membrane, and the HCV polyprotein is cleaved during translation and posttranslationally by host cellular proteases as well as HCV NS2-3 and NS3-4A proteases. Host cofactors involved in HCV replication include cyclophilin A, which binds to NS5A and yields conformational changes required for viral replication, and liver-specific host microRNA miR-122.

At least six distinct major genotypes (and a minor genotype 7), as well as >50 subtypes within genotypes, of HCV have been identified by nucleotide sequencing. Genotypes differ from one another in sequence homology by ≥30%, and subtypes differ by approximately 20%. Because divergence of HCV isolates within a genotype or subtype and within the same host may vary insufficiently to define a distinct genotype, these intragenotypic differences are referred to as *quasispecies* and differ in sequence homology by only a few percent. The genotypic and quasispecies diversity of HCV, resulting from its high mutation rate, interferes with effective humoral immunity. Neutralizing antibodies to HCV have been demonstrated, but they tend to be short lived, and HCV infection does not induce lasting immunity against reinfection with different virus isolates or even the same virus isolate. Thus, neither *heterologous* nor *homologous* immunity appears to develop commonly after acute HCV infection. Some HCV genotypes are distributed worldwide, whereas others are more geographically confined (see "Epidemiology and Global Features"). In addition, differences exist among genotypes in responsiveness to antiviral therapy but not in pathogenicity or clinical progression (except for genotype 3, in which hepatic steatosis and clinical progression are more likely).

Currently available, third-generation immunoassays, which incorporate proteins from the core, NS3, and NS5 regions, detect anti-HCV antibodies during acute infection. The most sensitive indicator of HCV infection is the presence of HCV RNA, which requires molecular amplification by PCR or transcription-mediated amplification (TMA) (Fig. 360-7). To allow standardization of the quantification of HCV RNA among laboratories and commercial assays, HCV RNA is reported as international units (IUs) per milliliter; quantitative assays with a broad dynamic range are available that allow detection of HCV RNA with a sensitivity as low as 5 IU/mL. HCV RNA can be detected within a few days of exposure to HCV—well before the appearance of anti-HCV—and tends to persist for the duration of HCV infection. Application of sensitive molecular probes for HCV RNA has revealed the presence of replicative HCV in peripheral blood lymphocytes of infected persons; however, as is the case for HBV in lymphocytes, the clinical relevance of HCV lymphocyte infection is not known.

Hepatitis E Previously labeled *epidemic* or *enterically transmitted non-A, non-B hepatitis*, HEV is an enterically transmitted virus that causes clinically apparent hepatitis primarily in India, Asia, Africa, and Central America; in those geographic areas, HEV is the most common cause of acute hepatitis; one-third of the global population appears to have been infected. This agent, with epidemiologic features resembling those of hepatitis A, is a 27- to 34-nm, nonenveloped, HAV-like virus with a 7200-nucleotide, single-strand, positive-sense RNA genome. HEV has three open reading frames (ORF) (genes), the largest of which, *ORF1*, encodes nonstructural proteins involved in virus replication. A middle-sized gene, *ORF2*, encodes the nucleocapsid protein, the major nonstructural protein, and the smallest, *ORF3*, encodes a structural protein whose function remains undetermined. All HEV isolates appear to belong to a single serotype, despite genomic heterogeneity of up to 25% and the existence of five genotypes, only four of which have been detected in humans; genotypes 1 and 2 appear to be more virulent, whereas genotypes 3 and 4 are more attenuated and account for subclinical infections. Contributing to the perpetuation of this virus are animal reservoirs, most notably in swine. No genomic or antigenic homology, however, exists between HEV and HAV or other picornaviruses; and HEV, although resembling caliciviruses, is sufficiently distinct from any known agent to merit its own classification as a unique genus, *Hepevirus*, within the family Hepeviridae. The virus has been detected in stool, bile, and liver and is excreted in the stool during the late incubation period. Both IgM anti-HEV during early acute infection and IgG anti-HEV predominating after the first 3 months can be detected. Currently, availability and reliability of serologic/virologic testing for HEV infection is limited but can be done in specialized laboratories (e.g., the Centers for Disease Control and Prevention).

