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# Surveillance of antimicrobial resistance among *Escherichia coli* from chicken and swine, China, 2008–2015

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ABSTRACT

The objective of this study was to investigate the antimicrobial resistance trend in *Escherichia coli* from food animals in China. During 2008–2015, a total of 15,130 *E. coli* were isolated from chicken and swine from seven provinces. The susceptibilities of these isolates to nine classes of antimicrobial agents were determined using broth microdilution susceptibility method. The findings of this study include: (1) multi-drug resistance was highly prevalent in *E. coli*; (2) these *E. coli* isolates showed high resistant rate (>80%) to several old drugs, including ampicillin, tetracycline and sulfisoxazole; (3) increasing resistance to colistin, florfenicol and ceftiofur was observed; (4) the *E. coli* isolates from different provinces had different resistance patterns. All these data highlight the rising problem of antimicrobial resistance. It is urgent to improve the management of animal production and enhance the proper use of antimicrobials in China as well as the other countries.



## 1. Introduction

Antimicrobial resistance (AMR) in bacteria is of great concern to the health and welfare of both human and animals (McDermott et al., 2016; Zawack et al., 2016). It has been reported that AMR kills around 50,000 people a year in the US and Europe, and is estimated to kill more than 700,000 people globally (O'Neill, 2016). If no action was made to reduce AMR, probably, 10 million people would die every year from drug-resistant infections by the year of 2050 (O'Neill, 2016). Academic studies suggest that the use of antimicrobial agents in agriculture increases the number of infections caused by drug-resistant bacteria in humans. Thus the monitoring system of AMR should not only focus on humans but also on animals as well as associated environments (O'Neil, 2015). Like many other countries, China established the surveillance system for AMR in humans since 2004.

Usually, *E. coli* are part of the normal human intestinal flora. However, certain types of *E. coli* can cause diarrheal disease (Kaper et al., 2004), and pathogenic *E. coli* are responsible for an estimated 209,500 deaths per year globally (Lozano et al., 2013). These *E. coli* pathogens carried drug-resistant genes, which are undoubtedly more likely to be associated with treatment failure for limited therapeutic drugs are available (O'Neill, 2016). Notably, bacteria in farm animals are widely considered as the reservoir for antibiotic resistance genes (Hu et al., 2016). It is worth mentioning that the plasmid-borne carbapenems resistance gene *NDM-1* and colistin resistance gene *mcr-1* are successively found in bacterial strains of both humans and animals (Delgado-Blas et al., 2016; Liu et al., 2016; Shaheen et al., 2013; Sheng et al., 2013). This is of great concern as these antimicrobials are always considered as last-sort

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drugs for human infections caused by multi-drug resistant pathogens (Shaheen et al., 2013).

In China, several investigations focusing on AMR in *E. coli* from livestock at the local level or within limited years have been reported recently (Lei et al., 2010; Li et al., 2014). Here, we present a national surveillance report regarding the current conditions and trends of AMR in food animal-derived *E. coli* from seven major food producing provinces during 2008–2015.

## 2. Materials and methods

### 2.1. Sampling design and isolation of E. coli isolates

During 2008–2015, faecal samples of chickens and pigs from conventional farms were collected in seven provinces, including Sichuan, Guangdong, Shanghai, Henan, Shandong, Liaoning, and Inner Mongolia (Fig. 1). The detailed protocols for the isolation and identification of *E. coli* were described in the previous study (Xia et al., 2011). Briefly, all the faecal samples obtained from individual animals from 333 different farms (181 chicken farms and 152 swine farms) were collected by disposable sterile swabs. Most of these farms were sampled more than once in different years. All these samples were brought to local laboratory and subjected to bacterial isolation immediately (Lei et al., 2010). All the *E. coli* isolates were further confirmed using polymerase chain reaction (PCR) (Bej et al., 1991).

### 2.2. Antimicrobial susceptibility testing

The antimicrobial susceptibilities of *E. coli* to nine antimicrobial agents were determined using the broth microdilution susceptibility method described by CLSI (CLSI, 2008). The interpretation of the result was according to CLSI criteria VET01-A4 (ceftiofur and enrofloxacin) (CLSI, 2013), M100-S25 (ampicillin, amoxicillin/clavulanic acid, gentamicin, tetracycline and sulfisoxazole) (CLSI, 2015) and epidemiological cutoff values (EUCAST, www.eucast.org) (colistin and florfenicol).

