Detection and coexistence of six categories of resistance genes in *Escherichia coli* strains from chickens in Anhui Province, China

Lin Li, Ying Wang, Shuai Feng, Xingyong Dai, Yanfei Yang, Jinnian Li, Minghua Zeng
College of Animal Science and Technology, Anhui Agricultural University, Hefei, China

Abstract

The aim of this study was to characterise the prevalence of class 1 integrons and gene cassettes, tetracycline-resistance genes, phenicol-resistance genes, 16S rRNA methylase genes, extended-spectrum β-lactamase genes and plasmid-mediated fluoroquinolone resistance determinants in 184 *Escherichia coli* isolates from chickens in Anhui, China. Susceptibility to 15 antimicrobials was determined using broth micro-dilution. Polymerase chain reaction and DNA sequencing were used to characterise the molecular basis of the antibiotic resistance. High rates of antimicrobial resistance were observed; 131 out of the 184 (72.3%) isolates were resistant to at least six antimicrobial agents. The prevalences of class 1 integrons, tetracycline-resistance genes, phenicol-resistance genes, 16S rRNA methylase genes, extended-spectrum β-lactamase genes and plasmid-mediated fluoroquinolone resistance determinants were 49.5, 17.4, 15.8, 0.5, 57.6 and 46.2%, respectively. In 82 isolates, 48 different kinds of coexistence of the different genes were identified. Statistical (χ²) analysis showed that the resistance to amoxicillin, doxycycline, florfenicol, ofloxacin and gentamicin had significant differences (P<0.01 or 0.01<P<0.05) among the strains that carried and did not carry the resistance genes, which showed a certain correlation between antimicrobial resistance and the presence of resistance genes.

Materials and methods

**Bacterial isolates**

In this study, *E. coli* isolates (n=184) were collected from chicken cloacae at four different farms located in Anhui Province, China, from March to May 2012. The data and location of each farm are as follows: No. 1 chicken farm (n=46, located in Hefei city), No. 2 chicken farm (n=44, located in Changfeng county), No. 3 chicken farm (n=44, located in Feixian county), and No. 4 chicken farm (n=50, located in Feidong county). Sterile cotton swabs were used to collect fecal samples from chicken cloacae. The swabs were immediately transferred to sterile collection containers containing Luria-Bertani (LB) broth and were cultured at 37°C overnight. The cultures were inoculated in *E. coli* Chromogenic Medium and were grown at 37°C for 18-24 h. Then picked up a single colony which was routinely grown in LB or LB agar at 37°C for 18-24 h.

**Antimicrobial susceptibility testing**

The minimum inhibitory concentrations (MICs) of 15 antimicrobials (amoxicillin (AMX), ceftriaxone (CRO), cefotaxime (CTF), amikacin (AMI), gentamicin (GEN), apramycin (APR), doxycycline (DC), oxytetracycline (OTC), florfenicol (FFC), enrofloxacin (ERO), ofloxacin (OFX), lomefloxacin (LOM), ceftiofur (CQN), sarafloxacin (SAR), sulfamethoxazole (SUL)) were determined using the broth micro-dilution method, according to the guidelines issued by the Clinical and Laboratory Standards Institute. *E. coli* ATCC 29922 was used as the reference strain.

Corresponding author: Prof. Minghua Zeng, College of Animal Science and Technology, Anhui Agricultural University, Hefei 230036, China. Tel. +86.551.65786556 - Fax. +86.551.65786516. E-mail: wangkay1234@163.com

Key words: *Escherichia coli*; Antimicrobial resistance; Chicken; Coexistence.

Acknowledgments: this work was supported by grants from the National Natural Science Foundation of China (31201957), and the Annual Disciplinary and Academic Degree Construction Projects in 2013 (XKWD2013006).

Contributions: LL and YW conceived and designed the experiments. YW and SF performed the experiments. XY and YF analysed the data. JN and MH contributed to reagents/materials/analysis tools. LL and YW contributed equally to the work and wrote the paper. YW, SF, XY and YF collected *E. coli* isolates from chickens at four farms.

