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Published in:
Journal of Medical Microbiology

DOI:
10.1099/jmm.0.05488-0

2004
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Received 30 September 2003
Accepted 12 January 2004

Brachyspira hyodysenteriae and other strongly β-haemolytic and indole-positive spirochaetes isolated from mallards (Anas platyrhynchos)

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The aims of the current study were to collect intestinal spirochaetes (genus Brachyspira) from farmed and wild mallards (Anas platyrhynchos) and to identify and classify those isolates that phenotypically resembled Brachyspira hyodysenteriae, an enteric pathogen of pigs. The isolation rate of Brachyspira spp. was high from both farmed (93 %) and wild mallards (78 %). In wild mallards, it appeared that Brachyspira spp. were more likely to be found in migratory birds (multivariate analysis: RR = 1.8, 95 % CI 1.1–3.1) than in mallards sampled in a public park. Pure cultures of putative B. hyodysenteriae were obtained from 22 birds. All five isolates from farmed mallards and ten randomly selected isolates with this phenotype were used for further studies. All isolates from farmed mallards and two of the isolates from wild mallards were PCR-positive for the tlyA gene of B. hyodysenteriae. Two isolates from farmed mallards were selected for pulsed field gel electrophoresis (PFGE) and randomly amplified polymorphic DNA (RAPD) analysis. These isolates clustered with the type and reference strains of B. hyodysenteriae. 16S rDNA sequence analysis performed on 11 of the strains showed that they were all closely related to each other and to the B. hyodysenteriae – Brachyspira intermedia cluster. Three of the mallard isolates had 16S rDNA sequences that were identical to those of B. hyodysenteriae strains R1 and NIV-1 previously isolated from common rheas (Rhea americana). To conclude, the isolates from farmed mallards and two isolates from wild mallards were classified as B. hyodysenteriae based on the fact that they could not be differentiated by any of the applied methods from type, reference and field strains of B. hyodysenteriae. The remaining isolates could not be assigned irrefutably to any of the presently recognized Brachyspira species. These results point to a broader host spectrum of B. hyodysenteriae than is generally recognized, and to the presence in mallards of strongly β-haemolytic and indole-producing spirochaetes that possess many, but not all, of the currently recognized characteristics of B. hyodysenteriae.

INTRODUCTION

Spirochaetes have long been known to colonize the intestines of some birds (Jansson et al., 2001). Reports on potentially pathogenic Brachyspira species in chickens and common rheas, as well as the availability of simple biochemical classification schemes, specific PCR assays and various
DNA fingerprinting methods, have led to increased knowledge of the complexity of intestinal spirochaetes in avian species, especially poultry. Information about intestinal spirochaetes in wild birds is, however, very limited. Wild-living waterbirds in Australia and the United States seem to be commonly infected (Swayne & McLaren, 1997; Oxberry et al., 1998). Waterbirds have been suggested as potential natural reservoirs and transmitters of Brachyspira pilosicoli to animals and humans (Oxberry et al., 1998; Duhamel, 2001).

Brachyspira hyodysenteriae is recognized as the aetiologic agent of swine dysentery, a mucosa-haemorrhagic diarrhoeic disease of pigs (Ochiai et al., 1997; Harris et al., 1999). This agent has also been suggested as the cause of necrotizing typhlocolitis in common rheas (Rhea americana) (Sagartz et al., 1992; Buckles et al., 1997). Furthermore, B. hyodysenteriae may be present in wild rodents on farms with infected pigs (Duhamel, 2001). The natural occurrence of B. hyodysenteriae in other mammalian and avian species has not been verified. Interestingly, neither B. hyodysenteriae nor any other intestinal spirochaete has been isolated from wild boars in Sweden (Fellström & Jacobsson, 2002).

B. hyodysenteriae is routinely diagnosed by culture, phenotypic traits, which consist of strong β-haemolysis, indole production, the inability to cleave hippurate and α-galactosidase activity (Fellström et al., 1999), and by specific PCR assays (Leser et al., 1997; Ateyo et al., 1999; Fellström et al., 2001). Several atypical B. hyodysenteriae isolates of porcine origin have recently been described. These include isolates that do not produce indole (Fellström et al., 1999) and those that are negative for a B. hyodysenteriae-specific 23S rDNA-based PCR test (Murray et al., 2003). PFGE, randomly amplified polymorphic DNA (RAPD) and phylogenetic analysis based on 16S rRNA sequence analysis showed that these atypical variants are genetically closely related to typical porcine B. hyodysenteriae (Fellström et al., 1999; Murray et al., 2003).

