

Low occurrence of *Brachyspira hyodysenteriae* in Swiss pig herds with diarrhoea

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Short communication

Brachyspira (B.) hyodysenteriae is one of the agents causing Swine Dysentery (SD), a severe enteric disease occurring worldwide.⁶ Decreased daily weight gain, poor feed conversion, animal losses and treatment costs result in economic losses. The occurrence of SD varies between countries and studies. Control of the disease became of major importance as *B. hyodysenteriae* isolates with decreased susceptibility to clinically important antimicrobials are increasingly reported.^{6,9} Eradication is a powerful tool to eliminate the agent from a herd when correctly performed.¹⁰ In Swiss herds, *B. hyodysenteriae* has been officially reported for the first time in 2008.¹³ This report and the detection of *B. hyodysenteriae* in a multiplier herd⁸ enforced the systematic examination of *B. hyodysenteriae* in Swiss herds. In 2011, monitoring in member herds of the Pig Health Service (PHS; SUISAG) started. On average, approximately 50% of the Swiss fattening farms are a member of the PHS (SUISAG). All Swiss nucleus and multiplier herds (breeding herds) are tested at least twice a year and are clinically monitored. Other herds are tested in case of SD suspicion. Positive breeding herds have to undergo a herd specific eradication, which can be e. g. a partial depopulation with medication, a modified partial depopulation, or a total depopulation. While not mandatory, an eradication is also strongly recommended for other positive herds. Until 2020, 211 positive herds and herds linked to positive ones were detected within the monitoring approach and 148 eradications were performed (Fig. 1).

In Switzerland, the *B. hyodysenteriae* isolated from pigs over the past 10 years belonged to four sequence types (ST6, ST66, ST196, ST197) with ST196 being predominant.⁵ The low number of genetic lineages and the presence of the same predominant ST196 over time suggests a presumably low number of sources for *B. hyodysenteriae* in the pig production pyramid of Switzerland prompting us during this project to i) establish

a culture and molecular-based surveillance system for pig herds with SD, ii) try to trace back sources of the different *B. hyodysenteriae* of a same ST using information associated with the life path of the pigs to identify common origins; and iii) identify possible new emerging strains.

In herds with diarrhoea in weaned to finishing pigs, five individual rectal faecal swabs were taken from diseased but untreated pigs and submitted for a free-of-charge *Brachyspira* spp. examination between October 2019 and December 2020. The samples were taken by veterinarians as part of the regular diagnostic approach in diseased herds only, thereby not requiring animal experiment authorization. The samples had to be sent together with a submission form covering herd data, date of sampling, and data of sampled pigs. The farmers agreed with the submission, that the data will be used within this study and that they would provide further information in case of a *B. hyodysenteriae* positive result.

Faecal swabs were streaked onto selective BJ agar⁴ (trypticase soy agar supplemented with either 5% of cattle or sheep blood supplemented with colistin, vancomycin, spectinomycin, spiramycin, and rifampicin) and incubated under anaerobic conditions at 42 °C for 5–6 days. The bacterial lawn was analysed for the presence of spirochaetes using dark-field microscopy. Spirochaete positive plates were subcultured on Columbia agar containing 5% of sheep blood (Becton, Dickinson and Company; Thermo Fisher Diagnostics AG) for 3 days at 42 °C and species identification was done by a multiplex real-time PCR discriminating between the 23S rDNA gene of *B. hyodysenteriae*, *B. pilosicoli*, and three other *Brachyspira* spp. (*B. intermedia*, *B. innocens*, *B. murdochii*).¹ High resolution melting assay was determined to further identify *B. hampsonii*.¹²

The ST of one *B. hyodysenteriae* isolate per positive herd was determined by multi-locus sequence typing using

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Table 1: Herd characteristics and laboratory results of three Swiss fattening herds with detection of *Brachyspira hyodysenteriae* (BH). Herd characteristics data of positive herds were collected by a questionnaire-based interview.

