Hepatitis E virus investigation on farrowing and nursery pigs from a farm free of in-feed antimicrobials: a case report.

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Background

Hepatitis E virus (HEV) is an emerging zoonotic agent associated with acute and possibly fatal hepatitis in humans, especially in immunosuppressed patients and pregnant women. There are eight different HEV genotypes out of which genotypes 3, 4 and 7 are zoonotic [3]. In pigs, HEV infection is subclinical and can be detected in blood, liver and feces [5]. Infection in humans might occur through consumption of pork-derived products or by the ingestion of food and water contaminated with swine waste. Occupational risk is a concern since farmworkers are directly exposed to the infection source.

In a previous study we detected anti-HEV antibodies by ELISA in slaughtered pigs [2]. The pigs examined were from a family-raised pig farm and without the use of antimicrobials in the feed at Embrapa Swine and Poultry (UD-Concordia). Testing UD-Concordia, antibodies were detected on sows and finishers (90.3% and 91%, respectively) [2]. Concerning a persistence of HEV in that herd, the objectives of this study were to understand the dynamics of the infection and to identify the possible source of HEV.

Materials and Methods

Two sites were studied: site 1 (UD-Concordia) and site 2, a nursery-finishing (20 km away) in Sede Brum Concordia-SC, Brazil (SB-Concordia). The sows selected were the mothers of the HEV seropositive animals by ELISA (PrioCHECK® HEV Ab porcine), previously mentioned [2]. Samples from sows and their novel litters were collected for 3 days postpartum and weekly until weaning. Thus, the first group of collections was carried out at the UD-Concordia, which included two sows (before and after farrowing) and their litters at birth and during the suckling phase. Sow samples included blood, feces, placenta, oral fluid, colostrum and milk. Samples of feces, blood, oral and nasal fluid were collected from the piglets. To evaluate environmental contamination, swabs were collected from the farrowing grids, creepers and the floor of the maternity stalls. Samples of potential vectors (flies and mouse droppings) were also collected. All protocols, including RNA extraction, followed procedures established in the laboratory for the detection of viral RNA. The second collection took place in the nursery phase or site 2 SB-Concordia. The weaned piglets were housed with other pigs from different origins. For this collection, environment, feces, and vectors samples from the pre and post housing were collected, packaged and processed as mentioned above. The third and last collection was carried out from the same pigs (SB-Concordia), which were already older, in the finishing phase. In summary, collections were performed at weeks 1, 2, 3, 4 and 20 of the pigs' lives. The individually extracted samples were tested by RT-qPCR for HEV genotype 3 (HEV-3), the essay aimed for conserved genomic fragments described previously [1]. In the meantime, additional liver samples from finished animals were processed and tested by RT-qPCR for HEV-3. These samples originated from those first seropositive pigs [2].

Results

RT-qPCR for HEV-3 results indicated the absence of HEV-3 RNA in all the samples collected from sows or piglets in all phases. Environmental or vector samples collected in this study from the two analyzed farms, in their different phases of growth and development, also tested negative. Furthermore, all 120 liver samples analyzed were also negative to HEV-3 RNA.

Discussion

In this work, we searched for a possible source of infection or persistence/environmental contamination in pig herds from a farm previously positive for anti-HEV antibodies. HEV can persist for months in food products or in the environment (soil, water, sediment, and inanimate surfaces). Thus, we collected both environmental and biological samples trying to uncover the source of HEV infection to pigs and to humans. Similar to other countries, the prevalence of anti-HEV in pigs and humans in southern Brazil is high and deserves continuing investigation regarding the source of infection [2,7].

We used a test previously standardized by Da Silva et al. (2018) for HEV-3, which is the most common genotype linked to HEV infections in Europe and America, as genotype 4 is more present in Asia and Europe [4]. However, when performing the essay, all results were negative. To better understand the dynamics or source of infection in the studied farms, studies with other litters, batches and different HEV genotypes will be necessary. Complementary ongoing research will expand the knowledge of viral variability and health status of the pig farms.

Conclusions

Understanding the epidemiology, pathogenesis and dynamics of viral infection and monitoring of pig herds must be carried out to avoid zoonotic HEV transmission and harm to public health.

References

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