In a previous study, we cultured a putative B. hyodysenteriae isolate from a mallard (Anas platyrhynchos) on a gamebird farm (Jansson et al., 2001). The present study was designed to confirm this finding, to investigate whether the same spirochaete phenotype was present in wild-living mallards and to identify these isolates. Finally, we wanted to examine whether age, season, sex or migratory status was associated with the presence of Brachyspira spp. in wild mallards. We chose the mallard as our target species because it is the most numerous and widespread of all ducks. The mallard is an omnivorous dabbling duck that lives on wetlands, sometimes in close association to human populations. In addition, it is a common game species and is also the ancestor of domestic ducks.

METHODS

Strains and isolates. All strains and isolates of porcine, canine and avian origin that were used for phenotyping, PCR and genetic analyses are shown in Table 1. One of those isolates from a mallard on a gamebird farm (AN383/2/00) has previously been described phenotypically (Jansson et al., 2001). A further 27 cloacal swabs were obtained in June 2000 from adult mallards on the same farm. The sampling was approved by the Swedish Ethical Committee for Scientific Experiments (protocol C33/99). Samples from wild mallards were collected independently from two separate locations. Between November 2000 and May 2001, 33 wild mallards were sampled in a public park with an ornamental lake in southern Sweden (Pildammsparken, Malmo; 55°35’ N 12°58’ E). These samples were collected as freshly deposited faeces. Additionally, 184 migrating mallards were consecutively caught on an island in southeastern Sweden during October and November 2002 (Ottenby Bird Observatory, Oland; 56°12’ N 16°24’ E). The birds were caught in a duck funnel trap with the approval of the Swedish Museum of Natural History/Swedish Environmental Protection Agency (protocol 412-1038-02 Nf) and the sampling was approved by the Swedish Ethical Committee for Scientific Experiments (protocol M109/02). The samples were obtained either as cloacal swabs or as fresh faeces. In the latter case, birds were confined individually to boxes on clean newspaper until they defecated, and their faeces were collected. The sex and age of the birds were determined as described previously (Boyd et al., 1975). Birds less than 1 year old were considered as juveniles, and older birds as adults. All the sampled mallards were clinically healthy and showed no signs of diarrhoea. The samples were transported at ambient temperature by surface mail in Amies medium and cultured within 24–48 h at the Department of Bacteriology, National Veterinary Institute, Uppsala, Sweden. Spirochaetes were thereafter isolated and classified according to previous descriptions (Fellström et al., 1999).

PCR analysis. PCR for detection of the tlyA haemolysin gene of B. hyodysenteriae was used according to previously described protocols (Fellström et al., 2001), with some modifications. Each sample was tested twice. In total, ten type, reference and field strains of porcine origin, one chicken isolate, one isolate from a dog and 15 mallard isolates were analysed by PCR.

PFGE. PFGE was performed as described previously (Fellström et al., 1999). A dendrogram was created with the GelCompar program based on combined gels of MluI- and Sall-digested DNA, using a matrix of band-matching coefficients by the unweighted pair group method with arithmetic mean (UPGMA) clustering fusion strategy. Ten type, reference and field strains of porcine origin, one chicken isolate, one isolate from a dog and two mallard isolates with a biochemical phenotype consistent with group I spirochaetes were studied by PFGE.

RAPD. Two mallard isolates with a biochemical phenotype consistent with group I spirochaetes, one chicken isolate and ten type, reference and field strains of porcine origin were studied by RAPD, as described previously (Quednau et al., 1998), with a few modifications. The cells were lysed by boiling and the isolates were typed with primers P1254 (5’-CCGCAAGCCAA-3’) and P73 (5’-ACGGCGCCCT-3’), separately, which resulted in two sets of banding patterns. Those patterns were combined in the GelCompar program with the combined gels option.

