DNA. Retroviruses contain an RNA-dependent DNA polymerase (a reverse transcriptase) that directs the synthesis of a DNA form of the viral genome after infection of a host cell. The designation *retrovirus* denotes that information in the form of RNA is transcribed into DNA in the host cell—a sequence that overturned a central dogma of molecular biology: that information passes unidirectionally from DNA to RNA to protein. The observation that RNA was the source of genetic information in the causative agents of certain animal tumors led to a number of paradigm-shifting biologic insights regarding not only the direction of genetic information passage but also the viral etiology of certain cancers and the concept of oncogenes as normal host genes scavenged and altered by a viral vector.

The family Retroviridae includes seven subfamilies (Table 225e-1). Members of two of the families infect humans with pathologic consequences: the deltaretroviruses, of which human T cell lymphotropic virus (HTLV) type 1 is the most important in humans; and lentiviruses, of which HIV is the most important in humans.

The wide variety of interactions of a retrovirus with its host range from completely benign events (e.g., silent carriage of endogenous retroviral sequences in the germline genome of many animal species) to rapidly fatal infections (e.g., exogenous infection with an oncogenic virus such as Rous sarcoma virus in chickens). The ability of retroviruses to acquire and alter the structure and function of host cell sequences has revolutionized our understanding of molecular carcinogenesis. The viruses can insert into the germline genome of the host cell and behave as a transposable or movable genetic element. They can activate or inactivate genes near the site of integration into the genome. They can rapidly alter their own genome by recombination and mutation under selective environmental stimuli.

Most human viral diseases occur as a consequence of tissue destruction either directly by the virus itself or indirectly by the host's response to the virus. Although these mechanisms are operative in retroviral infections, retroviruses have additional mechanisms of inducing disease, including the malignant transformation of an infected cell and the induction of an immunodeficiency state that renders the host susceptible to opportunistic diseases (infections and neoplasms; Chap. 226).

TABLE 225e-1 CLASSIFICATION OF RETROVIRUSES: THE FAMILY RETROVIRIDAE

Genus	Example(s)	Feature
Alpharetrovirus	Rous sarcoma virus	Contains *src* oncogene
Betaretrovirus	Mouse mammary tumor virus	Exogenous or endogenous
Gammaretrovirus	Abelson murine leukemia virus	Contains *abl* oncogene
Deltaretrovirus	HTLV-1	Causes T cell lymphoma and neurologic disease
Epsilonretrovirus	Walleye dermal sarcoma virus	Not known to be pathogenic in humans
Lentivirus	HIV-1, -2	Causes AIDS
Spumavirus	Simian foamy virus	Not known to be pathogenic in humans

STRUCTURE AND LIFE CYCLE

All retroviruses are similar in structure, genome organization, and mode of replication. Retroviruses are 70–130 nm in diameter and have a lipid-containing envelope surrounding an icosahedral capsid with a dense inner core. The core contains two identical copies of the single-strand RNA genome. The RNA molecules are 8–10 kb long and are complexed with reverse transcriptase and tRNA. Other viral proteins, such as integrase, are also components of the virion particle. The RNA has features usually found in mRNA: a cap site at the 5′ end of the molecule, which is important in the initiation of mRNA translation, and a polyadenylation site at the 3′ end, which influences mRNA turnover (i.e., messages with shorter polyA tails turn over faster than messages with longer polyA tails). However, the retroviral RNA is not translated; instead it is transcribed into DNA. The DNA form of the retroviral genome is called a *provirus*.

The replication cycle of retroviruses proceeds in two phases (Fig. 225e-1). In the first phase, the virus enters the cytoplasm after binding to one or more specific cell-surface receptors; the viral RNA and reverse transcriptase synthesize a double-strand DNA version of the RNA template; and the provirus moves into the nucleus and integrates into the host cell genome. This proviral integration is permanent. Although some animal retroviruses integrate into a single specific site of the host genome in every infected cell, the human retroviruses integrate randomly. This first phase of replication depends entirely on gene products in the virus. The second phase includes the synthesis and processing of viral genomes, mRNAs, and proteins using host cell machinery, often under the influence of viral gene products. Virions are assembled and released from the cell by budding from the membrane; host cell membrane proteins are frequently incorporated into the envelope of the virus. Proviral integration occurs during the S-phase of the cell cycle; thus, in general, nondividing cells are resistant to retroviral infection. Only the lentiviruses are able to infect nondividing cells. Once a host cell is infected, it is infected for the life of the cell.

Retroviral genomes include both coding and noncoding sequences (Fig. 225e-2). In general, noncoding sequences are important recognition signals for DNA or RNA synthesis or processing events and are located in the 5′ and 3′ terminal regions of the genome. All retroviral genomes are terminally redundant, containing identical sequences called *long terminal repeats* (LTRs). The ends of the retroviral RNA genome differ slightly in sequence from the integrated retroviral DNA. In the latter, the LTR sequences are repeated in both the 5′ and the 3′ terminus of the virus. The LTRs contain sequences involved in initiating the expression of the viral proteins, the integration of the provirus, and the polyadenylation of viral RNAs. The primer binding site, which is critical for the initiation of reverse transcription, and the viral packaging sequences are located outside the LTR sequences. The coding regions include the *gag* (group-specific antigen, core protein), *pol* (RNA-dependent DNA polymerase), and *env* (envelope) genes. The *gag* gene encodes a precursor polyprotein that is cleaved to form three to five capsid proteins; a fraction of the Gag precursor proteins also contain a protease responsible for cleaving the Gag and Pol polyproteins. A Gag-Pol polyprotein gives rise to the protease that is responsible for cleaving the Gag-Pol polyprotein. The *pol* gene encodes three proteins: the reverse transcriptase, the integrase, and the protease. The reverse transcriptase copies the viral RNA into the double-strand DNA provirus, which inserts itself into the host cell DNA via the action of integrase. The protease cleaves the Gag-Pol polyprotein into smaller protein products. The *env* gene encodes the envelope glycoproteins: one protein that binds to specific surface receptors and determines what cell types can be infected and a smaller transmembrane protein that anchors the complex to the envelope. Fig. 225e-3 shows how the retroviral gene products make up the virus structure.