

028

Hepatitis E virus: an investigation of within-herd transmission and factors affecting risk of infection in slaughter age pigs

Withenshaw S.¹, Grierson S.², Choudhury B.², Martelli F.³, Smith R.¹

¹Animal and Plant Health Agency, Department of Epidemiological Sciences, Addlestone, United Kingdom, ²Animal and Plant Health Agency, Department of Virology, Addlestone, United Kingdom,

³Animal and Plant Health Agency, Department of Bacteriology, Addlestone, United Kingdom

Introduction

Human infection with Hepatitis E virus (HEV) is an increasing public health concern in Europe. The virus is endemic in parts of Asia and Africa, where genotypes 1 and 2 dominate and are transmitted between people via sewage-contaminated drinking water. HEV in Europe was previously associated with travel to endemic regions, but incidence of indigenously acquired infection has increased over the last decade due to the emergence of HEV genotype 3 (G3), which also infects pigs and is associated with zoonotic transmission (Adlhoch *et al.*, 2016). Foodborne transmission of HEV G3 is believed to be an important route for human infection in Europe. HEV RNA has been detected in pork products (e.g. Berto *et al.*, 2012) and consuming pork products has been identified as a risk factor for infection (Said *et al.*, 2014). Efforts to reduce the risk of HEV contamination in the pork food chain have so far largely focused on developing methods for viral inactivation during processing. Measures to prevent HEV entering the food chain in the first place are also needed, but have received relatively little attention. Developing such measures requires an understanding of HEV transmission within the farm environment, which is currently lacking. Furthermore, on-farm practices that might mitigate the risk of actively infected pigs going to slaughter must be identified and investigated. Here we present the results of an on-farm pilot study that begins to address these knowledge gaps.

Methods

The HEV infection status of a cohort of pigs was followed from farrowing to pre-slaughter on an indoor English farrow-to-finish farm. The cohort comprised 153 piglets born to 11 sows. Five sampling visits took place from May-October 2018 to coincide with key management events for the cohort as follows: pre-farrowing, pre-weaning, prior to movement into grower accommodation, prior to movement into finisher accommodation, and one week prior to slaughter.

Throughout production, pigs were housed as several groups in multiple pens. Observational data collected from a UK abattoir study suggested that late mixing of finisher pigs could be a risk factor for active infection at slaughter. We therefore used coloured ear tags to identify pigs from different litters and track group mixing throughout production. At each visit, fresh faecal droppings were collected from each group and tested for HEV RNA using a qPCR. Viral shedding in faeces was used as a proxy for infection status. HEV presence was determined per group and HEV prevalence was estimated across the entire study cohort on each sampling occasion. In addition, HEV prevalence in all growers and finishers present on the farm was estimated at each visit to investigate general trends within the herd. Environmental samples (including wildlife faeces, standing water, and swabs of farm equipment) were also tested for HEV RNA to identify potential sources of contamination in the farm environment.

Results

Prevalence across all growers was consistently high at all visits (75-87%; Figure 1a) and always higher than in finishers (10-38%; Figure 1b). HEV RNA was detected in 43/67 environmental samples and was found in all production areas (farrowing, weaner, grower, and finisher accommodation), including a cleaned, unoccupied pen.

HEV prevalence in the study cohort fluctuated over time (Figure 1c). HEV was not detected in any sow sampled pre- or post-farrowing, nor in any litter sampled just prior to weaning. After weaning, the cohort was sorted into seven groups of ~30 pigs and placed into weaner accommodation. Seven weeks later, HEV prevalence in the cohort was 26% but HEV was only present in 2/7 groups.

The cohort was subsequently sorted into two larger groups of approximately 60 and 100 pigs and housed in grower accommodation. After six weeks, HEV was present in both groups and prevalence across the cohort was 100% (Figure 1c). The larger group subsequently retained a stable composition for the remainder of the fattening period, and prevalence fell to 23% when sampled one week prior to slaughter. Pigs in the smaller group were sent to slaughter before they could be sampled as finishers, therefore a comparison of HEV presence between study cohort finisher groups was not possible. However, prevalence in the remaining cohort group was generally lower than prevalence in the non-cohort finisher buildings, where pigs had experienced a greater degree of late-stage mixing.

