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

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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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Professional Status of the Speaker

Postdoc

Junior Scientist Status

Yes, I am a Junior Scientist.

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