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Divergent Genotype of Hepatitis A Virus in Alpacas, Bolivia, 2019

Inhalt

Hepatitis A virus (HAV) is a common human pathogen causing acute hepatitis. Human HAV belongs to species Hepatovirus A, genus Hepatovirus, family Picornaviridae. HAV strains of Hepatovirus A are only found in humans (genotypes I-III) and monkeys (genotypes IV-VI), with no non-primate reservoir host. We screened serum and faeces of 70 alpacas and llamas from Bolivia for novel viruses using undirected Illumina High Throughput Sequencing, and detected a divergent HAV. In a PCR screen of 64 alpacas and 6 llamas, we detected HAV RNA in serum and/or faeces of ~9% of alpacas, but not in llamas. In ELISA analysis, we found HAV antibodies in ~64% of alpacas and ~67% of llamas, suggesting HAV infection is common. Complete-genome analysis of alpaca HAV suggests that it is a novel non-primate genotype of Hepatovirus A. Phylogenetic analysis indicates a long association of HAV with alpacas. HAV in alpacas is similar to human HAV infection: RNA is present in serum and faeces at viral loads comparable to human infection, and immunity builds up over life. Alpaca HAV might belong to the same serotype as genotypes I-VI. Consequently, HAV vaccinations, especially for camelid handlers, should be considered to reduce spillover risk.

Keywords

HAV, alpaca, metagenomics, virus discovery, virus taxonomy

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Yes, I am a Junior Scientist.

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