Sequence analysis of the 16S rRNA gene. 16S rDNA sequences of 11 of the selected Brachyspira isolates from farmed and wild-living mallards were determined as described by Pettersson et al. (1996), with some modifications. The 16S rDNA gene was first amplified with the PCR primers listed in Table 2. The sequencing system (Pettersson et al., 1996) was adapted to the ABI Prism 3100 Genetic Analyzer (Applied Biosystems) with the primers listed in Table 2. Labelled terminators (Big Dye; Applied Biosystems) were used in the cycle sequencing reactions. The primer sequences are given in Table 2. Contigs were created using the ContigExpress program included in the Vector NTI suite (Informax). The 16S rDNA sequences were aligned manually using Genetic Data Environment software (Smith, 1992), to a prealigned set of
Table 1. Biochemical characteristics, PCRs and GenBank accession nos of porcine, canine and avian *Brachyspira* strains included in this study

Ind, Indole production; Hipp, hippurate cleavage; α-gal, α-galactosidase activity; NA, not available; ND, not done; +/−, different results were obtained when duplicated.

<table>
<thead>
<tr>
<th>Strain</th>
<th>Species</th>
<th>Animal of origin</th>
<th>β-Haemolysis</th>
<th>Ind</th>
<th>Hipp</th>
<th>α-Gal</th>
<th>tlyA*</th>
<th>GenBank accession no.</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td>B78T</td>
<td><em>B. hyodysenteriae</em></td>
<td>Pig</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>U14930</td>
<td>Harris et al. (1972)</td>
</tr>
<tr>
<td>B204</td>
<td><em>B. hyodysenteriae</em></td>
<td>Pig</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>U14932</td>
<td>Kinyon et al. (1977)</td>
</tr>
<tr>
<td>R1</td>
<td><em>B. hyodysenteriae</em></td>
<td>Rhea</td>
<td>Strong†</td>
<td>+†</td>
<td>NA</td>
<td>−†</td>
<td>NA</td>
<td>U23035</td>
<td>Sagartz et al. (1992)</td>
</tr>
<tr>
<td>NIV-1</td>
<td><em>B. hyodysenteriae</em></td>
<td>Rhea</td>
<td>Strong†</td>
<td>+†</td>
<td>NA</td>
<td>−†</td>
<td>NA</td>
<td>U23036</td>
<td>Jensen et al. (1996)</td>
</tr>
<tr>
<td>AN983 : 90</td>
<td><em>B. intermedia</em></td>
<td>Pig</td>
<td>Weak</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>U14933</td>
<td>Pettersson et al. (1996)</td>
</tr>
<tr>
<td>PWS/AR</td>
<td><em>B. intermedia</em></td>
<td>Pig</td>
<td>Weak</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>U23033</td>
<td>Stanton et al. (1997)</td>
</tr>
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<td>C378</td>
<td><em>Brachyspira murdochii</em></td>
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<td>Weak</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>U14918</td>
<td>Pettersson et al. (1996)</td>
</tr>
<tr>
<td>56-150R</td>
<td><em>B. murdochii</em></td>
<td>Pig</td>
<td>Weak</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>U14920</td>
<td>Kinyon &amp; Harris (1979)</td>
</tr>
<tr>
<td>C173</td>
<td><em>Brachyspira innocens</em></td>
<td>Pig</td>
<td>Weak</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>U14921</td>
<td>Pettersson et al. (1996)</td>
</tr>
<tr>
<td>B256T</td>
<td><em>B. innocens</em></td>
<td>Pig</td>
<td>Weak</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>U14920</td>
<td>Kinyon &amp; Harris (1979)</td>
</tr>
<tr>
<td>P43/6/78T</td>
<td><em>B. pilosicoli</em></td>
<td>Pig</td>
<td>Weak</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>U14927</td>
<td>Pettersson et al. (1996)</td>
</tr>
<tr>
<td>AN497 : 93</td>
<td><em>B. pilosicoli</em></td>
<td>Pig</td>
<td>Weak</td>
<td>+</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>U14927</td>
<td>Pettersson et al. (1996)</td>
</tr>
<tr>
<td>C1T</td>
<td><em>Brachyspira alvinipulli</em></td>
<td>Dog</td>
<td>Weak</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>U23030</td>
<td>Swarowsky et al. (1992); Stanton et al. (1998)</td>
</tr>
<tr>
<td>AN4578/01</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Weak</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>U349933</td>
<td>K.-E. Johansson and others (unpublished)</td>
</tr>
<tr>
<td>AN383 : 200</td>
<td><em>B. hyodysenteriae</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>AY352291</td>
<td>Jansson et al. (2001); this study</td>
</tr>
<tr>
<td>AN3355 : 2/00</td>
<td><em>B. hyodysenteriae</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>U352289</td>
<td>This study</td>
</tr>
<tr>
<td>AN3055 : 3/00</td>
<td><em>B. hyodysenteriae</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>ND</td>
<td>This study</td>
</tr>
<tr>
<td>AN3049 : 2/00</td>
<td><em>B. hyodysenteriae</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>ND</td>
<td>This study</td>
</tr>
<tr>
<td>AN3060 : 1/00</td>
<td><em>B. hyodysenteriae</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>ND</td>
<td>This study</td>
</tr>
<tr>
<td>AN3052 : 1/00</td>
<td><em>B. hyodysenteriae</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>ND</td>
<td>This study</td>
</tr>
<tr>
<td>AN1409 : 2/01</td>
<td><em>B. hyodysenteriae</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>+</td>
<td>AY352281</td>
<td>This study</td>
</tr>
<tr>
<td>AN1418 : 2/01</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>AY352282</td>
<td>This study</td>
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<td>AN3599 : 2/02</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>AY352283</td>
<td>This study</td>
</tr>
<tr>
<td>AN3624 : 2/02</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>AY352284</td>
<td>This study</td>
</tr>
<tr>
<td>AN3886 : 2/02</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>AY352285</td>
<td>This study</td>
</tr>
<tr>
<td>AN3902 : 2/02</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>AY352286</td>
<td>This study</td>
</tr>
<tr>
<td>AN3907 : 2/02</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>AY352287</td>
<td>This study</td>
</tr>
<tr>
<td>AN3930 : 2/02</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>AY352288</td>
<td>This study</td>
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<td>AN3931 : 2/02</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>AY352289</td>
<td>This study</td>
</tr>
<tr>
<td>AN3949 : 2/02</td>
<td><em>Brachyspira spp.</em></td>
<td>Mallard</td>
<td>Strong</td>
<td>+</td>
<td>−</td>
<td>−</td>
<td>−</td>
<td>AY352290</td>
<td>This study</td>
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</tbody>
</table>

