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Occurrence of Brachyspira hyodysenteriae and Brachyspira pilosicoli in Polish pig herds

Dors A.[1], Czyżewska-Dors E.[1], Furtak E.[1], Woźniakowski G.[1]

[1]The National Veterinary Research Institute, Department of Swine Diseases, Pulawy, Poland

Introduction

Pathogenic intestinal spirochetes of pigs include *Brachyspira hyodysenteriae*, the cause of swine dysentery, and *Brachyspira pilosicoli*, the cause of porcine colonic spirochetosis. Most *Brachyspira* species have a restricted host range, whereas *B. pilosicoli* colonizes a wide range of hosts including humans and has natural potential to be transmitted between species (Hampson and Burrough 2019). There is potential for zoonotic transmission, especially in places where animals and humans live in close proximity, or for people working with intensively farmed pigs or chickens due to increased risk of exposure. Some species of the genus *Brachyspira* including *B. pilosicoli* can cause disease in human. There are few reports about *B. pilosicoli*-associated human intestinal spirochetosis (HIS). Most of these studies have involved observation of colorectal biopsy specimens that show spirochetes attached to the epithelial surface, to form a "false brush border" (Hampson 2018).

Subclinical colonization of pigs with *B. pilosicoli* occurs commonly on some farms (Biksi et al. 2007) On other farms, the spirochete may be isolated from diseased pigs alone or as part of a mixed infection with other enteric pathogens (Stege et al. 2000; Reiner et al. 2011). Recent changes in the management of pig farms and movement of pigs within the EU have resulted in shift in the relative prevalence of pathogenic *Brachyspira* species. Very few studies report the prevalence of *B. hyodysenteriae* in pig in Poland but only one concerning *B. pilosicoli*. The aim of the study was to preliminary assess current occurrence of *Brachyspira hyodysenteriae* and *Brachyspira pilosicoli* in Polish pig herds.

Material and Methods

Between 2017 and 2019, a total of 247 samples of pig feces were submitted to The National Veterinary Research Institute (NVRI). These samples were obtained form 60 different Polish pig herds form pigs older than 7 weeks. All these samples were submitted to NVRI to be evaluated for swine dysentery and/or porcine proliferative enteritis. Some of them were obtained from pigs subjected to routine monitoring and other came from pigs with clinical sings of diarrhea. Total genomic DNA was extracted from the fecal samples using commercial isolation kit (Genomic Mini, A&A Biotechnology, Gdynia, Poland), according to the manufacturer's recommendations.