Received for publication: 10 February 2015. Accepted for publication: 15 September 2015.

This work is licensed under a Creative Commons Attribution NonCommercial 3.0 License (CC BY-NC 3.0).

©Copyright. Li et al., 2015 Licensee PAGEPress, Italy. Italian Journal of Animal Science 2015; 14:3897 doi:10.4081/ijas.2015.3897

Genotypic resistance characterisation

Class 1 integrons and gene cassettes, tetracycline-resistance genes (tetA and tetM), phenicol-resistance genes (floR and fexA), 16S rRNA methylase genes (armA and rmtB), ESBL genes (*blaCTX-M*, *blaTEM* and *blaSHV*) and PMQR genes (*qnrA*, *qnrB*, *qnrC*, *qnrD*, *qnrS*, *aac(6’)-Ib-cr* and *qepA*) were detected by PCR using the primers listed in Table 1. All the PCR amplons were confirmed by dideoxy DNA sequencing. The DNA sequences obtained were compared with those in GenBank using the BLAST program (http://blast.ncbi.nlm.nih.gov/).
Results

Antimicrobial susceptibility of *Escherichia coli* isolates

High rates of resistance to OTC (97.8%), SUL (97.3%), DC (90.2%), AMX (82.6%), LOM (77.7%), CRO (70.1%), OFX (67.4%), ERO (55.9%), and FFC (52.7%) were observed among the 184 *E. coli* isolates. Low rates of resistance to AMI (7.6%) and SAR (2.2%) were observed. The resistance rates of *E. coli* isolates from four chicken farms to 15 antimicrobials can be seen in Figure 1. One hundred and thirty-one (72.3%) of the isolates were resistant to at least five antimicrobial agents, while 25 (13.6%) were resistant to at least 10 of these drugs (Figure 2).

Detection of the six categories of resistance determinants

The PCR results showed that 91 (49.5%) strains harbored class 1 integrons. Seventy of the 91 *intI*-positive isolates carried gene cassettes, which were *dfrA1*-qnrS1-adfA1 (45/70), *dfrA2-aadA2* (16/70) and *dfrA1-aadA1* (9/70); 21 isolates did not carry gene cassettes.

Tetracycline-resistance genes were detected in 32 of 184 (17.4%) isolates (*tetA*, *n*=27; *tetM*, *n*=5). Twenty-nine (15.8%) isolates possessed *phenicol*-resistance genes (*floR*, *n*=29); no isolates were positive for *rmtB*.

ESBL genes were detected in 106 of the 184 (57.6%) isolates (*blaCTX-M*, *n*=40; *blaTEM*, *n*=46; *blaSHV*, *n*=30; *blaOXY*, *n*=16; *blaPER*, *n*=16). Fifty-six (30.5%) isolates contained *bla* genes, while 31 (16.8%) harbored both *bla* and ESBL genes. The PCR results showed that 91 (49.5%) strains harbored class 1 integrons. Seventy of the 91 *intI*-positive isolates carried gene cassettes, which were *dfrA1*-qnrS1-adfA1 (45/70), *dfrA2-aadA2* (16/70) and *dfrA1-aadA1* (9/70); 21 isolates did not carry gene cassettes.


tetA

Tetracycline-resistance genes were detected in 32 of 184 (17.4%) isolates (*tetA*, *n*=27; *tetM*, *n*=5). Twenty-nine (15.8%) isolates possessed *phenicol*-resistance genes (*floR*, *n*=29); no isolates were positive for *rmtB*.

ESBL genes were detected in 106 of the 184 (57.6%) isolates (*blaCTX-M*, *n*=40; *blaTEM*, *n*=46; *blaSHV*, *n*=30; *blaOXY*, *n*=16; *blaPER*, *n*=16). Fifty-six (30.5%) isolates contained *bla* genes, while 31 (16.8%) harbored both *bla* and ESBL genes.

