

Title: Prevalence, genotyping and subtyping of hepatitis E virus in market weight pigs in the United States (NPB #18-021)

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Scientific Abstract:

Foodborne hepatitis E virus (HEV) infection is an emerging public health concern in industrialized countries including the United States. Swine is a major reservoir for genotypes 3 and 4 HEV which are known to infect humans. Since market weight pigs from slaughterhouses are the entry point into the food chain, knowledge of the prevalence and genotype of HEV in slaughtered pigs is of paramount importance since viremic pigs can potentially contaminate pork supply chains through HEV-containing blood at the time of slaughter. In this study, we tested serum samples collected from 5,033 market weight pigs from 25 slaughterhouses in different States for the prevalence of IgG anti-HEV and HEV RNA, using a commercial ELISA kit and RT-qPCR, respectively. RT-qPCR positive samples with high viral RNA copy number were further amplified for the viral capsid gene region by a nested RT-PCR assay, and the resulting PCR products are sequenced. The results show that approximately 6.32% (318/5033) of the sera are positive for HEV RNA, and approximately 39.88% of the sera are positive for IgG anti-HEV. Sequence and phylogenetic analyses reveal that the prevalent HEV genotype in slaughterhouse pigs in the United States is the zoonotic genotype 3, belonging to subgenotype Gt3 group 2 (i.e Gt3abchij). The finding from this comprehensive study indicates that a small proportion of the market weight pigs from slaughterhouses in the United States are still viremic at the time of slaughter and thus may contaminate pork supply chains causing potential pork safety concern.

These research results were submitted in fulfillment of checkoff-funded research projects. This report is published directly as submitted by the project's principal investigator. This report has not been peer-reviewed.

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