The Detection and Phylogenetic Analysis of Bovine Hepacivirus in China

Hepacivirus has been identified in cattle in Africa, Europe, and South America. In this survey of bovine hepacivirus (BovHepV) in 131 serum samples from Chinese cattle herds using RT-PCR, five of 131 sera were BovHepV positive, with the infection rate of 3.82%. Phylogenetic analysis based on the partial NS3 coding sequence showed that the BovHepV of the five positive samples clustered with other BovHepV but formed a separate branch. The results indicated that these new BovHepV represent emerging and novel strains. Further investigations are necessary to determine the epidemiology and viral pathogenesis of these BovHepV strains, as well as the potential threat to ruminant and livestock workers in China.
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