*Primer for PCR taken from Fellström et al. (2001).
†Data from Trott et al. (1996).
‡Mallards were: a, farmed bird, faecal sample; b, farmed bird, cloacal swab; c, wild bird in a public park, faecal sample; d, wild migrating bird, faecal sample.
§Sequence not deposited; preliminary data on 800 bp show close similarity to the sequence of R1 and NIV-1.
Brachyspira spp. sequences retrieved from the Ribosomal Database Project (Maidak et al., 2001).

Statistical analyses. Relative risks between isolation rate of intestinal spirochaetes and sampling sites, seasons, age groups and sexes were calculated, and the confidence intervals were precision based (Kleinbaum et al., 1982). To examine which of the potential risk factors (age, sex, migratory status and season) were most important for finding Brachyspira spp., a log linear model specified as a multivariate generalized linear model, with a Poisson distribution of the error term and log link function, was used. For inclusion in the final model, a \( P \) value, 0.01 was required.

RESULTS AND DISCUSSION

Strains and isolates

Brachyspira spp. were isolated from 25 of 27 (93 %) cloacal swabs collected from mallards on the game farm and from 169 of 217 (78 %) samples from wild mallards. The results of spirochaete cultures from wild mallards and relative risks are shown in Table 3. On average, 1.5 spirochaete isolates with different phenotypes were obtained from each infected wild mallard. The multivariate analyses indicated that the presence of Brachyspira spp. among the wild mallards examined appeared to be determined by whether the birds were migrating or not (\( RR = 1.8, 95 \% \) CI 1.1–3.1).

