Phenotypic and genotypic characterization of *Bordetella bronchiseptica* strains isolated from pigs in Poland

K. Stępniewska, K. Urbaniak, I. Markowska-Daniel

Department of Swine Diseases, National Veterinary Research Institute
Al. Partyzantów 57, 24-100 Puławy, Poland

Abstract

A total of 209 *Bordetella bronchiseptica* (*Bbr*) strains isolated from pigs were examined. Phenotypic study included: biochemical characterization (motility, catalase, oxidase, urease activity, nitrate reduction and growth on MacConkey agar) and antimicrobial susceptibility (disc diffusion method). Genotypic studies based on detection of three genes encoded virulence factors, such as: flagella (*fla*), dermonecrotoxin (*dnt*), and exogenous ferric siderophore receptor (*bfrZ*), using PCR.

Most of the *Bbr* strains tested had a homogeneous biochemical profile. 97.6% of them provided suitable results in biochemical tests. All *Bbr* isolates tested showed high resistance to penicillin (100%), linco-spectin (100%) and ceftiofur (97.9%). Over 57% and 43% of *Bbr* strains were resistant to ampicillin and amoxicillin, respectively. All *Bbr* isolates showed high sensitivity to most chemotherapeutics used such as enrofloxacin (97.9%), tetracycline (97.9%), oxytetracycline (97.9%), amoxicillin with clavulonic acid (95.8%), florfenicol (90.4%), and gentamicine (77.6%). Over of 94% of *Bbr* strains were moderately susceptible to norfloxacine.

Molecular analysis confirmed that almost all evaluated *Bbr* strains (94.7%) possessed the *fla* gene. A lower percentage of isolates had the *dnt* gene (72.7%) and the lowest percentage of strains (51.7%), had the *bfrZ* gene.

Key words: swine, *Bordetella bronchiseptica*, phenotypic and genotypic characterization, antimicrobial susceptibility

Introduction

*Bordetella bronchiseptica* (*Bbr*) was isolated for the first time by Ferry in 1910 from the respiratory tract of dogs (Goodnow 1980). The bacterium was renamed many times before receiving its final name. *Bordetella bronchiseptica* is an upper respiratory tract pathogen of many animal species such as: swine, dogs, cats, rabbits, horses, rats and guinea pigs. *Bordetella bronchiseptica* was also isolated from wild animals such as: bears, leopards, foxes, seals, koalas and raccoons (Ross et al. 1967, Woode and McLeod 1967, Bemis et al. 1977, Musser et al. 1987, Winn et al. 2006, Bemis et al. 2010). Occasionally it affects man.
Depending on the health of the pig herd Bbr alone can cause a mild to moderate form of atrophic rhinitis (AR) with nonprogressive turbinate bone atrophy; however, in combination with dermonecrotic Ppasteurella multocida (Pm) strains it can cause a more severe progressive form of AR (Jong De 2006, Pomorska-Mól et al. 2011, Register 2012). Other Bordetella spp. which belong to the Alcaligenaceae family do not cause diseases of animals (Bordetella hinzii, B. holmesii, B. trematum, B. petrii), although B. hinzii is isolated from the respiratory tract of poultry. In contrast Bordetella hinzii, B. holmesii and B. trematum are connected with human opportunistic infections (Be mis et al. 2010).

Many studies suggested that three species: Bbr, Bordetella pertussis (Bp) and Bordetella parapertussis (Bpp) are closely related (Parkhill et al. 2003, Parton 2005). These studies were based on a phenotypic and genotypic comparison between Bordetella species. Phenotypic analyses included biochemical properties and antigenic structure. Genotypic analyses were related to DNA-DNA hybridization analyses, mean G+C contents of their genomic DNA, sequence similarity of 23S rRNA and phage typing, as well as the comparison of the whole genome of each analyzed species. Phylogenetic analysis and the results of insertion sequence (IS) typing demonstrated that both Bp and Bpp are derived from Bbr. Comparison of genomic sequences of reference strains confirmed that the nucleotide sequence similarity is very high in conservative regions. This suggests that these strains have evolved from a Bbr-like ancestor (Gerlacha et al. 2001, Parkhill et al. 2003, Parton 2005, Sebaihia et al. 2006).

