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1 *Brachyspira hyodysenteriae* isolated from apparently healthy pig herds following an evaluation  
2 of a prototype commercial serological ELISA

3

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16

17 **Abstract**

18 Swine dysentery (SD) is a disease mainly of grower/finisher pigs characterised by severe  
19 mucohaemorrhagic colitis. The classical aetiological agent is the anaerobic intestinal spirochaete  
20 *Brachyspira hyodysenteriae*, although “*Brachyspira hampsonii*” and *Brachyspira suanatina*  
21 also cause SD. This study reports on the unexpected isolation of *B. hyodysenteriae* from pigs in  
22 apparently healthy herds that gave positive reactions when tested with a prototype commercial  
23 serological ELISA for detecting herds infected with *B. hyodysenteriae* (Priocheck<sup>®</sup> Brachyspira  
24 porcine Ab ELISA). The ELISA was tested with sera collected at abattoirs from 1,770  
25 slaughtered pigs from 30 Australian herds, including 12 with a history of SD and 18 that were  
26 considered by their consulting veterinarians to be healthy. The latter herds had no history of  
27 SD and did not routinely use antimicrobials that may have masked the disease. Based on the  
28 recommended ELISA cut-off value, 25 herds were recorded as showing evidence of infection,  
29 including 11 of 12 herds that were considered infected by the submitters and 14 of the 18  
30 “healthy” herds. When faecal or colonic wall samples from 11 of the 14 “false positive” herds  
31 subsequently were culturing 6-24 months after the original ELISA testing was completed,  
32 different strains of *B. hyodysenteriae* were isolated from six herds, including a high-health  
33 status breeding herd. The existence of apparently healthy herds that are colonised by *B.*  
34 *hyodysenteriae* has major implications for the control of SD. Had the ELISA not been trialled  
35 it is unlikely that colonic samples from these herds would have been cultured and the  
36 colonisation identified.

37

38 *Keywords:* Swine dysentery; *Brachyspira hyodysenteriae*; diagnosis; ELISA; MLST

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42

43 **1. Introduction**

44 Swine dysentery (SD) is endemic in many regions of the world. The disease typically presents  
45 as a severe mucohaemorrhagic colitis mainly in grower and finisher pigs, although clinical  
46 signs may be ameliorated or prevented by the use of antimicrobial agents (Hampson 2012).

47 The classical agent of SD is the strongly haemolytic anaerobic intestinal spirochaete  
48 *Brachyspira hyodysenteriae*, but latterly the related strongly haemolytic species *Brachyspira*  
49 *suanatina* and “*Brachyspira hamptonii*” also have been shown to be able to cause SD  
50 (Råsbäck et al. 2007; Burrough et al. 2012; Chander et al. 2012; Rubin et al. 2013; Mushtaq et  
51 al. 2015).

52  
53 Diagnosis of SD largely rests on observation of clinical signs and pathology, together with  
54 demonstration and identification of the aetiological spirochaetes in the colon or faeces.

55 *Brachyspira* spp. grow slowly on specialised selective agar plates under anaerobic conditions,  
56 and their subsequent identification traditionally has been difficult and time consuming. The  
57 application of PCR technology to identify spirochaetes growing on plates or on DNA extracted  
58 from faecal or colonic samples represented an important diagnostic advance (Atyeo et al. 1998;  
59 La et al. 2003). Although culture and PCR can detect spirochaetes in the faeces of pigs that  
60 have diarrhoea and are excreting them in large numbers, they may not detect low numbers in  
61 healthy carrier animals (Fellström et al. 2001). Consequently these methods are not well suited  
62 for routine screening of apparently healthy herds to detect animals with low levels of  
63 colonisation, mainly because very large numbers of samples need to be tested and this is  
64 expensive and time consuming.