Table 1. Polymerase chain reaction primers and annealing temperatures.

| Gene | Sequence (5’-3’) | Annealing temperature, °C | Reference |
|------|-----------------|--------------------------|-----------|
| blactXM | F:CATGAGCTTTCTAGGAGGAGG | 50 | This study |
| blactXM | F:CCGATGGAAGGAGGAAGG | 59 | This study |
| blaqNR | F:TTAATCCCTGTCGAGGCAACCC | 55 | This study |
| qnrB | F:GATCGCAATTTTACACCC | 54 | Wang et al. (2012) |
| qnrC | F:CCGATCAATTAGATGCG | 58 | This study |
| qnrD | F:GGATCTGACATGCACAGC | 50 | Xia et al. (2010) |
| qnrS | F:GACCTTTGATGTTCCAGATG | 52 | Yuan et al. (2009) |
| aac(6’)-Ib-cr | F:CGAATAGCTGGAAGGAGG | 58 | This study |
| qepA | F:CCGATGGAAGGAGGAAGG | 50 | This study |
| intI | F:CCGATGGAAGGAGGAGG | 55 | del Castillo et al. (2013) |
| intI-class1 | F:GCAATGGAAGGAGGAAGG | 58 | del Castillo et al. (2013) |
| armA | F:CCGATGGAAGGAGGAAGG | 56 | Yan et al. (2004) |
| rmfB | F:CCGATGGAAGGAGGAAGG | 56 | Yan et al. (2004) |
| floA | F:CCGATGGAAGGAGGAAGG | 55 | Sáenz et al. (2004) |
| floX | F:GTCATTGCTCAGATGGAAGG | 57 | Keihrenberg and Schwarz (2005) |
| tetA | F:GAACTGGAAGGAGGAAGG | 60 | Giovanni et al. (2003) |

Figure 1. Resistance rates of *Escherichia coli* isolates from four chicken farms to fifteen antimicrobials. AMX, amoxicillin; CRO, ceftriaxome; CTF, cefotiofur; AMI, amikacin; GEN, gentamicin; APR, apramycin; DC, doxycycline; OTC, oxytetracycline; FFC, fleroxacin; ERO, enrofloxacin; OFX, ofloxacin; LOM, lomefloxacin; CQN, cefquinome; SAR, sarafloxacin; SUL, sulfamonomethoxine.
n=49; and blaTEM-26, n=17); no isolates were positive for the blasSH gene. Eighty-five out of the 184 (46.2%) isolates possessed PMQR determinants. Twenty-two (11.9%) isolates carried the qnr determinant and 63 (34.2%) carried aac(6\')-Ib-cr. Among the qnr determinants, only the qnrS-type gene was detected; no isolates were positive for qnrA, qnrB, qnrC, qnrD or qepA genes.

Coexistence of different resistance genes

Coexistence of different resistance genes was identified in 82 E. coli isolates. There were 48 different kinds of coexistence of resistance genes (Table 2). Twenty-six isolates carried four genes and three carried five genes. Only one isolate harbored six genes, which were dfrA2-aadA12, tetA, tetM, blaTEM-1, qnrS and aac(6\')-Ib-cr. The combination of dfrA1-tnpAIS26-aadA1 and aac(6\')-Ib-cr was observed in eight E. coli isolates.

Relationship between resistance genes and antibiotic resistance of the 184 Escherichia coli isolates

A \( \chi^2 \) test was used to determine the relationship between resistance genes and antimicrobial resistance of the 184 E. coli isolates. Compared the resistance to AMX, DC, FFC, OFX and GEN, the results of strains carrying resistance genes were significantly different (P<0.01 or 0.01<P<0.05) from the strains not carrying resistance genes, while resistance to the remaining 10 antimicrobials showed no difference (P>0.05) (Table 3).