### 2.3. Statistical analysis

The AMR of the drugs tested in this study are reported as a pooled prevalence estimate with a 95% confidence interval to represent annual resistance from 2008 to 2015. An overall combined estimate of AMR from 2008 to 2015 with a 95% confidence interval for each of the drugs tested is also reported. The minimum and maximum AMR to represent the range of antibiotic resistance of each drug tested and the raw data, i.e., the number of isolates testing positive for resistance of each drug ($r$) and the total number of isolates tested for measuring the AMR of each drug ($n$) are also reported for each pooled estimate, respectively.

The pooled estimates and the 95% confidence interval for the AMR prevalence of each drug tested were estimated using the meta-analysis of proportions. The raw proportions were transformed using the Freeman-Tukey transformation to normalize the sampling distribution of the proportions and to stabilize their variances (Freeman and Tukey, 1950). The transformed proportions were fitted to a random-effects model using the DerSimonian and Laird method to estimate the variance between trials (DerSimonian and Kacker, 2007). The transformed pooled estimates and 95% confidence intervals obtained from the random-effects model were back-transformed to proportions at a normal scale (Miller, 1978) and reported as discussed above. All the statistical analysis was performed in R version 3.3.1 (Team, 2016). Pooled prevalence was estimated using metafor package

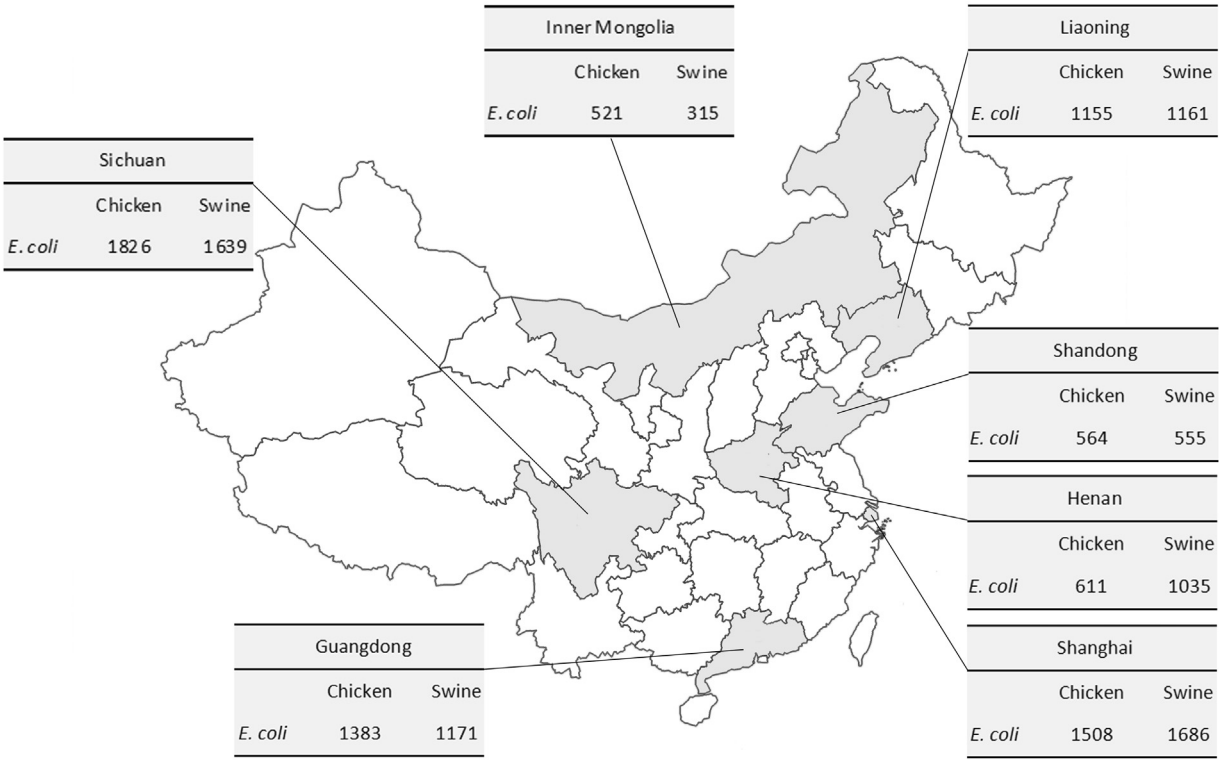


**Fig. 1.** Sample collection regions in China during 2008–15. Each label shows the region, animal species and the number of recovered *E. coli* isolates.