65  
66 Enzyme-linked immunosorbent assays (ELISAs) have the potential to be used for quantifying  
67 serum antibodies to pathogens, and hence providing indirect evidence of past exposure to the  
68 pathogen. As a consequence they are very useful in routine screening of apparently healthy

69 animals at the abattoir to assess the likely status of the herd of origin, particularly where the  
70 herd may have sub-clinical infection. ELISAs using either sonicated whole cells of *B.*  
71 *hyodysenteriae* or extracted lipooligosaccharide (LOS) as plate-coating antigens have been  
72 reported to be sensitive enough to allow detection of SD at a herd level, if sufficient numbers  
73 of pigs are tested (Joens et al. 1982; Wright et al. 1989; Smith et al. 1991; Mhoma et al. 1992;  
74 Song et al. 2012). Unfortunately as these antigens potentially could be shared by other  
75 *Brachyspira* species and generate false-positive cross-reactions this has hampered their further  
76 commercial development (La and Hampson 2001). To overcome cross-reactivity, recombinant  
77 specific conserved surface proteins of *B. hyodysenteriae* have been trialled as ELISA antigens.  
78 One such antigen, Bhlp29.7 (formerly BmpB) has been used in a serological ELISA to identify  
79 infected herds (La et al. 2009a). Unfortunately the test also has potential for cross-reactivity  
80 with strains of the non-pathogenic *Brachyspira innocens* (La et al. 2005), and more importantly  
81 the *Bhlp29.7* gene was found to be absent in a significant number of *B. hyodysenteriae* strains  
82 (Barth et al. 2012). More recently an immunogenic surface protein named H114 was shown to  
83 be widespread amongst *B. hyodysenteriae* strains and to have potential to be used as an ELISA  
84 antigen to detect infected herds (Song et al. 2015). In the current study a prototype test using  
85 H114 developed by Prionics AG (Prionics<sup>®</sup> Brachyspira porcine Ab ELISA) was tested on  
86 sera from pigs in 30 herds with or without a history of having SD. Fourteen of these herds gave  
87 apparently false positive results, but subsequent investigation by culture and PCR revealed that  
88 at least six were colonised with strains of *B. hyodysenteriae*.

89

## 90 **2. Materials and Methods**

### 91 *2.1. Permissions*

92 This study was conducted with the approval of the Murdoch University Animal Ethics  
93 Committee under permit number R2292/09.

94

95 *2.2. Herds and sample collection*

96 Serum samples originating from 30 pig herds were collected by members of the Australian Pig  
97 Veterinarians (APV), a special interest group of the Australian Veterinary Association. The  
98 herds all had >500 sows, and were located in the States of Western Australia (n=10), Victoria  
99 (n=9), New South Wales (n=8) and South Australia (n=3). The samples were from 12 herds  
100 where clinical SD had been recorded and where it was considered still to be present, even  
101 though controlled, and 18 where the consulting specialist veterinarian considered that the  
102 infection did not occur. Disease status was assessed based on clinical history, lack of use of  
103 routine medication in healthy herds, regular abattoir monitoring for disease signs and  
104 diagnostic testing of faecal samples from pigs with diarrhoea, including PCR for *Brachyspira*  
105 species. One of these herds was a breeding herd that was considered to be of very high health  
106 status. In most cases a minimum of 40 blood samples per herd was collected as a batch from  
107 healthy slaughter-aged pigs during exsanguination at the abattoir. Additional batches of sera  
108 were collected from seven herds where less than 40 samples were obtained at the initial  
109 sampling, or where consulting veterinarians questioned the initial results and sought additional  
110 testing. The blood samples were allowed to stand overnight at 4°C and the serum was pipetted  
111 off and tested within 48 hours.

112

113 *2.3. ELISA testing*

114 The testing was conducted blind to the origin of the samples. Serum samples were tested in a  
115 prototype commercial serological ELISA (Priocheck<sup>®</sup> *Brachyspira* porcine Ab ELISA; Prionics  
116 AG), as optimised by the manufacturer and following their detailed instructions. Recombinant  
117 antigen H114 was pre-coated on the plates by the manufacturer. Single strong positive, weak  
118 positive and negative control sera were supplied and included in each test run. Serum samples  
119 were diluted 1:20, added to wells on the plate, incubated at room temperature for 60 minutes,  
120 and after washing as recommended were reacted with a peroxidase labelled anti-pig antibody

