Molecular characterisation and antibiotic sensitivity profile of Pasteurella multocida isolated from poultry farms in Malaysia

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ABSTRACT. Fowl cholera has caused significant economic losses in many poultry producing countries worldwide. In Malaysia, outbreaks of fowl cholera are frequently reported and encountered in different types of poultry productions. The objective of this study was to characterise 13 avian Pasteurella multocida, isolated from fowl cholera outbreaks in Central Peninsular Malaysia in the period between 2000 and 2018. The isolates were subjected to multiplex polymerase chain reaction (PCR) for capsular serotyping, disc diffusion method for antimicrobial susceptibility profiles, and molecular genotyping using pulsed-field gel electrophoresis (PFGE) and multilocus sequence typing (MLST). The capsular serotyping showed all 13 Pasteurella multocida isolates belonging to capsular serotype A. The antimicrobial susceptibility showed several multidrug resistance strains among the P. multocida isolates. All the isolates were resistant to erythromycin (100%), streptomycin (68%), tetracycline (37%), enrofloxacin (37%), florfenicol (23%), penicillin G (14%), gentamicin (14%), and amoxicillin (14%). The PFGE analysis clustered the isolates into three clones. Group A included isolates with a similarity of 87% from the year 2000, 2013, and 2018. Three sequence types were identified using MLST typing namely, ST129, ST231, and ST355. The ST355 was assigned for the first time in the Rural Industries Research and Development Corporation (RIRDC) database. Besides, ST129 has been reported in India, China, and Sri Lanka, which highlights the possibility of transmission between Asian countries. This study provides an insight into epidemiological information of Pasteurella multocida that causes fowl cholera outbreaks in the central region of Peninsular Malaysia.

Key words: antimicrobial susceptibility, MLST, Pasteurella multocida, PFGE.

INTRODUCTION

Pasteurella multocida (P. multocida) is a Gram-negative bacterium that can cause a wide range of diseases in animals, such as fowl cholera in poultry, haemorrhagic septicaemia in bovine, and atrophic rhinitis in swine (Wilkie et al. 2012, Wilson and Ho 2013). Fowl cholera is an epizootic, highly contagious avian disease that could affect several avian species including commercial chickens (Botzler 1991). Since it was discovered, it has caused significant economic losses in the poultry industry worldwide (Harper et al. 2006). The disease may occur as an acute septicaemia form with high morbidity and mortality (up to 100%), or as a localised chronic infection (Heddleston et al. 1964, Harper et al. 2006). Sudden death for a large number of birds is usually the first clinical sign in acute fowl cholera (Glisson et al. 2013). Pasteurella multocida can currently be subdivided into four subspecies: subsp. multocida, subsp. gallicida, subsp. septica, and subsp. tigris. All subspecies, excluding tigris, have been isolated from fowl cholera outbreaks (Harper et al. 2006). Serotype A is the dominant serotype of P. multocida causing fowl cholera while serotypes B, D, and F have been less reported to cause disease in poultry (Wilkie et al. 2012). Outbreaks were reported in Asia and all over the world (Wang et al. 2013, Jones et al. 2013, Singh et al. 2013). Antibiotics are widely used in the treatment of P. multocida infections in poultry, which have increased antibiotic resistance (Murray 1992). A study conducted in Brazil showed 19.64% of P. multocida strains isolated from chicken and turkey farms were multidrug-resistant to three or more drugs in different categories using the disc diffusion method (Furian et al. 2016). A number of epidemiological studies were conducted to investigate the distribution of P. multocida strains in several countries (Sarangi et al. 2016, Li et al. 2018, Peng et al. 2018). Pulsed-field gel electrophoresis (PFGE) is a genotyping technique that analyses bacterial chromosomes using restriction enzyme into DNA fragments. The PFGE fragments pattern can be used to study the strain variation and evolution (Gunawardana et al. 2000). PFGE also has been used to study outbreaks of fowl cholera in poultry (Kardos and Kiss 2005, Selley et al. 2017). However, multilocus sequence typing (MLST) is the current gold standard typing method for P. multocida, which uses seven housekeeping genes to characterise and study the global distribution of P. multocida sequence types (STs) (Kardos and Kiss 2005, Subaaharan et al. 2010, Singh et al. 2013).

In Malaysia, avian P. multocida outbreaks were frequently reported in commercial and backyard farms (Arumugam et al. 2011, Nafizah et al. 2014, Khoo et al. 2017). However, information on P. multocida serogroups, antibiotic resistance profile, and molecular genotyping are poorly investigated. Therefore, the aim of this study is to molecular characterise P. multocida isolates from fowl cholera outbreaks submitted to the Laboratory of Bacteriology at Faculty of Veterinary Medicine, Universiti Putra Malaysia, Malaysia. The isolates undergo multiplex
PCR serotyping to determine the serogroup as well as the disc diffusion method to determine the resistance profile of the isolates. Additionally, genotyping was performed using PFGE and MLST to study the variation and evolution of the *P. multocida* isolates.

