Phylogenetic analysis of Hepatitis E virus and contamination sources in swine production network

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Viral contamination along the production chain is an important aspect of food safety and livestock have been reported to act as a reservoir for zoonotic, sometimes emerging viruses. Epidemiological studies have shown direct links between the consumption of uncooked pork meat and cases of hepatitis caused by the hepatitis E virus (HEV) genogroup 3 in humans. HEV can resist to low pH, to heat and to multiple freezing and thawing, making it persistent in the environment. Little is known on HEV distribution in pork meat primary production in Quebec.

In order to type HEV genogroup 3 strains and evaluate the contamination sources in a swine production network, 486 environment and faecal samples were collected from 10 farms and a slaughterhouse representing a single production network, including samples of trucks transporting animals, over a period of 11 months. Viral RNA was extracted and a nested RT-PCR was performed. Positive samples were sequenced and a phylogenetic analysis was performed.

HEV RNA was found in 38 samples both inside and outside the farm buildings, on the trucks, but most of them were found around the slaughterhouse, especially on the skid-loader. Phylogenetic analysis showed a wide diversity of HEV strains amongst samples. Interestingly, one strain detected in the slaughterhouse's field was homologous at 99% to a strain previously found in liver-transplanted immunosuppressed child who developed chronic hepatitis E infection.

According to the results, trucks and skid-loader circulations might play an important role in HEV dissemination on the slaughterhouse's site, and most likely beyond. HEV was mainly detected outside the farms and slaughterhouse, but few samples from inside the farms were positive. The cleaning work made inside seems effective and should be extended outside the farms, slaughterhouse and trucks, in order to maintain similar conditions throughout the swine production process.