121 in a direct ELISA. Colour development using TMB substrate was measured optically at a  
122 wavelength of 450nm. Percentage Positivity was calculated as the OD<sub>450nm</sub> of the sample  
123 minus the OD<sub>450nm</sub> of the negative control, divided by the OD<sub>450nm</sub> of the positive control  
124 minus the OD<sub>450nm</sub> of the negative control, multiplied by 100. Test samples with values equal  
125 to or above the cut-off of 30 Percent Positivity were considered positive in the test. Herds with  
126 one or more positive serum sample were considered to show evidence of infection with *B.*  
127 *hyodysenteriae*.

128

#### 129 2.4. Culture and PCR

130 For 22 of the herds, limited numbers of colon samples from pigs at the abattoir or faecal  
131 samples on farm subsequently were obtained for culture and PCR for *B. hyodysenteriae* (Table  
132 1). Sampling occurred 6 – 24 months after the original ELISA testing, and was not possible in  
133 all cases as some producers did not want to be involved, or there had been changes in  
134 management, and one had closed down. The preferred samples were colonic mucosa obtained  
135 at the abattoir following slaughter, where minor thickening or irregularities in the otherwise  
136 apparently normal colonic wall were identified by external palpation. Between 1 and 20  
137 colonic samples were obtained from 13 of the 22 herds. Faecal samples (between 1 and 50)  
138 were obtained from fattening pigs in 16 of the herds, including seven from herds where colon  
139 samples also were submitted. Loose faeces were requested, but in a number of cases the faeces  
140 received were of normal consistency and were considered unlikely to contain detectable levels  
141 of spirochaetes even if the animal was colonised.

142

#### 143 **Table 1 about here**

144

145 Samples were plated onto selective Trypticase Soy Agar (BBL) plates containing 5% (vol/vol)  
146 defibrinated ovine blood, 400 µg of spectinomycin per ml, and 25 µg each of colistin and

147 vancomycin (Sigma–Aldrich) per ml (Jenkinson and Wingar 1981). The plates were incubated  
148 for 5–7 days at 37 °C in an anaerobic environment of 94% H<sub>2</sub> and 6% CO<sub>2</sub> generated with  
149 anaerobic Gaspak plus sachets (BBL). The plates were examined for the presence of a low, flat,  
150 spreading growth and associated haemolysis. Surface growth was re-suspending in phosphate-  
151 buffered saline and examined under a phase-contrast microscope. The harvested growth on  
152 plates suspected to have spirochaete growth were subjected to a PCR reaction for *B.*  
153 *hyodysenteriae*, as previously described (La et al. 2003).

154

### 155 2.5. Multilocus sequence typing (MLST)

156 Six *B. hyodysenteriae* isolates obtained in pure culture were analysed by multilocus sequence  
157 typing (MLST), as previous described (La et al. 2009b). Two isolates came from herds where  
158 the veterinarian considered that SD was present and four came from apparently healthy herds.

159

## 160 3. Results

### 161 3.1. Culture and PCR

162 *B. hyodysenteriae* was isolated from faecal or colonic samples from nine of the 22 sampled  
163 herds, including three reported as being infected and six which were considered to be  
164 uninfected by their veterinarians (Table 1). Between one and 13 *B. hyodysenteriae* isolates  
165 were recovered from samples from these six herds, with their identity confirmed by PCR. All  
166 isolates were strongly beta-haemolytic.

167

### 168 3.2. MLST

169 The six isolates examined by MLST were confirmed as being *B. hyodysenteriae* on the basis of  
170 their clustering with other strains of the species, although they belonged to six different new  
171 sequence types (STs): ST140, ST144, ST149, ST158, ST160 and ST161. These STs have been  
172 submitted to the PubMLST database (<http://pubmlst.org/brachyspira/>).