Variable	Herd 1	Herd 2	Herd 3
Herd size	306	150	120
Number of batches in the 12 months before the interview	28 (24 placements)	18	6 (5 placements)
Number of source herds	9	13	6
Pig trader incoming pigs/slaughter pigs	A/none	B/B	C/C
Number of samples (BH positive /total)	2/5	3/5	5/5
Age or bodyweight of sampled pigs	16 weeks	30–40kg	5 months
Clinical signs	All five sampled pigs with diarrhoea (three pigs mucohaemorrhagic)	Two pigs with diarrhoea (pasty consistence). Other (treated, non-sampled) pigs in pen with haemorrhagic diarrhoea.	Five pigs with diarrhoea (two pigs haemorrhagic diarrhoea)

a published scheme¹¹ and the pubMLST database for *Brachyspira* spp. (<https://pubmlst.org/organisms/brachyspira-spp>).⁷

Farmers of positive herds were contacted by phone for a short questionnaire-based interview. The questionnaire covered herd characteristics, pig trade and transportation, and selected biosecurity aspects. The interview data were entered digitally (Microsoft Access 2016) and transferred into a data sheet for further descriptive ana-

lyses (Microsoft Excel 2016). Copies of pig trade documents were sent by the farmers and data were manually entered in the Excel sheet and complemented with the laboratory results.

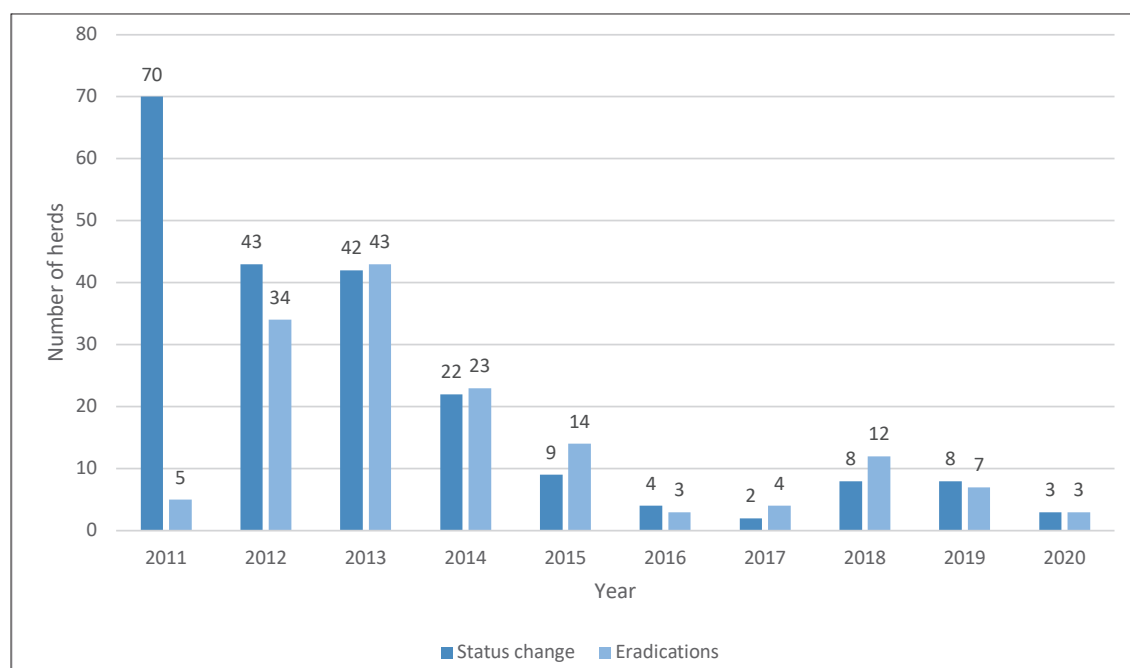
Of the 141 examined herds, three tested positive for *B. hyodysenteriae* (Herd 1, Herd 2, Herd 3; Tab. 1). No *B. hampsonii*, another agent of SD, was detected. All three *B. hyodysenteriae* positive herds were fattening herds with 120 to 306 places. Two of the herds were located in the eastern part of Switzerland, and one in the western part. Two farmers were members of the PHS. All three farmers had contracts for slurry management, but only one received foreign slurry. Two herds had access to outdoor areas. As contact to foxes was one of the risk factors for SD in a recent study,¹⁵ we asked specifically for this aspect. All three farmers reported foxes near their herds and also contacts of their pigs to the foxes.

In the 12 months before the sampling, the herds received between 385 and 855 pigs in six to 28 batches (Tab. 1). None of these sources was shared. Pig traders differed between the three positive herds. All piglets were transported by the traders to the farms. Only one farmer reported that his farm was the first one approached on the day of delivery and that the truck only contained piglets allocated to his farm. Selected characteristics of all 141 study herds are shown in Table 2.

MLST analysis revealed that isolates of two herds from the western and eastern part belonged to ST196, and the one from the second herd in the eastern part belonged to ST66. The two ST196 positive herds had no

Figure 1: Detection¹ of and eradication from *Brachyspira hyodysenteriae* in Pig Health Service (PHS, SUISAG) member herds since the introduction of guidelines for Swine Dysentery (RL 3.13).