**MATERIAL AND METHODS**

**BACTERIAL ISOLATES**

Thirteen *P. multocida* subspecies *multocida* isolates from the Bacteriology Laboratory, Faculty of Veterinary Medicine, Universiti Putra Malaysia, Malaysia were analysed in this study (table 1). The samples were submitted for diagnostic purposes, between the years 2000 to 2018 from fowl cholera outbreaks in backyard chicken farms located in Selangor, Malaysia. The bacteria isolates were obtained from chicken internal organs including liver, spleen, and lungs, and were subject to biochemical identification. The samples were cultured onto 5% blood agar (OXOID, UK). Suspected colonies showing *P. multocida* colony morphology, were subjected to biochemical tests, namely, oxidase, indole, Triple Sugar Iron (TSI), Sulfide Indole Motility (SIM), citrate, urease reactions and Ornithine Decarboxylase Test (ODC), trehalose, mannitol, D-sorbitol, and dulcitol.

**MOLECULAR IDENTIFICATION**

Genomic DNA was extracted using the boiling method. The bacteria were boiled at 97 °C for 10 min, then placed in an ice container for 5 min, then centrifugated for 10 min at room temperature. The isolates were confirmed as *P. multocida* using PCR targeting the KMT1 gene as described by Townsend et al (1998). *P. multocida* ATCC 12945 was used as a positive control.

**MULTIPLEX PCR CAPSULAR TYPING**

The isolates were subjected to capsular serotyping using the primers designed by Townsend et al (2001). Genomic DNA was extracted using the boiling method. The multiplex PCR was carried out with a final reaction volume of 50μl, 30 PCR cycles; 95°C for 45 sec, 56.2°C for 45 sec, 72°C for 45 sec. The PCR product was visualised using a UV transilluminator.

**ANTIMICROBIAL SUSCEPTIBILITY TEST**

Antimicrobial susceptibility test was carried out using the disc diffusion method following the Clinical and Laboratory Standards Institute standards (CLSI) VET01- A4 (4th ed.) and the M45 (3rd ed.). Two replicates were performed for each isolate against eight antibiotics, namely, streptomycin 10μg, amoxicillin 10μg, tetracycline 30μg, gentamicin 10μg, erythromycin 15μg, penicillin G 10μ, enrofloxacin 5μg, and florfenicol 30μg. The bacteria suspensions were cultured on Mueller-Hinton agar then the antibiotic where placed on the plates. After 24 hours of incubation, the average zone of inhibition was measured and interpreted. The *Escherichia coli* ATCC25922 and *Staphylococcus aureus* ATCC 29213 were used as quality control.

| Number | Year | Sample | PFGE | ST | Antibiotics resistance profile 2) |
|--------|------|--------|------|----|-----------------------------------|
| 1      | 2000 | PM201  | A3   | 129| E                                 |
| 2      | 2000 | PM202  | A3   | -  | E                                 |
| 3      | 2000 | PM203  | A3   | -  | E                                 |
| 4      | 2000 | PM204  | A3   | -  | E                                 |
| 5      | 2013 | PM205  | A1   | 129| ST, ENR, TE, E                    |
| 6      | 2013 | PM206  | A2   | -  | ST, ENR, TE, E, AMX, CN, P        |
| 7      | 2014 | PM207  | B    | 129| ST, ENR, TE, E, AMX, CN, P, FFC   |
| 8      | 2016 | PM208  | C1   | 355| ST, E                             |
| 9      | 2016 | PM209  | C2   | -  | ST, E                             |
| 10     | 2016 | PM210  | C3   | -  | ST, E                             |
| 11     | 2016 | PM211  | C3   | -  | E                                 |
| 12     | 2018 | PM212  | A1   | -  | ST, ENR, TE, E, FFC               |
| 13     | 2018 | PM213  | A1   | 231| ST, ENR, TE, E, FFC               |

2) List of antibiotics the isolates were resistant against, according to M45 (3rd ed.) and VET01- A4 (4th ed.) of the CLSI standard. ST= Streptomycin, AMX= Amoxicillin, TE= Tetracycline, CN= Gentamicin, E= Erythromycin, P= Penicillin G, ENR= Enrofloxacin, FFC= Florfenicol.
A single colony from each isolate was cultured in brain heart infusion broth (BHI) (OXOID, UK) and incubated at 37°C for 24 hr. The culture was then mixed to cell suspension buffer and adjusted to 0.6-0.7 of McFarland standard. The cell mixtures were pipetted into CHEF disposable plug moulds (Bio-Rad Laboratories, USA) and allowed to solidify for 10 min at 4°C. The plugs were transferred into 2 ml cell lysis buffer and incubated in a water bath at 56°C for 17 hr with one hour shaking at 100 rpm. The plugs were washed two times with deionised water for 10 min each at 50°C, followed by 5 times washing with the TE buffer. A small slice of each plug was placed in a 2 ml tube containing 200 µl per-restriction mixture for 15 min at 37°C. Then, a restriction mixture containing the ApaI enzyme was added and incubated at 37°C for 2 hr. Finally, the restriction mixture was removed, and 0.5 TBE buffer was added for 5-10 min. The electrophoresis was performed using the following conditions; initial switch time 1 sec, final switching time 40 sec, a constant voltage of 6 V, and an angle of 120. With a total running time of 23 hr and 14°C running temperature. BioNumerics 6.6 software was used to analyse the P. multocida PFGE profiles. The dendrogram was created with 1% optimization and 1% tolerance using the Dice similarity coefficient, by unweighted paired group method of arithmetic averages (UPGMA). Strains with more than three differences in DNA fragments and a similarity of <85% were classified into different PFGE types (Van Belkum et al 2007).

