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Association Between Ulcer Lesion Grade and Presence of *Helicobacter* Species in Pig Stomachs

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Introduction

Pigs with gastric ulcers show clinical signs of anorexia, chronic anemia, decreased weight gain, acute gastric hemorrhage and sudden death (3). Multiple etiologies with different risk factors have been suggested as causes of gastric ulcers in swine. Feed processing, housing, management and environmental factors are known to be linked to ulcer development. Infection of *Helicobacter* species has also suggested as a cause of gastric ulcers in pigs. In human, *H. pylori* is the most common. *H. heilmannii* has also been observed in human gastric pathology. Recently, *H. heilmannii* type 1 and type 2 have been identified in pig stomachs (1, 2). These results suggest that certain species of *Helicobacter* could be recognized as zoonotic pathogens, and pigs can be a potential source for human *Helicobacter* infection. The purpose of the present study was to investigate evidence of infection with *Helicobacter* species in slaughter pigs and to analyze an association between gastric ulcer lesion and *Helicobacter* infection.

Materials and methods

Over 400 pig stomachs were examined grossly for gastric ulcer lesions during 4 different visits to a slaughterhouse in Minnesota. A standard method was used to grade the gross stomach lesions; grade 0 for no lesion, grade 1 with evidence of parakeratosis, grade 2 with erosions of the epithelium, and grade 3 with active ulcers and cicatrization (3). Then, 40 samples from each grade level were randomly selected. Infection of *Helicobacter* species in pig stomach was examined using PCR with *Helicobacter* genus-specific primers.

Results

Of 160 stomach samples examined, 102 (63.8%) were positive by the PCR assay. The 40 samples each of the lesion grade 0, 1, 2 and 3 showed 22.5%, 52.5%, 85.0%, and 95.0% PCR positive results, respectively (Table 1). There was a significant trend ($P = <0.01$) in the proportions of PCR positive cases relative to severity of the lesion. About 80% of the 16S ribosomal RNA gene was amplified and PCR-restriction

fragment length polymorphism (RFLP) patterns were analyzed. Of 102 PCR positive samples, the PCR-RFLP patterns resulted in four different types, 32 samples being classified into type MN 1, 16 samples into type MN 2, 43 samples into type MN 3, and 11 samples into type MN 4.

Table 1. Identification of *Helicobacter* species by PCR in pig stomachs with different lesion grades

Lesion Grade	No. of sample examined	PCR positive samples
Grade 0	40	9 (22.5 %)
Grade 1	40	21 (52.5 %)
Grade 2	40	34 (85.0 %)
Grade 3	40	38 (95.0 %)
Total	160	102 (63.8 %)

Discussion and conclusion

The present results have demonstrated a significant association, the higher the lesion grade of ulceration the higher the detection rate of *Helicobacter* infection. The results have also confirmed the evidence of *H. suis* infection and identified novel *Helicobacter* species with high homology of human and rat origins in pigs. An interesting question remains whether swine and pork products infected with *Helicobacter* species can be a source for human infection.

References

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