¹The numbers include also herds which changed their status to «*B. hyodysenteriae* infected» due to epidemiologic links to positive herds but without an own diagnosis (sow pools herds). Furthermore, two herds tested positive twice and one three times indicating repeated eradications in these herds.



direct connection, neither via pig trade (different piglet producers and traders) nor geographically.

The occurrence of *B. hyodysenteriae* in Swiss pig herds with diarrhoea examined in this study was low (2,1%). In comparison, positive study herds of 18,9% in Spain and 32,1% Poland were reported.^{2,3} Also in Switzerland during the last decade, on average 21 herds per year tested positive or changed the *B. hyodysenteriae* status because of epidemiologic links to positive herds but without a final diagnosis (SUISAG). The current low occurrence might be the result of the intensive monitoring and eradication attempts in the PHS herds and other herds during the last ten years, and is in line with low numbers of SD cases observed by pig practitioners and veterinarians of the PHS (personal communication). The occurrence might be slightly higher than reported here as the participation in the study was voluntary and not all farmers with potential SD may have participated. However, we have made the study attractive by respecting strict confidentiality, free of charge

Brachyspira diagnostics and strategic advertisement on veterinary and pig producer platforms.¹⁴

As our study did not feature strategic monitoring in the pig population with sufficient sample size, random sampling, etc., we cannot determine the SD incidence. However, assuming that we did not miss a major number of SD cases, we might have a case incidence of less than 0,1% in Switzerland for the whole study period.

The finding of only three positive herds and the presence of two different STs does not allow to conclude for a common source. Furthermore, the two ST196 positive herds had no direct connection. Nevertheless, SD in Switzerland is still caused by *B. hyodysenteriae* belonging to STs (here: ST196 and ST66), which were detected over the past year in Switzerland.⁵ Therefore, monitoring and control of SD have to be continued as well as routine molecular typing introduced to also identify in time the emergence of new clones, which may show elevated mi-

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Table 2: Herd characteristics of 141 Swiss pig herds with diarrhoea in weaned to finishing pigs, tested for *Brachyspira hyodysenteriae*. Data are derived from the submission form.

Variable	Data of study herds	Switzerland	Comment
Herd type			
Piglet producing farm	n=20 (14,2%)	NA	
Farrow-to-finish farm	n=20 (14,2%)		
Fattening farm	n=87 (61,7%)		
Farm of sow pool system	n=10 (7,1%)		
Missing answers	n=4		
Geographic distribution of herds in Switzerland			
Eastern part	n=51 (36,2%)	30,1%*	East=cantons Aargau, Appenzells Inner and Outer Rhodes, Schaffhausen, St Gallen, Thurgau, Zurich
Middle-South part	n=53 (37,6%)	34,2%*	Middle-South=cantons Basel-Land, Lucerne, Ticino, Zug
Western part	n=37 (26,2%)	26,2%*	West=cantons Berne, Fribourg, Solothurn
Number of weaned and/or fattening pigs per herd			
Herd size	Median: 300 pigs (range: 12–2500)	NA	
Missing answers	n=21		
Clinical signs (faecal consistency in sampled pigs)			
Mucohaemorrhagic diarrhoea	n=24	NA	If different faecal consistencies were noted for the sampled pigs, only the worst one is shown
Liquid faeces (diarrhoea)	n=36		
Pasty faeces	n=41		
Soft and formed faeces	n=3		
Missing answers	n=37		

NA: Data nor available or question not applicable.

*: As only data from 2013 were publicly available (https://www.pxweb.bfs.admin.ch/pxweb/de/px-x-0702000000_231/-/px-x-0702000000_231.px/), only relative data are shown.

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nimum inhibitory concentrations to antibiotics currently used for SD treatment and eradication in Switzerland.

In summary, this study indicated a low occurrence of *B. hyodysenteriae* in Swiss pig herds and common sources for specific genetically related strains could not be identified and are rather unlikely. However, as identification of common sources was not possible hampering their targeted elimination and due to the fact that SD can have a cyclic occurrence, the disease must not be neglected. Constant monitoring of SD and analysis of genetic properties of *B. hyodysenteriae* including detection of antibiotic resistance mechanisms is essential to prevent or reduce the risk of uncontrolled spread of *B. hyodysenteriae* in Swiss pig herds. A molecular-based surveillance system of *B. hyodysenteriae* for pig herds with SD should be established and prevention of and eradications from SD should be continued on a high level to maintain or improve the current situation.

