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Data Article

Data on antibiogram and resistance genes harboured by *Salmonella* strains and their Pulsed-field gel electrophoresis clusters

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ABSTRACT

This article describes the Pulsed-field gel electrophoresis clustering of the predominant *Salmonella* strains (*Salmonella* ser. Albany, *Salmonella* ser. Brancaster, and *Salmonella* ser. Corvallis) isolated from poultry and processing environment in wet market and small-scale processing plant in Penang and Perlis, the northern states of Malaysia. Agar disk diffusion assay was performed to determine the phenotypic antibiotic resistance of these *Salmonella* strains. The most common antibiograms among the three predominant *Salmonella* serovars were reported. The presence of integrase genes and antibiotic resistance genes conferring to resistance against β-lactams, aminoglycosides, tetracyclines, quinolones, sulphonamides and chloramphenicol, was detected via PCR amplification.

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Specifications Table

Subject area	*Microbiology*
More specific subject area	Foodborne pathogen
Type of data	Table
How data was acquired	Antibiograms were determined using the agar disk diffusion assay. Antibiotic resistance genes were detected using PCR (TProfessional Standard Gradient96 Thermocyler, Biometra, Germany). Typing of the *Salmonella* strains was performed using Pulsed-field gel electrophoresis (PFGE) (Biorad CHEF Mapper system, Hercules, CA) coupled with Bionumerics software version 7.0 (Applied Maths, Kortrijk, Belgium).
Data format	Analysed
Experimental factors	Turbidity of the overnight broth cultures of *Salmonella* was adjusted to 0.5 McFarland Standard
Experimental features	Clustering of *Salmonella* strains using Pulsed-field gel electrophoresis (PFGE) fingerprints. The diameter of inhibition zones on agar was measured and interpreted as resistant by referring to breakpoints suggested by CLSI. The presence of antibiotic resistance and integrase genes were detected by PCR amplification.
Data source location	Perlis and Penang, the northern states of Malaysia
Data accessibility	Data are presented as Table 1 in this article, and Microsoft Excel Worksheet, which are provided as Supplementary data.

Value of the data

- The data on the presence of multidrug-resistant *Salmonella* in poultry and processing environment is a good indicator to extensive use of antibiotic in poultry.
- DNA fingerprinting will help in understanding the *Salmonella* contamination patterns.
- The data is a good indicator for the government to create a national surveillance program focusing on monitoring the antibiotic resistance profiles and DNA fingerprinting of foodborne *Salmonella* in poultry and processing environment.
- The data will aid in the discussion of the potential dissemination of antibiotic resistance genes in poultry and processing environment.

1. Data

Table 1 lists the antibiograms of multidrug-resistant (MDR) *S.* Corvallis, *S.* Brancaster and *S.* Albany strains isolated from poultry and processing environment in northern Malaysia. The Microsoft Excel Worksheet that is provided as Supplementary data (Table S1) for this article lists the antibiotic resistance and integrase genes harboured by these *Salmonella* strains, and the PFGE clustering of these strains.

2. Experimental design, materials and methods

2.1. *Salmonella* strains

Salmonella enterica subsp. *enterica* strains used in this study were previously isolated from a total of 182 poultry and environmental samples collected from wet markets and small-scale processing plant located in Penang and Perlis, the northern states of Malaysia. Seventeen different *Salmonella*