Discussion

No information is available about the occurrence and distribution of the different resistance determinants, such as integrons and gene cassettes, tetracycline-resistance genes, phenicol-resistance genes, 16S rRNA methylase genes, ESBL and PMQR genes in E. coli from chickens in Anhui Province, China, therefore we screened 184 E. coli isolates for the presence of these resistance determinants. 71.2% of the isolates were resistance to at least six antimicrobial agents, while 13.6% were resistance to at least 10 of these drugs, indicating a high prevalence of multiple antibiotic-resistant E. coli in chickens in Anhui Province.

In this study, 184 E. coli isolates were assayed for the presence of class 1 integrons. 49.5% of isolates carried class 1 integrons, harbouring gene cassettes such as dfrA1-tnpAIS26-aadA1, dfrA2-aadA12 and dfrA1-aadA1, which encode resistance to sulfonamides and aminoglycosides. There are differences in the prevalence of the class 1 integrons in China and abroad. 52% of E. coli isolated from poultry food possessed class 1 integrons (Soffi et al., 2011) in Tunisia. In Spain, a study suggested that the frequency of class 1 integrons was 51% (Marchant et al., 2013). In China, one study showed that 60.4% of E. coli isolates from chickens had class 1 integrons (Zhang et al., 2009). In addition, 89.9% E. coli collected from food-producing animals were positive for class 1 (Lin et al., 2011). In this study, the frequency of class 1 integrons is similar to the data obtained abroad, but lower than the domestic data.

In addition, we detected tetracycline-resistance genes, phenicol-resistance genes and aminoglycosides in 71.2% of isolates. The remaining 10 antimicrobials showed no difference (P>0.05) from the strains not carrying resistance genes.

Table 2. Coexistence of different resistance genes.

| Coexistence of different genes | Strains, n | Coexistence of different genes | Strains, n |
|-------------------------------|------------|-------------------------------|------------|
| dfrA2-aadA12+tetA+tetM+blaTEM-1+qnrS+aac(6\')-Ib-cr | 1          | dfrA1-tnpAIS26-aadA1+tetA+blaTEM-1+qnrS | 1          |
| dfrA1-tnpAIS26-aadA1+tetA+blaTEM-1+qnrS+aac(6\')-Ib-cr | 1          | dfrA1-aadA1+floR+blaTEM-1 | 1          |
| dfrA1-aadA1+tetM+flor+blaTEM-1+aac(6\')-Ib-cr | 1          | blactM-1+qnrS+aac(6\')-Ib-cr | 1          |
| dfrA1-tnpAIS26-aadA1+tetA+blaTEM-1+qnrS | 1          | floR+tetA | 1          |
| dfrA1-aadA1+blaTEM-1+qnrS | 1          | dfrA1-tnpAIS26-aadA1+aac(6\')-Ib-cr | 8          |
| dfrA1-aadA1+bactM-1+aac(6\')-Ib-cr | 1          | dfrA1-tnpAIS26-aadA1+bactM-1+aac(6\')-Ib-cr | 4          |
| dfrA1-aadA1+flor+blaTEM-1+aac(6\')-Ib-cr | 1          | dfrA1-tnpAIS26-aadA1+tetA | 4          |
| dfrA1-aadA1+flor+blaTEM-1+aac(6\')-Ib-cr | 3          | blactM-1+aac(6\')-Ib-cr | 4          |
| dfrA1-tnpAIS26-aadA1+bactM-1+aac(6\')-Ib-cr | 2          | dfrA2-aadA12+bactM-1 | 2          |
| dfrA1-tnpAIS26-aadA1+bactM-1+aac(6\')-Ib-cr | 4          | flor+aac(6\')-Ib-cr | 2          |
| tetA+bactM-1+aac(6\')-Ib-cr | 2          | bactM-1+aac(6\')-Ib-cr | 4          |
| dfrA2-aadA12+bactM-1+aac(6\')-Ib-cr | 2          | dfrA1-tnpAIS26-aadA1+bactM-1 | 1          |
| dfrA1-tnpAIS26-aadA1+bactM-1 | 1          | tetA+aac(6\')-Ib-cr | 1          |
| dfrA1-tnpAIS26-aadA1+fluor+qnrS | 1          | dfrA1-aadA1+aac(6\')-Ib-cr | 1          |
| dfrA1-aadA1+bactM-1+aac(6\')-Ib-cr | 1          | tetA+bactM-1 | 3          |
| dfrA2-aadA12+bactM-1+aac(6\')-Ib-cr | 1          | dfrA1-tnpAIS26-aadA1+fluor | 1          |
| dfrA1-tnpAIS26-aadA1+fluor+fluor+qnrS | 1          | flor+bactM-1 | 1          |
| dfrA1-tnpAIS26-aadA1+bactM-1+aac(6\')-Ib-cr | 1          | flor+bactM-1 | 1          |
| dfrA2-aadA12+bactM-1+aac(6\')-Ib-cr | 1          | blactM-1+aac(6\')-Ib-cr | 1          |
| dfrA1-tnpAIS26-aadA1+bactM-1 | 1          | tetA+bactM-1 | 1          |
### Table 3. Comparison of resistance between the strains carrying and not carrying resistance genes.