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References

- Borgström A, Scherrer S, Kirchgässner C, Schmitt S, Frei D, Wittenbrink MM.: A novel multiplex qPCR targeting 23S rDNA for diagnosis of swine dysentery and porcine intestinal spirochaetosis. *BMC Vet. Res.* 2017;16(13):42. doi:10.1186/s12917-016-0939-6.
- Carvajal A, de Arriba ML De Rodríguez H, Vidal AB, Duhamel GE, Rubio, P: Prevalence of *Brachyspira* species in pigs with diarrhoea in Spain. *Vet. Rec.* 2006;158:700–701. doi:10.1136/vr.158.20.700.
- Dors A, Czyżewska-Dors E, Woźniakowski G: A survey on the occurrence of *Brachyspira pilosicoli* and *Brachyspira hyodysenteriae* in growing-finishing pigs. F1000Research-2020;8:1702. doi:10.12688/f1000research.20639.2.
- Dünser M, Schweighardt H, Awad-Masalmeh M, Schuh M: Schweinedysenterie und Spirochaetendiarrhoe- vergleichende Untersuchungen serpulinenbedingter Enteritiden. *Wien. Tierarztl. Monatsschr.* 1997;84:151–161.
- García-Martín AB, Perreten V, Rossano A, Schmitt S, Nathues H, Zeeh F: Predominance of a macrolide-lincosamide-resistant *Brachyspira hyodysenteriae* of sequence type 196 in Swiss pig herds. *Vet. Microbiol.* 2018;226: 97–102. doi:10.1016/j.vetmic.2018.10.007.
- Hampson DJ, Lugsomya K, La T, Phillips ND, Trott DJ, Abraham S: Antimicrobial resistance in *Brachyspira* – An increasing problem for disease control. *Vet. Microbiol.* 2019;229: 59–71. doi:10.1016/j.vetmic.2018.12.019.
- Jolley KA, Bray JE, Maiden MCJ: Open-access bacterial population genomics: BIGSdb software, the PubMLST.org website and their applications. *Wellcome Open Res.* 2018;3:124. doi:10.12688/wellcomeopenres.14826.1.
- Löbert S, Zimmermann W, Bürki S, Frey J, Nathues H, Scheer P, Doherr MG, Stalder U, Zeeh F: Occurrence of *Brachyspira hyodysenteriae* in multiplier pig herds in Switzerland. *Tierarztl. Prax. Ausgabe G Grosstiere – Nutztiere.* 2016;44:13–18. doi:10.15653/TPG-150674.
- Mahu M, Pasmans F, Vranckx K, De Pauw N, Vande Maele L, Vyt P, Vandersmissen T, Martel A, Haesebrouck F, Boyen F: Presence and mechanisms of acquired antimicrobial resistance in Belgian *Brachyspira hyodysenteriae* isolates belonging to different clonal complexes. *Vet. Microbiol.* 2017;207:125–132. doi:10.1016/j.vetmic.2017.05.022.
- Neiryneck W, Boyen F, Chantziaras I, Vandersmissen T, Vyt P, Haesebrouck F, Dewulf J, Maes D: Implementation and evaluation of different eradication strategies for *Brachyspira hyodysenteriae*. *Porc. Heal. Manag.* 2020;6(1):27. doi:10.1186/s40813-020-00162-2.
- Råsbäck T, Johansson K-E, Jansson DS, Fellström C, Alikhani MY, La T, Dunn DS, Hampson DJ: Development of a multilocus sequence typing scheme for intestinal spirochaetes within the genus *Brachyspira*. *Microbiology.* 2007;153:4074–4087. doi:10.1099/mic.0.2007/008540-0.
- Scherrer S, Borgström A, Frei D, Wittenbrink MM: First screening for *Brachyspira hamptonii* in Swiss pigs applying a new high resolution melting assay. *Vet. Microbiol.* 2016;193:17–21. doi:10.1016/j.vetmic.2016.07.020.
- Speiser SA, Goy N, Albini S, Zimmermann W, Scheer P, Doherr MG, Zeeh F: Occurrence of *Brachyspira hyodysenteriae* and *Brachyspira pilosicoli* and assessment of risk factors in Switzerland, Oral Proceedings, 20th International Pig Veterinary Society Congress Durban, South Africa, 2008.

¹⁴ Zeeh F. Schweinedysenterie : Neue Erkenntnisse und ein neues Angebot. *Suisseporcs Inf.* 2019;11:20–21.

¹⁵ Zeeh F, Vidondo B, Nathues H: Risk factors for the infection with *Brachyspira hyodysenteriae* in pig herds. *Prev. Vet. Med.* 2020;174:104819. doi:10.1016/j.prevet-med.2019.104819.

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