



ELSEVIER

Contents lists available at ScienceDirect

Data in Brief

journal homepage: www.elsevier.com/locate/dib

Data Article

Data on the phylogenetic typing, integron gene cassette array analysis, multi-drug resistance analysis and correlation between antimicrobial resistance determinants in *Klebsiella* strains



Hao Wu^a, Mingyu Wang^a, Yuqing Liu^b, Xinhua Wang^c,
Yunkun Wang^c, Jinxing Lu^d, Hai Xu^{a,*}

^a State Key Laboratory of Microbial Technology, School of Life Sciences, Shandong University, Jinan 250100, Shandong, PR China

^b Shandong Key Laboratory of Animal Disease Control and Breeding, Institute of Animal Science and Veterinary Medicine, Shandong Academy of Agricultural Sciences, Jinan 250100, Shandong, PR China

^c School of Environmental Science and Engineering, Shandong University, Jinan 250100, Shandong, PR China

^d State Key Laboratory for Infectious Disease Prevention and Control, and National Institute for Communicable Disease Control and Prevention, Chinese Center for Disease Control and Prevention, Beijing 102206, PR China

ARTICLE INFO

Article history:

Received 6 June 2016

Received in revised form

4 July 2016

Accepted 11 July 2016

Available online 3 August 2016

Keywords:

Antimicrobial resistant *Klebsiella* species
Polymerase chain reaction–restriction fragment length polymorphism (PCR–RFLP)
Gene cassette arrays of integron
Statistical analysis

ABSTRACT

The antimicrobial resistance of *Klebsiella* species in the poultry industry is becoming a public concern. In support our recent publication “Characterization of antimicrobial resistance in *Klebsiella* species isolated from chicken broilers” (Wu et al., 2016) [1], multilocus sequence typing (MLST) and *gyrA* PCR–RFLP assays were conducted to identify the genetic relationships between and phylogenetic groups of the 90 antimicrobial resistant *Klebsiella* species isolated from a commercial broiler slaughter plant in Shandong, China. In addition, PCR–RFLP was performed to identify different gene cassette arrays in class 1 and 2 integrons, and the correlations between different antimicrobial resistance determinants were analyzed.

© 2016 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

DOI of original article: <http://dx.doi.org/10.1016/j.ijfoodmicro.2016.06.001>

* Corresponding author.

E-mail addresses: wuhao3075@163.com (H. Wu), wangmingyu@sdu.edu.cn (M. Wang), liuyuqing@163.com (Y. Liu), xinhuaawang@sdu.edu.cn (X. Wang), ykwang@sdu.edu.cn (Y. Wang), lujinxing@icdc.cn (J. Lu), haixu@sdu.edu.cn (H. Xu).

<http://dx.doi.org/10.1016/j.dib.2016.07.016>

2352–3409/© 2016 The Authors. Published by Elsevier Inc. This is an open access article under the CC BY license (<http://creativecommons.org/licenses/by/4.0/>).

Specifications Table

Subject area	Microbiology
More specific subject area	Food safety, antibiotic resistance
Type of data	Table, figure
How data was acquired	PCR, sequencing and statistical analysis
Data format	Analyzed
Experimental factors	Polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP), chi-square tests using SPSS
Experimental features	Identification of phylogenetic groups and different gene cassette arrays in class 1 and 2 integrons of <i>Klebsiella</i> species, analysis of the correlations between different antimicrobial resistance determinants
Data source location	Jinan, Shandong province of China.
Data accessibility	The data is available with this article

Value of the data

- The *gyrA* PCR-RFLP assay and MLST analysis in the *Klebsiella* isolates indicate the relationship of epidemiology of drug resistant bacteria in between clinical and poultry industry.
- The PCR-PFLP by *EcoRII* can be applied as a tool for detection of gene cassette arrays of integron 1 or 2.
- The statistical data and finding of a significant association of antimicrobial resistance determinants can be used as references for the investigation of other drug resistant bacteria.

1. Data

MLST was performed using seven housekeeping genes (*rpoB*, *gapA*, *mdh*, *pgi*, *phoE*, *infB*, and *tonB*), and primers of those genes for PCR amplification and sequencing were designed (Table 1) [2]. *gyrA* PCR-RFLP profiles showed nearly all (89/90) of the isolates were identified as Kpl-type and only one isolate was KplIII (Fig. 1). Antimicrobial susceptibility to nine antimicrobial agents was tested for the 90 *Klebsiella* isolates [1]. Among the isolates, 96.7% of them were resistant to more than three tested antimicrobial agents as well as 91.1% were resistant to more than three beta-lactam antibiotics (Fig. 2). A significant association between different antimicrobial resistance determinants was analyzed (Table 2). PCR-PFLP patterns of gene cassette arrays for integron 1 or 2 were performed (Fig. 3), and the detailed description was in the original article [1].

2. Experimental design, materials and methods

2.1. PCR Program

PCRs were prepared as follows: a final volume of 25 μ l containing 1 μ M of each primer, 0.2 mM dNTPs, 1.5 mM MgCl₂, and 1 unit of *Taq* polymerase (TransGen Biotech, Beijing, China). The conditions used for amplification were as described by the original article [1].

2.2. Primers designed for the MLST analysis of *Klebsiella* isolates

The primer pairs for seven housekeeping genes (*rpoB*, *gapA*, *mdh*, *pgi*, *phoE*, *infB*, and *tonB*) were designed for PCR amplification and sequencing (Table 1), as described previously [2].

Download English Version:

<https://daneshyari.com/en/article/6597484>

Download Persian Version:

<https://daneshyari.com/article/6597484>

[Daneshyari.com](https://daneshyari.com)