Bbr is small, Gram-negative, coccobacilli. The bacterium grows in obligatory aerobic conditions, optimally at 35°C. Bbr is a nonfermentative species with the ability to move, which is facilitated by peritrichous flagella (Goodnow 1980). Bbr has catalase, oxidase, and urease activity (in the case of urease, up to 4h). The bacterium also has the ability to cause decarboxylation of ornithine and nitrate reduction. Colonies of Bbr grow on routinely used agar media in 2-3 days, they grow more rapidly than other species of the Bordetella genus and are more resistant to variable physical and chemical conditions (Bemis et al. 1977, Parton 2005).

Some virulence factors have an important role in the pathogenicity of Bbr. Fimbriae, for example, are associated with bacterial attachment and colonization of nasal epithelium cells. Dermonecrototoxin is necessary for the induction of clinical signs in swine (Kume et al. 1986, Pullinger et al. 1996, Parton 2005), while iron is associated with the metabolism of Bbr and determines the bacterium’s ability to colonize and proliferate (Brickman et al. 2007).

The aim of this study was to analyze the phenotypic and genotypic properties of Polish Bbr strains isolated from nasal swabs of pigs.

Materials and Methods

Bordetella bronchiseptica strains

In total 209 Bbr strains were analyzed. They were isolated at the National Veterinary Research Institute in Pulawy between 2007-2011 from 912 nasal swabs of pigs from 106 farms located in 13 Polish provinces: Wielkopolskie (35), Śląskie (17), Kujawsko-Pomorskie (13), Mazowiecko-Pomorskie (10), Zachodnio-Pomorskie (8), Lubelskie (7), Warmińsko-Mazurskie (4), Łódzkie (3), Podlaskie (3), Lubuskie (2), Świętokrzyskie (2), Dolnośląskie (1) and Małopolskie (1). Figure 1 shows the results of isolation of Bbr from provinces and farms.

As a positive control Bbr vaccine strain (B16) and two reference Bbr strains from ATCC (4617 and 10580) were used. As a negative control, Bordetella parapertussis (ATCC 15311) and Bordetella pertussis (ATCC 8467) were included.

Culture conditions

The strains were isolated on G20G medium, supplemented with penicillinum crystallisatum (10 mg/ml, Polfa Tarchomin S.A.), gentamicin (0.25 mg/ml, Polfa Tarchomin S.A.), nitrofurantoine (10 mg/ml, Sigma Aldrich), and nystatinum (10 mg/ml, Sigma Aldrich). All plates were incubated at 37°C for 48-72 h. Blue-green suspected colonies were subcultured on agar medium with 5% horse blood.

Biochemical characterisation and classification

Identification of Bbr isolates was carried out using standard biochemical tests. Gram staining, motility, catalase and oxidase tests, urease activity, nitrate reduction, and growth on MacConkey agar were used as criteria for identification of Bbr.

Antimicrobial susceptibility

Isolates of Bbr were tested for their in vitro sensitivity to a panel of 14 commonly used chemotherapeutics by the disc diffusion method, following the
Fig. 1. Results of isolation of Bbr. Legend: red dot – provinces from which samples were tested, first number – number of farm tested from individual province, second – number of samples tested, third – number of Bbr isolates.

Table 1. Sequence of primers used for amplification of fla, dnt and bfrZ genes of Bbr.

