

## **BBD-PP-17**

### **TITLE**

**BRACHYSPIRA HYODYSENTERIAE; A GERM IN TRANSITION?**

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### **CONTENT**

#### Background and Objectives

Brachyspira hyodysenteriae infections are internationally known for their substantial economic losses in the pig industry. Topigs Norsvin tests fecal samples via PCR in their health monitoring system in addition to the observance for clinical signs. As some unexpected positive PCR results, in herds with no clinical signs, were found in the last years in Western Europe, it was decided to gather more information to better understand these non-clinical a modern Brachyspira hyodysenteriae infections.

#### Material & Methods

To confirm a positive PCR result in the monitoring additional samples were collected in a multiplication farm with 300 sows. Thirty samples we tested by an in-house NOX gene based RT-PCR (cut-off level CT-value 40), at GD Animal Health. Four individual animals were selected for postmortem examination. Four intestinal samples from post mortems and five additional fecal samples from other animals from the herd were send to TIHO (Germany) for culture. Positive culture samples were send for full genome sequencing to APHA-lab in Weybridge (UK).

#### Results

The initial positive monitoring sample had a CT-value of 38. Eight out of thirty additional samples were positive in the PCR. CT-values varied between 34 and 39. Macroscopic and histologic examination of four selected animals (by PCR result) showed no typical lesions for Brachyspira infections. In intestinal samples of two animals and in one fecal sample weakly hemolytic Brachyspira hyodysenteriae was detected by culture. Results of the full-genome sequence are not yet available.

#### Discussion & Conclusion

Whether this Brachyspira infection without disease or lesions is related to the herd circumstances or this infection is caused by a different subtype of Brachyspira hyodysenteriae appearing to be less pathogenic is not known yet. Further clarification of non-clinical Brachyspira hyodysenteriae infections could come from full genome sequencing currently being performed.