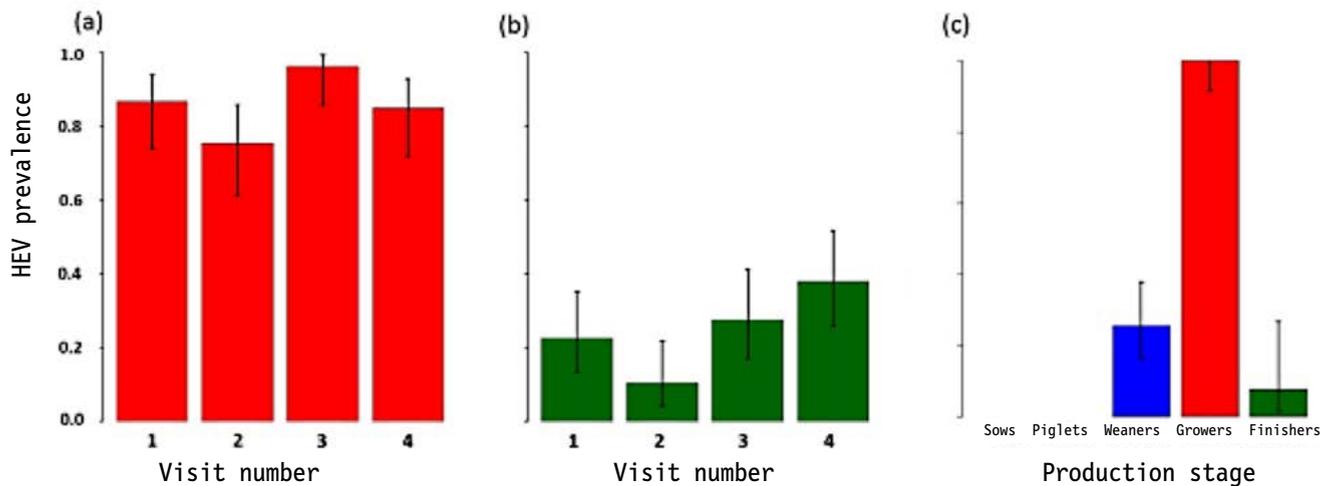


Figure 1: Prevalence of HEV RNA in faeces from (a) growers (b) finishers and (c) the study batch

Conclusion

The results suggest that HEV infection was persistent in this pig herd, and that contamination of the farm environment was widespread. Preventing infection in the herd completely is therefore unlikely to be a viable option for control.

HEV RNA was not detected in any sow faeces, either because they are not infected or they are infected but not shedding detectable levels of virus. Future studies will incorporate sampling of blood and other tissues to disentangle these mechanisms.

HEV RNA was first detected in the study cohort at the weaner stage. Infection may have therefore first entered the cohort after weaning, possibly after maternal antibodies had waned. However, latent infection in younger pigs is also possible, if maternal antibodies suppress viral shedding in faeces. HEV was not detected in all weaner groups. This variation may be linked to age at weaning or degree of mixing when weaned.

HEV appeared to rapidly spread through the cohort once introduced. All samples were positive by the end of grower stage. Only one group was available for sampling as finishers. This group had not experienced further mixing since leaving the weaner unit and HEV prevalence fell considerably by one week prior to slaughter. In contrast, other (non-cohort) finishers on the farm had experienced a greater degree of mixing as growers/finishers and prevalence in these pigs tended to be higher. This suggests that minimising group mixing between weaning and slaughter, especially in the latter part of the finishing period, may reduce the risk of active HEV infection and viraemia at slaughter.

Our study highlights that several factors are likely to contribute to the overall risk of active HEV

infection in slaughter pigs, including biological processes that mediate within-pig infection dynamics (e.g. presence of maternal antibodies) alongside management practices on farm that might influence exposure to infection during primary production (e.g. timing and degree of group mixing). The results from this study will inform further multi-farm investigations of HEV epidemiology in pig herds and the use of herd management strategies for limiting entry of swine-associated HEV to the human food chain.

References

Adlhoc, C. *et al.* (2016). Hepatitis E virus: Assessment of the epidemiological situation in humans in Europe, 2014/15. *J Clin Virology*, 82, 9-16.
 Berto, A. *et al.* (2012). Hepatitis E virus in pork food chain, United Kingdom, 2009-2010. *Emerg Inf Dis*, 18, 1358-1360.
 Said, B. *et al.* (2014). Hepatitis E virus in England and Wales: indigenous infection is associated with the consumption of processed pork products. *Epid & Inf*, 142, 1467-1475.