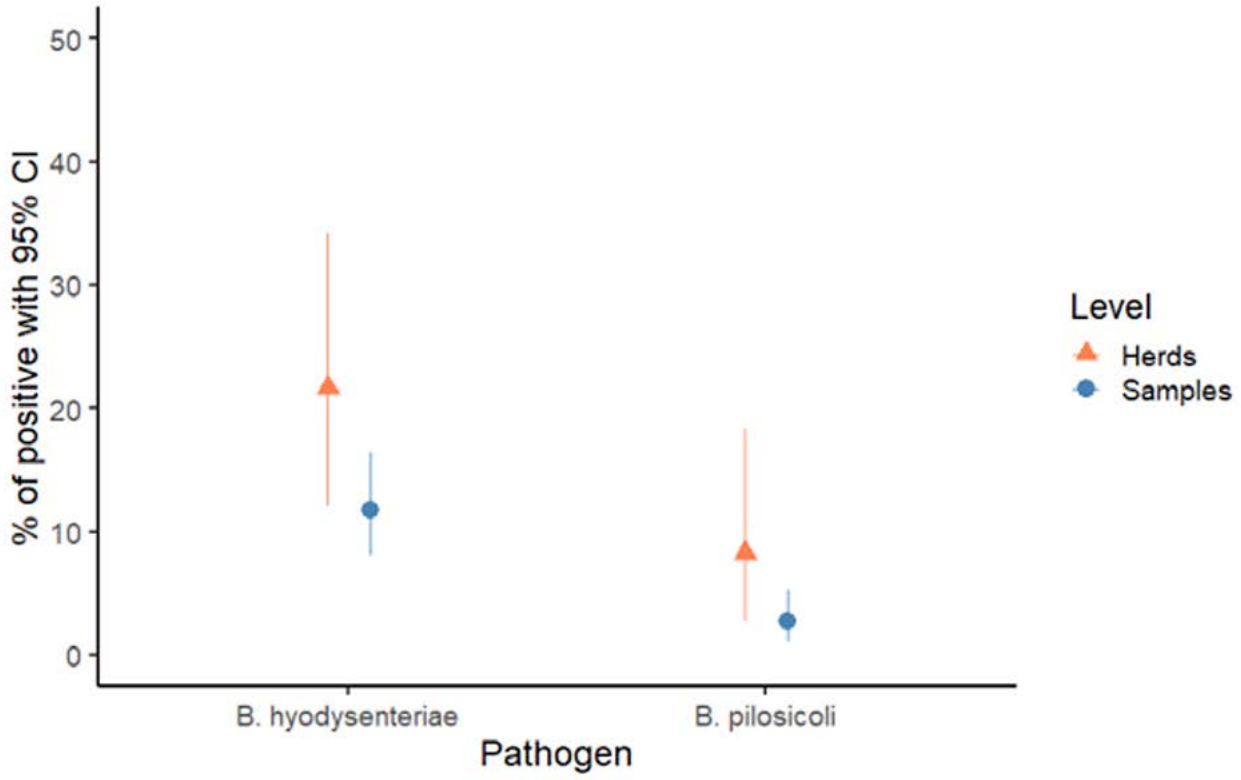

Figure 1: Occurrence of B. hyodysenteriae and B. pilosicoli in 247 samples from 60 Polish pig herds

Extracted DNA samples were stored at -20˚C until examination. All samples were tested by separated real time PCR assays for *B. hyodysenteriae* and *B. pilosicoli* according to the methods described previously (Zmudzki et al. 2012; Ståhl et al. 2011). A herd was defined as positive when at least one fecal sample taken from the herd had a positive PCR result. Percentages of positive samples/herds with a 95% two-sides exact binominal confidence interval (CI) were reported.

Results

Overall occurrence of *B. hyodysenteriae* and *B. pilosicoli* in pig herds in Poland is presented at Figure 1. Among total amount of 247 samples 138 were submitted to laboratory of NVRI for routine monitoring of pig herds. The remaining 109 samples originated from pigs with clinical problems such as diarrhea or enterocolitis. The real time PCR detected *B. pilosicoli* DNA in seven samples from pigs in 5 different herds. Which means that 2,8% (95% CI, 1,1% - 5,3%) of samples and 8,3% (95% CI, 2,8% - 18,4%) of herds were positive for *B. pilosicoli*. In terms of *B. hyodysenteriae* 11,7% of samples (95% CI, 8,0% - 16,4%) from 21,7% herds (95% CI, 12,1% - 34,2%) were positive in real time PCR. Samples in which *B. hyodysenteriae* were detected originated form pigs with clinical problems, all samples from routine monitoring programs were negative for this pathogen. In case of *B. pilosicoli* all positive samples were collected from apparently heathy pigs.

Discussion and Conclusion

The results of the study confirm that *B. pilosicoli* infections occur in Polish pig herds. Previous study reported only one positive sample among 127 tested from 23 pig farms was not fully reliable, especially if we taking into account lack of clinical signs (Pławińska et al. 2004). Our results show that *B. pilosicoli* is present in Polish pig herds but it seems that prevalence is rather low - 8,3% of positive herds. But it is interesting taking into account significantly higher prevalence of *B. pilosicoli* in other countries such as Germany - 31.6% (Reiner et al. 2011) or Denmark - 19% (Stege et al. 2000). Therefore, active sampling from Polish pig herds is necessary to assess true prevalence of *B. pilosicoli*. There is also a need for further investigation of the association between presence of *B. pilosicoli* in feces and the clinical signs or pig performance. The risk associated with zoonotic potential of this pathogen is difficult to assess, but it seems to be low based on obtained results - 2,8% of positive samples.

Another finding highlight that swine dysentery is still common cause of diarrhea among pigs from Polish herds despite of improving biosecurity, hygiene and management.

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