Isolates with a particular phenotype characteristic of B. hyodysenteriae were obtained in pure culture from five of 27 (19 %) farmed mallards and from 18 of 217 (8 %) wild mallards. Birds with strongly \( \beta \)-haemolytic Brachyspira spp. were distributed throughout the sampling period. This spirochaetal phenotype was cultured from birds of both sexes and from both juvenile and adult birds. In most cases,

Table 2. Primers used for PCR and sequencing of the 16S rRNA gene of Brachyspira spp.

Positions are numbered according to the Escherichia coli 16S rRNA sequence.

<table>
<thead>
<tr>
<th>Designation (direction)</th>
<th>Position</th>
<th>Sequence (5’–3’) or reference</th>
<th>Application</th>
</tr>
</thead>
<tbody>
<tr>
<td>kag-007 (forward)</td>
<td>11–35</td>
<td>GTTTGATYCTGGCTCAGARCKAACG</td>
<td>PCR</td>
</tr>
<tr>
<td>kag-009 (reverse)</td>
<td>1496–1520</td>
<td>CTTGGGTACGGMTCCCTTGTTACG</td>
<td>PCR</td>
</tr>
<tr>
<td>kag-008 (forward)</td>
<td>15–30</td>
<td>GATYCTGGCTCAGARC</td>
<td>Sequencing</td>
</tr>
<tr>
<td>584 (forward)</td>
<td>334–352</td>
<td>Johansson et al. (1998)</td>
<td>Sequencing</td>
</tr>
<tr>
<td>631 (reverse)</td>
<td>519–534</td>
<td>Johansson et al. (1998)</td>
<td>Sequencing</td>
</tr>
<tr>
<td>538 (forward)</td>
<td>800–818</td>
<td>Johansson et al. (1998)</td>
<td>Sequencing</td>
</tr>
<tr>
<td>kag-011 (reverse)</td>
<td>922–939</td>
<td>CTTGGGTACGGMTCCCTTG</td>
<td>Sequencing</td>
</tr>
<tr>
<td>597 (forward)</td>
<td>1175–1193</td>
<td>Johansson et al. (1998)</td>
<td>Sequencing</td>
</tr>
<tr>
<td>kag-010 (reverse)</td>
<td>1501–1518</td>
<td>TCCGCTACGGMTCCCTTG</td>
<td>Sequencing</td>
</tr>
</tbody>
</table>

Table 3. Results of Brachyspira spp. cultures in 217 wild mallards

\( RR \), Relative risk; CI, confidence interval. Birds of unknown age or sex were not included in the analyses.

<table>
<thead>
<tr>
<th>Variable</th>
<th>Brachyspira spp.</th>
<th>( RR ); 95 % CI limits</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Positives/sampled</td>
<td>Prevalence (%)</td>
</tr>
<tr>
<td><strong>Sampling site</strong></td>
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<td></td>
</tr>
<tr>
<td>Public park</td>
<td>15/33</td>
<td>45</td>
</tr>
<tr>
<td>Bird station (migratory birds)</td>
<td>154/184</td>
<td>84</td>
</tr>
<tr>
<td><strong>Sex</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>88/121</td>
<td>73</td>
</tr>
<tr>
<td>Female</td>
<td>79/94</td>
<td>84</td>
</tr>
<tr>
<td>Unknown</td>
<td>2/2</td>
<td>100</td>
</tr>
<tr>
<td><strong>Age</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Adults</td>
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<td>54</td>
</tr>
<tr>
<td>Juveniles</td>
<td>127/151</td>
<td>84</td>
</tr>
<tr>
<td>Unknown</td>
<td>15/16</td>
<td>94</td>
</tr>
<tr>
<td><strong>Season</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Spring (February to May)</td>
<td>9/18</td>
<td>50</td>
</tr>
<tr>
<td>Autumn (September to November)</td>
<td>160/199</td>
<td>80</td>
</tr>
</tbody>
</table>
inference that could distort the results of the statistical analyses. Thus, the several missing observations concerning age and sex that enable a firm conclusion on this issue. Moreover, there were migration as a risk factor. The current evidence does not finding and season (autumn) could also be important risk factors for promoted by migration. However, young age, sex (females) migratory seasons, or that the shedding of spirochaetes is susceptibility to spirochaetal infections is increased during al.