<table>
<thead>
<tr>
<th>Species</th>
<th>Primer</th>
<th>Gene</th>
<th>Sequence 5′→3′</th>
<th>Primer length (nt)</th>
<th>PCR product length (bp)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bbr</td>
<td>FlaF</td>
<td>fla</td>
<td>AGG CTC CCA AGA GAG AAA GGC T</td>
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<td>237</td>
</tr>
<tr>
<td></td>
<td>FlaR</td>
<td></td>
<td>TGG CGC CTG CCC TAT C</td>
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<td></td>
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<tr>
<td></td>
<td>dntF</td>
<td>dnt</td>
<td>GCG CTA CTT GGG ATA ATA GA</td>
<td>20</td>
<td>224</td>
</tr>
<tr>
<td></td>
<td>dntR</td>
<td></td>
<td>ATA AAG ATG AAT CGG CAT TG</td>
<td>20</td>
<td></td>
</tr>
<tr>
<td></td>
<td>BfrZf</td>
<td>bfrZ</td>
<td>GCA ATG ACC TGA ACC TGT ATT T</td>
<td>22</td>
<td>368</td>
</tr>
<tr>
<td></td>
<td>BfrZr</td>
<td></td>
<td>CAT GGG CAT GTT CTT CTT GT</td>
<td>20</td>
<td></td>
</tr>
</tbody>
</table>

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For analysis of antimicrobial susceptibility of *Bbr* isolates Müeller-Hinton medium with 5% sheep blood was used.

**DNA extraction**

DNA extraction from *Bbr* isolates was performed according to the Genomic Mini isolation kit protocol (A&A Biotechnology, Poland). Genetic material was used directly in PCR or stored at -80°C for further analysis.

**Primers**

Three sets of primers were used in PCR for detection of genes encoding selected virulence factors of *Bbr* such as flagella (*fla*), dermonecrotxin (*dnt*) and exogenous ferric siderophore receptor (*bfrZ*). Primers which amplify a 237 bp fragment of the *fla* gene were designed by Hozbor et al. (1999).

Primers which amplify *dnt* and *bfrZ* genes were designed by us, based on the analysis of their gene sequence available from GeneBank (BB3978 and BB4744, respectively), using the LaserGene computer programme. The specification of primers used is shown in Table 1.

**Reaction conditions**

All PCRs were performed in 0.2 ml individual PCR Tubes™ (BioRad, UK) in a T3-thermocycler (Biometra, Germany). Reactions were performed using an AmpliTaq Gold set containing 10xPCR Gold Buffer, 25 mM MgCl₂ solution, polymerase AmpliTaq Gold 5 U/mL (Applied Biosystem, Roche), 10 mM dNTPs (Fermentas) and 20 μM each of primer and water free from DNase and RNase. The total volume of reaction mixture was 25 μl, which included 2.5 μl of DNA and 22.5 μl of reagent mix. Each reaction mixture was subjected to an amplification regimen consisting of 10 min of initial denaturation at 95°C, followed by 40 cycles of 30 s of denaturation at 95°C, 30 s of annealing at 56°C, and 30 s of extension at 72°C. Final elongation was done for 10 min at 72°C.

**Detection of PCR products**

PCR products were separated by electrophoresis in 2% agarose gel with ethidium bromide at a concentration of 1 μl/ml. The electrophoresis was done in 1xTAE buffer, at 350 mA. 10 μl of reaction mixture and 2 μl of loading buffer 6xDNA Loading Dye (Fermentas) were inserted into each well. The molecular weight of the products obtained was determined by comparison to the molecular weight of marker GeneRuler™ 100 bp DNA Ladder Plus (Fermentas). The agarose gels were photographed under UV light using an EC3 Chemi HR 410 Imaging System (UK).

**Results**

Isolates of *Bbr* strains were obtained from 22.9% of nasal swabs taken from 3 groups of pigs: with AR, suspected of having the disease or of unknown health. All *Bbr* strains showed a high level of homogeneity. They had typical morphology, were Gram (-) and produced catalase. Over 99% of them had the ability to move (99.5%), produced urease (98.6%), gave positive results in an oxidase production test (99.5%) and reduced nitrate (97.6%). *Bbr* showed typical growth on MacConkey agar (99.5%).

Results of antimicrobial susceptibility show that all *Bbr* isolates were resistant to penicillin and linco-spectin. Over 97.9% of *Bbr* strains were also resistant to ceftiofur. In contrast, over 95% of strains were sensitive to amoxicillin with clavulanic acid (95.8%), oxytetracycline, tetracycline and enrofloxacin (97.9% each). The percentage of strains sensitive to florfenicol was 90.4%. 94.4% of strains were moderately susceptible to norfloxacin.

