



## BACTERIAL DISEASES

BBD-082

### LOW DIVERSITY AMONG *BRACHYSPIRA HYODYSENTERIAE* ISOLATES IN SWITZERLAND

F. Zeeh<sup>1</sup>, S. Schmitt<sup>2</sup>, A.B. García-Martín<sup>3</sup>, H. Nathues<sup>1</sup>, V. Perreten<sup>3</sup>.

<sup>1</sup> Clinic for Swine, Vetsuisse Faculty, University of Bern, Bern, Switzerland; <sup>2</sup> Institute of Veterinary Bacteriology, Vetsuisse Faculty, University of Zurich, Zurich, Switzerland; <sup>3</sup> Institute of Veterinary Bacteriology, Vetsuisse Faculty, University of Bern, Bern, Switzerland.

#### Introduction

*Brachyspira* (*B.*) *hyodysenteriae* infection can cause swine dysentery (SD), increased use of antimicrobials and economic losses. Control and eradication of SD rely on a better understanding of sources, transmission and spread. We analysed *B. hyodysenteriae* isolates from different Swiss pig herds using molecular typing methods and epidemiological data.

#### Material & Methods

*B. hyodysenteriae* isolates were obtained from a laboratory collection (SD cases, monitoring) and research projects and were analysed by multi-locus sequence typing. Epidemiological data (place & date of sampling) were recorded.

#### Results

Forty-seven isolates (1 to 8/ herd) originating from 24 herds (eastern Switzerland: 16, middle-western part: 8) were collected between 2010 and 2017. Isolates belonged to sequence type (ST) ST6 (n=3), ST66 (n=12), and the new STs ST196 (n=30) and ST197 (n=2). The herds located in eastern Switzerland harboured all four identified STs. In one of these herds, two STs (ST66 and ST196) were present. In herds from the middle and western parts, only ST196 (n=7) and ST66 (n=1) were present.

#### Discussion & Conclusion

Sequence typing of *B. hyodysenteriae* revealed a low genetic diversity and the presence of the same ST in different regions in Switzerland. This indicates that the *B. hyodysenteriae* strains very likely originate from a few common sources which contribute to the spread of the pathogen. In case of numerous sources, more STs would have been expected to be present. However, further analyses of more herds and samples including their epidemiological background are needed to confirm this hypothesis and to identify sources.