Birds through increased corticosteroid levels (Holberton et al., 1996; Ra˚berg et al., 1998), it cannot be excluded that their susceptibility to spirochaetal infections is increased during migratory seasons, or that the shedding of spirochaetes is promoted by migration. However, young age, sex (females) and season (autumn) could also be important risk factors for finding Brachyspira spp. or simply reduce the prominence of migration as a risk factor. The current evidence does not enable a firm conclusion on this issue. Moreover, there were several missing observations concerning age and sex that could distort the results of the statistical analyses. Thus, the inference that Brachyspira spp. is associated with migration should be considered indicative rather than conclusive.

**PCR assay**

The results of the PCR assay are shown in Table 1. All selected isolates from farmed mallards and two isolates from wild mallards (AN1409 : 2/01 and AN3907 : 2/02) were PCR-positive for the tlyA gene and were therefore classified as B. hyodysenteriae. The remaining isolates from wild mallards were negative for the tlyA gene and could not be classified by PCR.

**PFGE and RAPD**

The two isolates that were analysed by PFGE and RAPD originated from the mallard farm. The dendrogram based on RAPD analysis is shown in Fig. 1. The similarity values for both assays showed that the avian isolates were closely related to the reference strains B78 and B204 of B. hyodysenteriae, thus confirming their classification based on PCR as B. hyodysenteriae.

**Phylogenetic analysis**

The phylogenetic tree based on 16S rRNA sequence analysis is shown in Fig. 2. Accession numbers of the 16S rRNA gene of mallard isolates are given in Table 1. Phylogenetic analysis based on 16S rRNA sequences showed that all of the 11 studied Brachyspira strains grouped in the B. hyodysenteriae– Brachyspira intermedia cluster. The similarity values of the 16S rRNA sequences in this cluster varied from 99.4 to 100 %.

This observation, and the fact that there were no coherent subclusters comprising only representatives of the respective species, shows that it is not possible to distinguish between B. hyodysenteriae and B. intermedia by sequence analysis of 16S rDNA, in accordance with previously published results (Pettersson et al., 1996). Three of the mallard strains (AN383 : 2/00, AN1409 : 2/01 and AN3907 : 2/02) had identical sequences, that were also identical to two strains of B. hyodysenteriae (R1 and NIV-1) that have been isolated from common rheas from farms in Ohio and Iowa in the United States (Sagartz et al., 1992; Jensen et al., 1996). The mallard isolates possessing this sequence were from a farmed bird, and from the two wild birds. These two wild birds had been
sampled during different seasons, years and at separate locations. We believe that these three mallard isolates and the two previously described isolates from common rheas should be considered as \textit{B. hyodysenteriae}. This specific \textit{B. hyodysenteriae} genotype seems to be genetically rather stable, present on two continents in both farmed and wild-living avian hosts and possibly adapted to birds, as it has not been found in pigs. Two additional strains (AN39930:2/02 and AN39931:2/02) were also identical with respect to their 16S rRNA sequences, and differed from strains R1 and NIV-1 by only one nucleotide. These two latter isolates both originated from wild-living migrating mallards. Three strains from wild mallards (AN3599:2/02, AN3624:2/02 and AN3886:2/02) were also identical with respect to their 16S rRNA sequences, and differed from strains R1 and R358 from common rheas also failed to colonize the animals and they did not develop any lesions (Buckles, 1996). Furthermore, in inoculation experiments of pigs, \textit{B. hyodysenteriae} strains R1 and R358 from common rheas also failed to grow from caecal or colonic samples obtained at necropsy 4 weeks post-inoculation. All pigs remained healthy. In the case of mallards, we have at present no reason to believe that \textit{B. hyodysenteriae} or \textit{B. hyodysenteriae}-like variants are pathogenic. None of the sampled birds in this study showed any signs of disease or diarrhoea. However, we were not able to investigate any of the birds for histological evidence of lesions. This does not necessarily mean that \textit{B. hyodysenteriae} strains are pathogenic. Additional studies are needed to confirm this conclusion. Moreover, if these extended challenge trials should confirm the apathogenic nature of avian \textit{B. hyodysenteriae}, these isolates may serve as useful comparative tools in identifying pathogenicity mechanisms in other strains of \textit{B. hyodysenteriae}.