| Drugs | Carrying resistance genes | Not carrying resistance genes | χ² | P   |
|-------|---------------------------|-------------------------------|----|-----|
| AMX   | 87.3                      | 70.0                          | 7.58 | <0.01 |
| CRO   | 73.1                      | 62.0                          | 2.14 | >0.05 |
| CTF   | 18.7                      | 12.0                          | 1.17 | >0.05 |
| AMI   | 9.0                       | 4.0                           | 0.68 | >0.05 |
| CQN   | 14.9                      | 22.0                          | 1.13 | >0.05 |
| GEN   | 44.0                      | 24.0                          | 6.15 | 0.01< and <0.05 |
| APR   | 29.1                      | 24.0                          | 0.47 | >0.05 |
| DC    | 95.5                      | 78.0                          | 11.28 | <0.01 |
| OTC   | 98.5                      | 96.0                          | 0.22 | >0.05 |
| FFC   | 61.2                      | 32.0                          | 12.47 | <0.01 |
| ERO   | 60.4                      | 46.0                          | 3.07 | >0.05 |
| SAR   | 3.0                       | 0                             | 0.45 | >0.05 |
| OFX   | 73.9                      | 48.0                          | 11.02 | <0.01 |
| LOM   | 78.4                      | 74.0                          | 0.40 | >0.05 |
| SUL   | 96.3                      | 90.0                          | 1.73 | >0.05 |

AMX, amoxicillin; CRO, cefoxitin; CFF, cefotaxim; AMI, amikacin; CQN, cefquinone; GEN, gentamicin; APR, apramycin; DC, dicycloxacin; OTC, oxytetracycline; FFC, florenicol; ERO, eurofloxacin; SAR, sarafloxacin; OFX, ofloxacin; LOM, lonfloxacin; SUL, sulfonamethoxine. P>0.05, no differences; 0.01<P<0.05, difference; P<0.01, significant difference.

16S rRNA methylase genes. The results showed that in Anhui Province, the frequencies of tetA, tetM, and floR were 14.7, 2.7 and 15.8%, respectively. Only one isolate harbored a 16S rRNA methylase gene (rmfB). No isolates carried fexA and arrA. In other studies, the frequencies of tetA and tetM were 87.9 and 15.3%, respectively (Zhang et al., 2010), the prevalence of floR was 45.1% (Du et al., 2007) and the frequency of rmfB was 30.3% (Zhou et al., 2010). Thus the frequencies of these three genes in the current study were lower than those reported previously.