The highest diversity in susceptibility was noticed in the group of β-lactams, commonly using chemotherapeutics. Within this group, all *Bbr* isolates were resistant to penicillin and highly sensitive to amoxicillin with clavulanic acid. Just 4.2% of *Bbr* strains were moderately susceptible to amoxicillin with clavulanic acid. A high percent of *Bbr* strains were resistant to ampicillin (57.4%) and 29.9% of strains were susceptible to this antibiotic. Over 43% of *Bbr* strains were sensitive to amoxillin (43.9%), while 39% of strains were resistant to it.

All *Bbr* strains were resistant to ceftiofur, linco-spectin and penicillin. Figure 2. shows the results of antimicrobial susceptibility of *Bbr* strains. Additionally to phenotypic analysis of *Bbr* strains, genotypic characterisation was done. The presence of three genes was tested in *Bbr* strains by specific PCRs. 198 of 209 *Bbr* isolates (94.7%) from nasal swabs possessed the *fla* gene, which was indicated by presence of 237 bp product. This was the highest percentage of *Bbr* isolates which possessed this gene. In a lower number of tested *Bbr* strains the *dnt* gene was detected. 152 isolates were positive for the presence of this gene (72.7%). The *bfrZ* gene was
detected in the lowest number of Bbr strains. The gene was found only in 108 isolates, which was a little more than a half of all tested Bbr strains (51.7%).

**Discussion**

Classic bacteriological methods are still the “gold standard” in laboratory diagnostics. The success of isolation of Bbr strains mainly depends on the time between sample acquisition and further laboratory procedures, sample storage conditions and the presence of appropriate medium in swabs during transport (Markowska-Daniel and Stępniewska 2009).

Samples taken from the nasal cavity of pigs are specific. The pig is a digging animal species and has contact with other pigs and their secretions. Therefore the pig nasal cavity harbours many atypical bacterial species. As a consequence, competitive growth of bacteria could make the isolation of Bbr strains on blood agar more difficult and thereby extend the time of bacteriological examination.

Colony morphology on solid medium is commonly used as a microbial identification criterion in laboratory diagnosis. Isolation of Bbr directly from nasal swabs on blood agar medium is a little troublesome because of the small size of the Bbr colony and the fact that their growth might be blocked by mixed bacterial flora. Therefore, it is important to use selective media during Bbr isolation. Smith – Baskerville medium is in common use in the isolation of Bbr from biological material, especially when the number of Bbr present is low. The medium contains three antibiotics: 20 μg/ml penicillin, 20 μg/ml furaltadone, and 0.5 μg/ml gentamicin (Smith and Baskerville 1979, Lariviere et al. 1993, Register 2012). In our study G20G medium was used, which, similarly to Smith – Baskerville, contains penicillin and gentamicin, but additionally includes nitrofurantoin and nystatinum, which prevents the growth of fungal pathogens.

For identification of Bbr species, Lariviére et al. (1993), Bemis et al. (1997), Register and Ackerman (1997), Register and DeJong (2006) and Zhao et al. (2010) used a catalase, oxydase and urease test, growth on MacConkey medium, nitrate reduction and colony morphology analysis. Analogous tests were use in our studies. Most of the Bbr strains tested have a homogeneous biochemical profile. 97.6% of them obtained suitable results in biochemical tests.

The next part of this study was the evaluation of the sensitivity of Bbr isolates to commonly used chemotherapeutics. There are only few reports connected with drug resistance of Bbr strains.

Among swine respiratory pathogens examined such as: Bbr, Pm, Mannheimia haemolitica (M. haemolitica), Actinobacillus pleuropneumoniae (App), Streptococcus suis (S. suis) the highest MIC values for various concentrations of florfenicol for Bbr was achieved by Priebe and Schwarz (2003). Those results suggest low efficiency of florfenicol in low concentrations against Bbr, in comparison to other pathogens tested.