**Conclusions**

To conclude, we were able to classify the strongly \(\beta\)-haemolytic and indole-positive spirochaetes which were corrected for multiple substitutions (Saitou & Nei, 1987) from a distance matrix comprising 1399 nucleotide positions, which was based on few sequence differences and many of the nodes are not stable (bootstrap values lower than 67%).

**Clinical significance**

The clinical significance of \textit{B. hyodysenteriae} in non-porcine species remains somewhat unclear. In common rheas, the infection has been associated with necrotizing typhilocolitis and high mortality (Sagartz et al., 1992; Buckles et al., 1997). On the other hand, challenge infection of juvenile common rheas with the R1 rhea strain of \textit{B. hyodysenteriae} was inconclusive as to the development of lesions, although spirochaetes were seen in histological sections in 75% of the infected birds (Buckles, 1996). In the same study, mallard ducklings were infected by strain R1. Histological evaluation revealed spirochaetes in only 7% of the inoculated ducks and none of the birds developed any lesions (Buckles, 1996). Furthermore, in inoculation experiments of pigs, \textit{B. hyodysenteriae} strains R1 and R358 from common rheas also failed to colonize the animals and they did not develop any lesions (Stanton et al., 1997). In a preliminary challenge infection trial approved by the Swedish Ethical Committee for Scientific Experiments (protocol C17/2), we used one of the mallard isolates of \textit{B. hyodysenteriae} (AN3052:1/00) to inoculate three grower pigs twice orally (data not shown). We were not able to reisolate the bacterium from rectal swabs obtained daily from each pig, except from one pig within 24 h of the inoculation. Spirochaetes did not grow from caecal or colonic samples obtained at necropsy 4 weeks post-inoculation. All pigs remained healthy. In the case of mallards, we have at present no reason to believe that \textit{B. hyodysenteriae} or \textit{B. hyodysenteriae}-like variants are pathogenic. None of the sampled birds in this study showed any signs of disease or diarrhoea. However, we were not able to investigate any of the birds for histological evidence of lesions. This does not necessarily mean that \textit{B. hyodysenteriae} and \textit{B. hyodysenteriae}-like variants are avirulent in mallards; they seem more likely to be opportunistic or apathogenic to the host. Taken together, the current lack of evidence of pathogenicity of avian isolates of \textit{B. hyodysenteriae} in pigs indicates avirulence. Additional studies are needed to confirm this conclusion. Moreover, if these extended challenge trials should confirm the apathogenic nature of avian \textit{B. hyodysenteriae}, these isolates may serve as useful comparative tools in identifying pathogenicity mechanisms in other strains of \textit{B. hyodysenteriae}.

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**Fig. 2.** Evolutionary tree based on sequence analysis of the 16S rRNA gene showing the phylogenetic relations between \textit{Brachyspira} spp. isolated from mallards (shown in bold) and other strains of \textit{Brachyspira} spp. The tree was constructed by neighbour-joining (Saitou & Nei, 1987) from a distance matrix comprising 1399 nucleotide positions, which was corrected for multiple substitutions at single locations by the two-parameter method of Kimura (1980). \textit{Brachyspira aalborgi} was used as outgroup. Bootstrap percentages from 1000 resamplings of the dataset are given for some of the stable nodes. The scale bar shows the distance equivalent to one substitution per 100 positions.
spectrum of \textit{B. hyodysenteriae} than generally recognized, as well as to the presence of strongly β-haemolytic and indole-producing spirochaetes that possess many, but not all, of the currently recognized characteristics of \textit{B. hyodysenteriae}.

**ACKNOWLEDGEMENTS**

We thank Ulla Zimmermann and Marianne Persson for excellent laboratory assistance. We would also like to express our gratitude to the owner of the game bird farm, to K. Bengtsson and L. Blomquist for collecting samples from wild mallards in the public park and to P. Bohman and K. Carlsson who collected the samples from migrating mallards. This work was supported by grants from the Swedish Farmers’ Foundation for Agricultural Research.

**REFERENCES**