The blatTEM1 gene was the most common β-lactamase gene among E. coli isolates in Anhui Province. This was in agreement with previous findings (Xia et al., 2010). With respect to PMQR genes, qnrS and aac(6’)-Ib-cr were not detected in this study. Notably, 82 isolates carried more than two types of genes, resulting in 48 different kinds of coexistence of class 1 integrons and gene cassettes, tetracycline-resistance genes, phencil-resistance genes, ESBL and PMQR genes. Thus the coexistence of resistance genes was very common and varied in Anhui Province. The most frequent coexistence was dfrA1-tnpAIS26-aadA1 and aac(6’)-Ib-cr, which was found in eight E. coli isolates, while the others were found in 4 isolates. Six determinants, dfrA2-aadA12, tetA, tetM, blatTEM1, qnrS and aac(6’)-Ib-cr, were detected in an individual E. coli isolate. To the best of our knowledge, this is the first report of these six genes coexisting in an E. coli strain in China. In addition, statistical analysis indicated a correlation between antimicrobial resistance and the presence of resistance genes. Except for CQN, the frequency of resistance to the other 14 antimicrobial agents in those isolates that carried resistance genes was higher than those without resistance genes. This was especially the case for resistance to AMX, DC, FFC, OFX and GEN (P<0.01 or 0.01<P<0.05), which suggested that the prevalence of ESBL genes, tetracycline-resistance genes, phencil-resistance genes, PMQR genes and aadA was related, to a certain extent, to the observed resistance to AMX, DC, FFC, OFX and GEN.

### Conclusions

In conclusion, this is the first study describing the prevalence and characteristics of six categories of resistance determinants in E. coli isolates from chickens in Anhui Province, China. The most abundant genes were ESBL genes (57.6%), class 1 integrons (49.5%) and PMQR genes (46.2%). In 82 isolates, 48 different types of coexistence of the different genes were identified. Six genes, dfrA2-aadA12, tetA, tetM, blatTEM1, qnrS and aac(6’)-Ib-cr, were detected in an individual E. coli isolate for the first time. Resistance to AMX, DC, FFC, OFX and GEN was significantly different (P<0.01 or 0.01<P<0.05) among the strains that carried and did not carry resistance genes, which indicated that resistance genes contributed to the corresponding antimicrobial resistance.

