

Chronic Hepatitis C Virus Infection

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Introduction

Hepatitis C virus (HCV), part of the Hepacivirus genus in the Flaviviridae family, has a 9.6 kb positive-strand RNA genome that includes an internal ribosome entry site (IRES) and various nonstructural proteins critical for replication. There are six major genotypes, with genotypes 1, 2, and 3 being the most prevalent globally, though distribution varies by region. Notably, genotype 1b is associated with a higher risk of chronic infection following acute exposure (Zein, 2000; Moradpour & Penin, 2013).

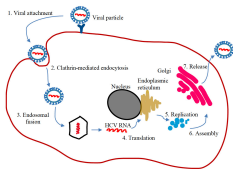


Figure 1: The schematic diagram represents the life cycle of HCV begins with the viral attachment, Clathrin-mediated endocytosis, endosomal fusion, RNA replication and finally viral assembly and release (Che Noh, C. I., Abu Bakar, R., Ahmad, I., 2023)

Pathophysiology of Chronic HCV infection

Hepatitis C virus (HCV) entry into hepatocytes is a multistep process involving viral attachment, receptor-mediated endocytosis, and endosomal fusion (Figure 1). HCV interacts with receptors such as scavenger receptor B1 (SRB1) and heparan sulfate proteoglycans to attach to liver cells. Following entry, HCV's positive-strand RNA genome is released into the cytoplasm, leading to polyprotein production through the endoplasmic reticulum (Manns et al., 2017). HCV replication is influenced by host factors like microRNA-122 and Cyclophilin A. The immune response to HCV involves both innate and adaptive mechanisms, with effective CD4⁺ and CD8⁺ T cell responses linked to viral clearance. Chronic infection can lead to liver damage, fibrosis, and steatosis, particularly associated with genotype 3. The interplay between viral persistence, immune evasion, and host response is critical in the progression of HCV-related liver disease (Schoggins & Rice, 2013).

References

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