173

### 174 3.3. ELISA

175 A total of 1,770 serum samples were obtained from the 30 herds (Table 1). Multiple sets of  
176 samples were submitted from seven herds, with a total of 42 batches of sera received from the  
177 30 herds. In the case of the 12 herds that were reported as being infected by the submitting  
178 veterinarians, 11 were positive by ELISA (91.7%). The herd that was negative by ELISA (herd  
179 12) was only sampled once. Herd 10 was negative with the first batch of sera test, but was  
180 positive with two other batches of sera. Faecal or colonic samples were collected from pigs  
181 from seven of the 12 herds considered to be infected, and single isolates of *B. hyodysenteriae*  
182 were detected by culture in three (including herd 12 that was negative by ELISA).

183

184 Of the other 18 herds that were classified as not being infected by the veterinarians, 14 (herds  
185 13 through 26) were positive by ELISA. Three of these herds had more than one batch of sera  
186 tested, and batches from two herds also were positive in the subsequent tests (herds 15 and 24).  
187 Faecal or colonic samples were obtained from 11 of these 14 herds, and *B. hyodysenteriae* was  
188 isolated from samples from six of these (54.5%). The final four herds (herds 27-30) were  
189 considered negative by their veterinarians and also gave a negative ELISA results. Faeces or  
190 colon samples cultured from three of these four herds were negative. Confirmatory samples  
191 were not made available for the fourth herd.

192

## 193 4. Discussion

194 Use of the prototype ELISA was able to correctly identify 11 of 12 herds that had a history of  
195 SD. Herd 10 was only correctly identified as infected when a second batch of 40 sera was  
196 examined, while herd 12 that was incorrectly recorded as uninfected by ELISA only had 40  
197 samples collected at a single time point. In this case the negative result may have arisen from  
198 the limitations of the sampling regimen. With a perfect test, and assuming an infected herd has

199 a 10% within-herd prevalence of infection, a sample size of 40 sera should achieve 95%  
200 confidence of detecting an individual infected pig, provided that the infection is uniformly  
201 distributed in the herd (Mhoma et al. 1992; Song et al. 2015). If additional samples had been  
202 tested from this herd, and preferable samples from another batch of pigs, the chances of  
203 identifying the herd as infected would have been improved (as it was for herd 10). Indeed, for  
204 routine surveillance it is recommended that the ELISA should be used regularly on different  
205 batches of serum samples: this regimen would both help detect new infections in disease-free  
206 herds, and could be used to monitor changes in the numbers of infected pigs in herds that are  
207 known to be colonised.

208  
209 Of the 18 herds reported to be non-infected, only four were ELISA negative. Samples from  
210 three of the latter were tested by culture and PCR and the negative results helped to confirm  
211 that they were likely to be true negative herds. On the basis of the overall findings it appeared  
212 that the ELISA had quite a poor specificity as a herd test. Of the other 14 “false positive” herds,  
213 however, six that initially were considered to be non-infected by the consulting veterinarians  
214 subsequently were shown to be colonised when *B. hyodysenteriae* was isolated from animals  
215 from the herds. Sampling occurred 6-24 months after ELISA testing, and it is possible that they  
216 were newly infected during this intervening period, but against this possibility was the fact that  
217 their clinical status of the herds did not change over this period and they remained healthy. As  
218 a result of this finding the apparent specificity of the test improved, and indeed it might have  
219 been even greater if more samples from others of the eight “false positive” herds were  
220 examined by culture and PCR. This was emphasised by the fact that *B. hyodysenteriae* was  
221 only isolated from samples from a minority of the 12 herds that were known to be infected. To  
222 obtain a better understanding of the true specificity of the ELISA it would be necessary to  
223 examine samples from many more herds that are confirmed to be uninfected based on prior  
224 extensive screening of large number of colonic samples by culture and PCR. Serological cross-

225 reactivities resulting from infection with other *Brachyspira* species also remain a possible way  
226 that false positive results could be generated. In this case the gene for H114 is present in some  
227 strains of “*B. hampsonii*”, *B. intermedia*, *B. murdochii* and *B. pilosicoli*, although at the  
228 translated amino acid level the similarity to H114 in *B. hyodysenteriae* is only 70-78%,  
229 meaning that serological cross-reactivity is unlikely (unpublished data). Such potential cross-  
230 reactivities also were screened for in the original selection of the ELISA antigen (Song et al.  
231 2015).

