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Serological survey and molecular detection of hepatitis E virus in rabbits of Belarus

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Statement of the Problem: Hepatitis E virus (HEV) infection is recognized as a zoonosis. The prevalence of HEV RNA and anti-HEV antibodies in different animal species has been reported, but the host range of HEV is unclear. Rabbit HEV is a novel genotype of HEV. In this study, we investigated biological material obtained from Belarusian rabbits for the presence of HEV RNA in feces, as well as anti-HEV IgG in serum, to determine the prevalence of HEV in Belarusian rabbits.

Methodology & Theoretical Orientation: The object of this study was blood, serum and feces from rabbits contained in Belarusian vivarium. Samples were collected from rabbits aged 2-12 month during 2014-2017 in different cities of Belarus. For detection of HEV RNA in fecal samples, we used nested reverse transcription PCR. Rabbit sera were tested for anti-HEV IgG using a commercial diagnostic ELISA kit.

Findings: During the study, we have tested 129 fecal samples of rabbits for HEV RNA. HEV RNA was detected in 29 samples (22.5%). Among 88 sera samples collected from rabbits, the positive rate for HEV-specific IgG was 25% (22). Phylogenetic analysis showed that the isolates of HEV RNA from Belarusian rabbits form a single cluster with isolates obtained from rabbits in China, as well as isolates from rabbits in Moscow and Moscow region with similarity of the nucleotide sequence 86%. The allocated cluster is independent, close, but not related to the HEV3.

Conclusion & Significance: This study showed that rabbit HEV is closest to the third genotype, but apparently it is an independent subtype of the virus. The obtained data suggest that there is an epidemic process of HEV in rabbit population of Belarus and rabbits have been confirmed to be a reservoir of HEV in Belarus.

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