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The Global Prevalence of Hepatitis E Virus Infection and Susceptibility: A Systematic Review

Immunization, Vaccines and Biologicals

World Health
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Rakesh Aggarwal, MD, DM, MSc (Epidemiology)
Department of Gastroenterology
Sanjay Gandhi Postgraduate Institute of Medical Sciences
Lucknow, India

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World Health Organization
Department of Immunization, Vaccines and Biologicals
CH-1211 Geneva 27, Switzerland
• *Fax:* + 41 22 791 4227 • *Email:* vaccines@who.int •

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Contents

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Background

Hepatitis E virus

Hepatitis E virus (HEV) is a small, non-enveloped virus, approximately 27-34 nm in diamter. The virus has a polyadenylated, single-stranded RNA genome, approximately 7.2 kilobases in length, with a positive polarity and a cap at its 5’-end. The viral genome contains short non-coding regions at both the 5’ and the 3’ ends, and contains three discontinuous and partially overlapping open reading frames. The largest open reading frame (ORF), known as ORF1, codes for viral non-structural proteins and contains several conserved domains, including putative methyltransferase, protease, helicase and RNA-dependent RNA polymerase. The ORF2 codes for the viral capsid protein, and the ORF3 for a small phosphoprotein with uncertain function. HEV is the only member of the genus *Hepevirus* and is placed in the family *Hepeviridae*.

The genus *Hepevirus* consists so far of two species: (i) mammalian HEV, which causes human disease and infects several other mammalian species, in particular pigs; and (ii) avian HEV, which is responsible for big liver and spleen disease in chicken, and is known to infect other birds such as turkeys. The avian HEV is believed not to be transmitted to man.

Viral genotypes

On genomic sequence analysis, human and swine HEV isolates group into four genotypes, namely genotypes 1, 2, 3 and 4, each with several subtypes. Avian isolates of HEV have a shorter (6.6 kb) genome with only approximately 50% sequence homology with mammalian isolates. These isolates thus constitute a genetically distinct group, which though initially proposed to be a fifth HEV genotype, appears to be a separate genus. All HEV genotypes share at least one major, serologically cross-reactive epitope and belong to a single serotype. Each HEV genotype appears to have a specific