232  
233 The most important finding in this study was the demonstration that *B. hyodysenteriae* is  
234 present in a number of Australian pig herds that are not showing signs of disease, including in  
235 a high health status breeding herd that does not routinely use antimicrobials. There had been no  
236 reason to suspect that these herds were colonised, and they would not have been investigated  
237 for SD had they not submitted serum samples as being from “negative control SD-free herds”.  
238 It is apparent that routine herd screening based simply on observation of clinical signs,  
239 checking production records and submitting faecal samples from healthy pigs to look for *B.*  
240 *hyodysenteriae* by culture and/or PCR may fail to identify colonisation in apparently healthy  
241 herds. A more reliable means of routine screening of healthy herds can be achieved at the  
242 abattoir by culturing any thickened areas of the colonic wall in pigs after slaughter.

243  
244 Although the sampled herds were not randomly selected, *B. hyodysenteriae* was detected by  
245 culture in six of the 18 healthy herds. Although this is a small sample size, it does give a  
246 remarkably high 33% prevalence of infection amongst apparently healthy Australian herds.  
247 Interestingly, this is the same as in a much earlier study where 35 of 106 randomly selected  
248 Western Australian herds were considered to be infected based on testing blood collected at  
249 abattoirs in a serological ELISA using extracted *B. hyodysenteriae* LOS as the plate coating  
250 antigen (Mhoma et al. 1992). It appears that colonisation of herds may be more common than

251 is generally appreciated, and that colonisation does not necessarily result in typical disease at  
252 the herd level.

253  
254 A similar situation to that described here was reported in an Australian study published in 1992,  
255 where an isolate of *B. hyodysenteriae* was recovered from a pig in a high-health status herd  
256 with minimal antimicrobial usage and no disease (Hampson et al. 1992). Significantly, this  
257 isolate caused typical SD when it was used to experimentally challenge pigs in a research  
258 facility. The reason for lack of disease expression in the herd of origin was unclear, but it is  
259 known that dietary ingredients may influence the occurrence and severity of SD by creating  
260 conditions within the large intestine that influence colonisation by the spirochaete (Pluske et al.  
261 1996; Siba et al. 1996; Thomsen et al. 2007; Hansen et al. 2010, 2011). In this scenario, should  
262 isolates from healthy herds be transmitted to other herds where different conditions exist then  
263 disease eventually may develop (Hampson et al. 2015).

264  
265 A question remains as to the pathogenic potential of the isolates in the current study that were  
266 recovered from herds where signs of disease were not observed. Six different sequence types of  
267 *B. hyodysenteriae* were detected for six isolates, including four STs for the four isolates tested  
268 from herds without disease. This demonstrates that the absence of disease in these colonised  
269 herds was not associated with one shared strain of low virulence. Isolates of *B. hyodysenteriae*  
270 with low or reduced virulence have been described previously in Europe and North America  
271 (Lyson et al. 1982; Jensen and Stanton 1993; Achacha et al. 1996; Thomson et al. 2003), and it  
272 will be important to test the current isolates in a standardised experimental infection model to  
273 evaluate their potential to colonise and cause disease. If they prove to have reduced capacity to  
274 cause disease then the molecular basis of this will need to be investigated further (La et al.  
275 2011; La et al. 2014). Interestingly when the prototype test kit was used in Europe and the  
276 USA it was again found to be sensitive but apparently lacking in specificity, but in this case the

277 “false positive” herds were not investigated further (unpublished data). It seems likely that at  
278 least some of these herds also were colonised. Use of the ELISA could help alert veterinarians  
279 to the possibility that a healthy herd is colonised, so that it can undergo further investigation,  
280 and as such the test should be a useful addition to the available diagnostic repertoire.

281

## 282 **Conflict of interest**

283 The Prionics test kits were produced under licence from Murdoch University and the  
284 Australian Pork CRC. The authors declare that they have no personal potential conflicts of  
285 interest with the research and/or publication of this study.