Kadlec et al. (2004) conducted studies on the susceptibility of Bbr isolates from pigs collected between 2001-2003 in Germany. Their results showed high sensitivity of Bbr isolates tested to tetracycline, enrofloxacin and gentamicin. These antibiotics in a concentration of 0.5-2 μg/ml inhibited the growth of 90% of Bbr strains. Polish Bbr isolates were also sensitive to these three antibiotics. Kadlec et al.
(2004) also showed that the MICs values to ampicillin and ceftiofur for Bbr strains were the highest (MIC90=16). The ceftiofur from the cephalosporin group of antibiotics, could be used against a wide range of pathogens of the pig respiratory tract and is in common use against Salmonella spp., Pm, App, S. suis and Escherichia coli, whereas it is not effective against Bbr (Burton et al.1996). Among our Bbr isolates, significant resistance to ampicillin and ceftiofur was also observed.

Mortensen et al. (1989) showed high sensitivity of Bbr strains to tetracycline. This antibiotic in a concentration of 2 μg/ml inhibits the growth of 90% of Bbr strains isolated from people and pigs. For American and German Bbr strains MIC90 values to ampicillin and SXT were similar, but to gentamicin and tetracycline MIC values were higher in the case of strains obtained from the USA.

Assignment of Bbr based on MIC values for different antibiotics into susceptible, moderately susceptible and resistant strains is problematic, because the range of antimicrobial susceptibility published by CLSI contains data only for florfenicol.

The efficiency of some chemotherapeutics on Bbr may depend on the growth phase of the bacterium. Ishikawa et al. (1988) showed that Bbr in the C growth phase was more resistant to ampicillin than in the X phase. Bannatyne and Cheung (1984) showed that strains which lost some functional structural antigens were more resistant to antibiotic in comparison to the wild type.

Isolation of Bbr is time-consuming, and may take 3-7 days. Commercial ELISA tests for Bbr detection are not available. Serological tests, which use Bp antigen cannot differentiate infection caused by Bpp from Bbr. Furthermore, Jenkins (1977) who tested cross reactivity of ELISA, showed that 2.7% and 13% serum samples from growing pigs and mature hogs, respectively, reacted with Pm antigen. Boot et al. (1993) suggested that ELISA be used in cases of monitoring infection caused by Bbr in rabbits and guinea pigs.

A more sensitive, specific and accurate method used in diagnosis of Bbr infection is PCR.

In our study the specific sequence of the fla gene was amplified in PCR. The main reason why the fla gene was used was the fact that Bbr strains are ciliated bacteria and have the ability to move, in comparison to Bp and Bpp, which are nonmotile. Hozbor et al. (1999) used primers which amplify the 237 bp fragment of this gene. Evaluation of its specificity show that they were specific only for Bbr. The specificity was tested also with such pathogens as Staphylococcus aureus, M. hyopneumoniae, Aspergillus fumigatus, Candida albicans, Streptococcus pneumoniae, Streptococcus pyogenes, Streptococcus agalactiae and Chlamydia pneumoniae. PCR results showed that this gene was present in 94.7% of Bbr strains.

For detection of dermonecrotxin traditional bacteriological methods, such as cytotoxic tests using cell lines, or biological test (laboratory animals) can be used but they are time consuming, and therefore PCR seems to be a good tool. As was shown by Stepniewska and Markowska (2010) primers for amplification were specific only for Bbr and the sensitivity of the elaborated test was high. It is important that PCR based on the dnt gene can be use directly to nasal swabs with no need of bacteria isolation.

In the pathogenicity of Bbr the siderophore receptor gene is no less important than dermonecrotxin or flagella. The bfrZ gene is only present in the genome of Bbr. The lowest number of Bbr strains with this gene may suggest that other siderophore receptor genes were expressed.

Our results show the common presence of Bbr strains in Polish pig herds. The presence of fla, dnt and bfrZ genes in 94.7%, 72.7% and 51.5% respectively in Bbr strains confirm a high level of pathogenicity among Polish Bbr isolates. It is suggested that fla, dnt and bfrZ genes can be use as markers of pathogenicity of Bbr strains (Stepniewska and Markowska 2012).

According to our best knowledge there are no other reports on phenotypic and genotypic characterisation of Polish isolates of Bbr from nasal swabs of pigs.

References