MULTILOCUS SEQUENCE TYPING

One isolate representing each year was characterised via the MLST scheme. Briefly, PCR amplification was carried out for seven housekeeping genes, using the primers designed by Subaaharan et al (2010), then the sequences were analysed using the P. multocida MLST RIRDC database to get the P. multocida sequence type (ST).
A recently published study in China reported that 84% of avian Pasteurella multocida isolates were ST129, and they suggested that ST129 is a significant and high virulence ST of Pasteurella multocida in southwestern China, causing fowl cholera infections in many types of poultry species (Li et al. 2018). The study also found that most of the ST129 isolates exhibited multidrug resistance for antibiotics, including amoxicillin, tetracycline, florfenicol, and streptomycin, which is very similar to the resistance pattern findings for the ST129 isolates in this study (table 1). Furthermore, Pasteurella multocida ST129 was also reported in India in fowl cholera outbreaks (Sarangi et al. 2016). And in Iran from chicken fowl cholera outbreak according to the RIRDC MLST database. On the other hand, the ST129 was also reported to cause hemorrhagic septicemia in bovine in Sri Lanka (Hotchkiss et al. 2011), as well as infection in pigs according to the RIRDC MLST database. As a result, ST129 was suggested as adaptable to many types of hosts (Hotchkiss et al. 2011, Peng et al. 2018). Although the distribution of the ST129 was discovered in India, it was suggested as a result of possible transmission from China and Sri Lanka (Sarangi et al. 2016). In the current study, ST129 was identified in several fowl cholera cases among poultry in Malaysia and had a relatively similar antibiotic profile to the ST129 isolates reported in southwestern China (Li et al. 2018). This finding shows the high possibility of transmission of ST129 from or to China into Malaysia. Besides, Pasteurella multocida was proved to spread between different countries. In a study of the fowl cholera outbreaks in Denmark and Sweden, it shows that migrating birds had spread a strain of Pasteurella multocida, which caused several fowl cholera outbreaks among these countries (Christensen and Bisgaard 2000, Petersen et al. 2001). Regarding our study, Malaysia is a significant winter home for many species of migratory birds coming from the north due to its stable weather (DeCandido et al. 2004). Thus, increasing the possibility of transmission of new strains into the country.

MLST is an effective tool to study Pasteurella multocida genotype variation and evolution (Subaaharan et al. 2010). Pasteurella multocida ST231 belongs to the CC129 and shared six alleles (esp, pmx, Zwf, mdh, gdh, pgp) with ST129 single locus variant (SLV) besides sharing a relatively similar antibiogram (table 1), which suggested that it evolved from ST129. Another study had published a complete genome sequence of Pasteurella multocida serotype A, isolated from haemorrhagic septicemia infection in buffaloes in Malaysia under the accession No. CP007205 in NCBI GenBank (Jabeen et al 2017). Based on the analysis of the RIRDC MLST database, this strain belongs to ST201, which also belongs to CC129. This isolate is SLV with ST129, this finding suggested that it evolved from ST129 and caused haemorrhagic septicemia infection in buffaloes.
in Malaysia. Haemorrhagic septicaemia was reported to be endemic and of significant economic importance in many countries, including Malaysia (Benkirane and De Alwis 2002). The investigation provides significant insights into the epidemiological importance of CC129 in Malaysia. In contrast, recently published in China, there is a report on a double-locus variant (DLV) genotype from the CC129 identified as the first hypervirulent and multi-antimicrobial resistant avian *P. multocida* (ST342) (Zhu et al. 2020). In India, SLV from CC129 (ST280) was also reported causing fowl cholera outbreaks (Sarangi et al. 2016). These findings highlight the threat of *P. multocida* CC129 as ubiquitous and causing infections in many animal host species in Asian countries.

Overall, this study provides important epidemiological data on the diversity of *P. multocida* causing fowl cholera infection in Malaysia and highlighted the high potential of transmission of the same sequence type among the nearby countries. This study also reported the CC129 is a big threat to the poultry industry in Malaysia, and as a wildly reported CC causing fowl cholera in South Asian countries. The high antibiotic resistance shown among isolates in this study warrants the prudent use of antimicrobial agents in the poultry production in Malaysia.

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