286

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294 collection of the samples.

295

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406 **Table 1**

407 Comparison of reported health status of the 30 herds, and results in ELISA and by culture of  
 408 faeces and/or colonic contents where available

| Herd | Reported herd SD status | ELISA results <sup>a</sup>   | Samples subsequently tested by culture and PCR <sup>b</sup> | Number of positive samples |
|------|-------------------------|--|---|----------------------------|
| 1    | Positive                | 2/45 positive  | NT  | NT                         |
| 2    | Positive                | 5/40 positive  | NT  | NT                         |
| 3    | Positive                | 5/60 positive  | 10 faeces, 2 colon samples                                  | Negative                   |
| 4    | Positive                | 1/39 positive  | 2 colon samples   | Negative                   |
| 5    | Positive                | 8/62 positive  | NT  | NT                         |
| 6    | Positive                | 1/40 positive<br>60/60 negative (2 <sup>nd</sup> test)   | NT  | NT                         |
| 7    | Positive                | 5/40 positive  | 1 colon sample  | Negative                   |
| 8    | Positive                | 3/39 positive  | 12 faeces samples   | Negative                   |
| 9    | Positive                | 5/20 positive<br>45/45 negative (2 <sup>nd</sup> test)   | 4 faeces, 2 colon samples                                   | Positive (1)               |
| 10   | Positive                | 40/40 negative<br>2/40 positive (2 <sup>nd</sup> test)<br>1/60 positive (3 <sup>rd</sup> test) | 10 faeces samples   | Positive (1)               |
| 11   | Positive                | 25/25 negative<br>2/25 positive (2 <sup>nd</sup> test)   | 1 faeces sample   | Negative                   |
| 12   | Positive                | 40/40 negative   | 6 faeces, 7 colon samples                                   | Positive (1)               |
| 13   | Negative                | 1/47 positive  | 8 faeces samples  | Positive (1)               |
| 14   | Negative                | 8/40 positive  | 36 faeces, 4 colon samples                                  | Positive (9)               |

|    |          |  |                                |               |
|----|----------|--|--------------------------------|---------------|
| 15 | Negative | 2/40 positive<br>3/40 positive (2 <sup>nd</sup> test)<br>57/57 negative (3 <sup>rd</sup> test)<br>2/30 positive (4 <sup>th</sup> test) | 22 faeces, 17 colon<br>samples | Positive (1)  |
| 16 | Negative | 5/63 positive  | 50 faeces samples              | Positive (13) |
| 17 | Negative | 6/61 positive  | 6 faeces samples               | Positive (4)  |
| 18 | Negative | 2/40 positive  | 6 colon samples                | Positive (1)  |
| 19 | Negative | 1/17 positive<br>43/43 negative (2 <sup>nd</sup> test)<br>56/56 negative (3 <sup>rd</sup> test)  | 42 faeces, 2 colon samples     | Negative      |
| 20 | Negative | 5/57 positive  | 41 faeces samples              | Negative      |
| 21 | Negative | 1/50 positive  | 20 faeces samples              | Negative      |
| 22 | Negative | 1/40 positive  | 2 colon samples                | Negative      |
| 23 | Negative | 3/60 positive  | 20 colon samples               | Negative      |
| 24 | Negative | 5/35 positive<br>9/35 positive (2 <sup>nd</sup> test)<br>1/16 positive (3 <sup>rd</sup> test)  | NT                             | NT            |
| 25 | Negative | 2/30 positive  | NT                             | NT            |
| 26 | Negative | 2/60 positive  | NT                             | NT            |
| 27 | Negative | 40/40 negative   | 2 faeces, 2 colon samples      | Negative      |
| 28 | Negative | 40/40 negative   | NT                             | NT            |
| 29 | Negative | 20/20 negative   | 2 faeces samples               | Negative      |
| 30 | Negative | 33/33 negative   | 11 colon samples               | Negative      |

409 NT, not tested

410 <sup>a</sup>Second, third and fourth tests conducted 2-6 months after the first test

411 <sup>b</sup>Samples collected 6-24 months after serological testing