





Spread of multidrug-resistant *Pseudomonas aeruginosa* in animal-derived foods in Beijing, China

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Abstract

Pseudomonas aeruginosa is the most common bacterium occurred in nosocomial infections and is also an important indicator of food spoilage. The worldwide spread of multidrug resistant (MDR) *P. aeruginosa* is threatening public health. However, the prevalence and spread of MDR *P. aeruginosa* through the food chain is little referred under the One Health perspective. Here, we collected a total of 259 animal-derived foods (168 chicken and 91 pork) from 16 supermarkets and farmer's markets in six regions of Beijing, China. The prevalence of *P. aeruginosa* in chicken and pork was 42.1%. The phenotypic antimicrobial susceptibility testing showed that 69.7% of isolates were MDR, and isolates from Chaoyang district exhibited a higher resistance rate compared to that from Xicheng district ($p < 0.05$). *P. aeruginosa* isolates exhibited high levels of resistance against β -lactams (91.7%), cephalosporins (29.4%), and carbapenems (22.9%). Interestingly, none of strains showed resistance to amikacin. Whole-genome sequencing showed that all isolates carried various kinds of antimicrobial resistance genes (ARGs) and virulence genes (VGs), especially for *bla*_{OXA} genes and *phz* genes. Multilocus sequence typing (MLST) analysis indicated that ST111 (12.8%) was the most predominant ST. Notably, the emergence of ST697 clones in food-borne *P. aeruginosa* was firstly reported. In addition, the toxin pyocyanin was detected in 79.8% of *P. aeruginosa* strains. These findings help to decipher the prevalence and the strong toxigenic ability of MDR *P. aeruginosa* from animal-derived foods and highlight the effective supervision of animal-derived food hygiene should be strengthened to prevent the spread of ARGs in a One Health strategy.

Sample collection and bacterial isolation

A total of 259 samples of pork ($n=91$) and chicken ($n=168$) were collected in 2020 from 16 supermarket and farmer's markets in six different districts (Dongcheng, Xicheng, Chaoyang, Changping, Fengtai, and Xicheng) in Beijing, China. Labplas TWIRL'EM sterile homogeneous bags (Labplas, Canada) were used for preservation before the samples were delivered to the laboratory and CHROMagar *Pseudomonas* (CHROMagar, Paris, France) were used for bacteria screening. All the samples were cultivated on...

Prevalence and distribution of *P. aeruginosa* from animal-derived foods

Overall, 109 non-duplicate *P. aeruginosa* isolates were identified from 259 chicken and pork samples from six districts of Beijing, China, of which 91 were from chicken and 18 were from pork (Table 1 and Table S1). The overall prevalence rate of *P. aeruginosa* was 42.1%, and the prevalence rate in chicken (54.2%) was significantly higher ($p<0.05$) than that in pork (19.8%). Regarding the regional differences, the prevalence rate varies from 20.8% in Haidian to 60.0% in Fengtai among the 6...

Discussion

P. aeruginosa is an opportunistic pathogen associated with hospital infections, drinking water contamination, and food spoilage (Del Barrio Tofiño et al., 2020; Wei et al., 2020). The rapid emergence and dissemination of MDR *P. aeruginosa* is threatening public health and food safety (Kupferschmidt, 2016). To date, many studies have tended to focus on the clinical detriment of MDR *P. aeruginosa*, while few comprehensive surveillance data have been reported from animal-derived foods. Here, we...

Conclusions

This study firstly characterized the spread and prevalence of MDR *P. aeruginosa* in animal-derived foods in Beijing, China. *P. aeruginosa* contamination in chicken is more serious than that in pork. Isolates show MDR phenotypes, especially β -lactams and carbapenems. The β -lactamase genes *bla*_{OXA} are the main ARGs in CRPA isolates. ST111 is the dominant clones in MDR *P. aeruginosa* in animal-derived foods. Importantly, the emergence of ST697 clones in food-borne *P. aeruginosa* is firstly reported. *P. ...*