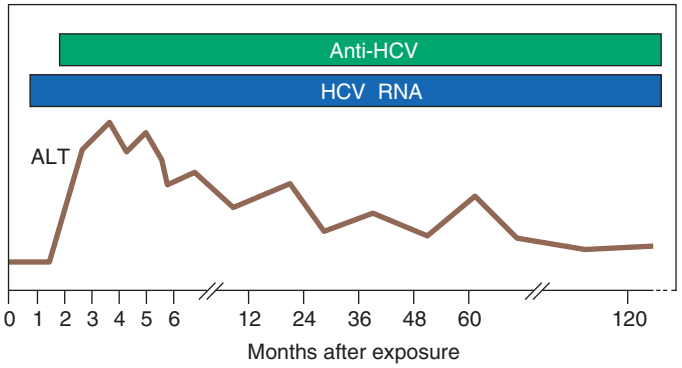

FIGURE 360-7 Scheme of typical laboratory features during acute hepatitis C progressing to chronicity. Hepatitis C virus (HCV) RNA is the first detectable event, preceding alanine aminotransferase (ALT) elevation and the appearance of anti-HCV.

PATHOGENESIS

Under ordinary circumstances, none of the hepatitis viruses is known to be directly cytopathic to hepatocytes. Evidence suggests that the clinical manifestations and outcomes after acute liver injury associated with viral hepatitis are determined by the immunologic responses of the host. Among the viral hepatitides, the immunopathogenesis of hepatitis B and C has been studied most extensively.

Hepatitis B For HBV, the existence of inactive hepatitis B carriers with normal liver histology and function suggests that the virus is not directly cytopathic. The fact that patients with defects in cellular immune competence are more likely to remain chronically infected rather than to clear HBV supports the role of cellular immune responses in the pathogenesis of hepatitis B–related liver injury. The model that has the most experimental support involves cytolytic T cells sensitized specifically to recognize host and hepatitis B viral antigens on the liver cell surface. Nucleocapsid proteins (HBcAg and possibly HBeAg), present on the cell membrane in minute quantities, are the viral target antigens that, with host antigens, invite cytolytic T cells to destroy HBV-infected hepatocytes. Differences in the robustness and broad polyclonality of CD8+ cytolytic T cell responsiveness; in the level of HBV-specific helper CD4+ T cells; in attenuation, depletion, and exhaustion of virus-specific T cells; in viral T cell epitope escape mutations that allow the virus to evade T cell containment; and in the elaboration of antiviral cytokines by T cells have been invoked to explain differences in outcomes between those who recover after acute hepatitis and those who progress to chronic hepatitis, or between those with mild and those with severe (fulminant) acute HBV infection.

Although a robust cytolytic T cell response occurs and eliminates virus-infected liver cells during acute hepatitis B, >90% of HBV DNA has been found in experimentally infected chimpanzees to disappear from the liver and blood before maximal T cell infiltration of the liver and before most of the biochemical and histologic evidence of liver injury. This observation suggests that components of the innate immune system and inflammatory cytokines, independent of cytopathic antiviral mechanisms, participate in the early immune response to HBV infection; this effect has been shown to represent elimination of HBV replicative intermediates from the cytoplasm and covalently closed circular viral DNA from the nucleus of infected hepatocytes. In turn, the innate immune response to HBV infection is mediated largely by natural killer (NK) cell cytotoxicity, activated by immunosuppressive cytokines (e.g., interleukin [IL] 10 and transforming growth factor [TGF] β), reduced signals from inhibitory receptor expression (e.g., major histocompatibility complex), or increased signals from activating receptor expression on infected hepatocytes. In addition, NK cells reduce helper CD4+ cells, which results in reduced CD8+ cells and exhaustion of the virus-specific T cell response to HBV infection. Ultimately, HBV-HLA-specific cytolytic T cell responses of the adaptive immune system are felt to be responsible for recovery from HBV infection.