### References

- Carattoli, A., 2001. Importance of integrons in the diffusion of resistance. Vet. Res. 32:243-259.
- Dai, L., Lu, L.M., Wu, C.M., Li, B.B., Huang, S.Y., Wang, S.C., Qi, Y.H., Shen, J.Z., 2008. Characterization of antimicrobial resistance among Escherichia coli isolates from chickens in China between 2001 and 2006. FEMS Microbiol. Lett. 286:178-183.
- del Castillo, B.R., Vinue, L., Roman, E.J., Guerra, B., Carattoli, A., Torres, C., Martínez-Martínez, L., 2013. Molecular characterization of multiresistant E. coli producing or not producing extended-spectrum β-lactamases. BMC Microbiol. 13:84.
- Du, X.D., Li, X.S., Zhang, S.M., Mo, J., Wu, N.P., Cui, B.A., 2007. Detection of the floR genes in florfenicol resistant Escherichia coli isolated from diseased chickens. J. Henan Agr. Univ. 41:188-191.
- Giovannetti, E., Brenziani, A., Lupidi, R., Roberts, M.C., Varaldo, P.E., 2003. Presence of the tet(O) gene in erythromycin- and tetracycline-resistant strains of Streptococcus pyogenes and linkage with either the mef(A) or the erm(A) gene. Antimicrob. Agents Ch. 47:2844-2849.
- Hall, R.M., Collis, C.M., 1995. Mobile gene cassettes and integrons: capture and spread of genes by site-specific recombination. Mol. Microbiol. 15:593-600.
- Kehrenberg, C., Schwarz, S., 2005. Florfenicol-chloramphenicol exporter gene fexA is
part of the novel transposon Tn558. Antimicrob. Agents Ch. 49:813-815.
Lin, J.C., Chen, Y.L., Cao, S.J., Shu, G., Wen, X.T., 2011. Molecular characterization of integron-gene cassettes in multidrug-resistant E. coli isolates from food-producing animals. Acta Vet. Zoot. Sinica 42:77-81.
Lin, J.C., Zhuo, J.Z., Jiang, H.X., Liu, J.H., Zeng, Z.L., 2009. Surveillance of antimicrobial resistance among Escherichia coli isolates from swine and poultry in different regions. J. South China Agr. Univ. 30:86-88.
Ma, Q.C., Gu, X., Zhang, K.Y., Jin, L.Y., Xue, F.Q., 2009. Identification, isolation and antimicrobial susceptibility of Escherichia coli from poultry in Shanghai. China Poultry 31:11-13.
Marchant, M., Vinue, L., Torres, C., 2013. Change of integrons over time in E. coli isolates recovered from healthy pigs and chickens. Vet Microbiol. 163:124-132.
Maynard, C.J., Fairbrother, M., Bekal, S., Sanschagrin, F., Levesque, R.C., Brousseau, R., Masson, L., Lariviére, S., Harel, J., 2003. Antimicrobial resistance genes in enterotoxigenic Escherichia coli O149:K91 isolates obtained over a 23-year period from pigs. Antimicrob. Agents Ch. 47:3214-3221.
Sáenz, Y., Briñas, L., Domínguez, E., Ruiz, J., Zarazaga, M., Vila, J., Torres, C., 2004. Mechanisms of resistance in multiple-antibiotic-resistant Escherichia coli strains of human, animal and food origins. Antimicrob. Agents Ch. 48:3996-4001.
Soufi, L., Sáenz, Y., Laura, V., Abbassi, M.S., Ruiz, E., Zarazaga, M., Hassen, A.B., Hammami, S., Torres, C., 2011. E. coli of poultry food origin as reservoir of sulphonamide resistance genes and integrons. Int. J. Food Microbiol. 144:497-502.
Wang, Y., He, T., Han, J., Wang, J., Foley, S.L., Yang, G.Y., Wan, S.X., Shen, J.Z., Wu, C.M., 2012. Prevalence of ESBLs and PMQR genes in fecal Escherichia coli isolated from the non-human primates in six zoos in China. Vet Microbiol. 159:53-59.
Xia, L.N., Li, L., Wu, C.M., Liu, Y.Q., Tao, X.Q., Dai, L., Qi, Y.H., Lu, L.M., Shen, J.Z., 2010. A survey of plasmid-mediated fluoroquinolone resistance genes from Escherichia coli isolates and their dissemination in Shandong, China. Foodborne Pathog. Dis. 7:207-215.
Yan, J.J., Wu, J.J., Ko, W.C., Tsai, S.H., Chuang, C.L., Wu, H.M., Lu, Y.J., Li, J.D., 2004. Plasmid-mediated 16S rRNA methylases conferring high-level aminoglycoside resistance in Escherichia coli and Klebsiella pneumoniae isolates from two Taiwanese hospitals. J. Antimicrob Ch. 54:1007-1012.
Yuan, L., Liu, J.H., Hu, G.Z., Pan, S.Y., Liu, Z.M., Mo, J., Wei, Y.J., 2009. Molecular characterization of extended-spectrum β-lactamase-producing Escherichia coli isolates from chickens in Henan Province, China. J. Med. Microbiol. 58:1449-1453.
Yuan, L., Wu, H., Liu, Z.M., Fu, X.L., Hu, G.Z., 2010. Surveillance of antimicrobial resistance among strains of Escherichia coli isolated from chickens in Henan. Acta Agric. Jiangxi 22:128-130.
Zhang, C.P., Ning, Y.B., Song, L., 2010. Resistance to tetracycline and distribution of tetracycline resistance determinants in commensal Escherichia coli isolated from clinically healthy chickens and pigs. Sci. Agr. Sin. 43:2578-2583.
Zhang, X.Y., Ding, L.J., Yue, J., 2009. Occurrence and characterization of class 1 and 2 integrons in resistant E. coli isolates from animals and farm workers in Northeastern China. Microb. Drug Resist. 15:323-328.
Zhou, Y., Yu, H., Guo, Q., Xu, X., Ye, X., Wu, S., Guo, Y., Wang, M., 2010. Distribution of 16S rRNA methylases among different species of Gram-negative bacilli with high-level resistance to aminoglycosides. Eur. J. Clin. Microbiol. 29:1349-1353.