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**Abstract:**

Hepatitis E virus (HEV) is a positive-stranded RNA virus with a 7.2 kb genome that is capped and polyadenylated. The virus is currently unclassified: the organisation of the genome resembles that of the Caliciviridae but sequence analyses suggest it is more closely related to the Togaviridae. Hepatitis E virus is an enterically transmitted virus that causes both epidemics and sporadic cases of acute hepatitis in many countries of Asia and Africa but only rarely causes disease in more industrialised countries. Initially the virus was believed to have a limited geographical distribution. However, serological studies suggest that HEV may be endemic also in the United States and Europe even though it infrequently causes overt disease in these countries. Many different animal species worldwide recently have been shown to have antibodies to HEV suggesting that hepatitis E may be zoonotic. Although two related strains have been experimentally transmitted between species, direct transmission from an animal to a human has not been documented. There are four currently recognised genotypes and two of the four contain viruses isolated from swine as well as from humans. Regardless of country of origin or genotype of the virus, most, if not all, strains belong to a single serotype. A promising recombinant vaccine candidate comprised of a truncated capsid protein is currently under evaluation in Nepal.