

Session: OS175 Origin, dissemination and impact of mcr genes

Category: 3b. Resistance surveillance & epidemiology: Gram-negatives

25 April 2017, 10:48 - 10:58
OS0875

Comprehensive resistome analysis reveals the prevalence of bla_{NDM} and mcr-1 in Chinese poultry production

Yang Wang*¹, Rongmin Zhang², Zuwei Wu³, Stefan Schwarz⁴, Qijing Zhang³, Timothy R. Walsh⁵, Jianzhong Shen⁶

¹*China Agricultural University; College of Veterinary Medicine*

²*China Agricultural University*

³*Iowa State University*

⁴*Institute of Farm Animal Genetics, Friedrich-Loeffler-Institut (FLI)*

⁵*Infection and Immunity, School of Medicine, Cardiff University*

⁶*China Agricultural University; Beijing Advanced Innovation Center for Food Nutrition and Human Health, College of Veterinary Medicine*

Background: By 2030, the global population will be 8.5 billion placing pressure on international poultry production of which China is a key producer. As of April 2017, China will invoke the withdrawal of colistin as growth promoter removing over 8000 tons/year from the Chinese farming sector. Here we aim to understand the impact of banning colistin and the epidemiology of multi-drug resistant *Escherichia coli* (using bla_{NDM} and mcr-1 as marker genes) in the Chinese farming sector/food chain.

Material/methods: We undertook a comprehensive sampling strategy including poultry, farmers, dogs, sewage, wild birds and flies. Direct sample testing (DST) for bla_{NDM} and mcr-1 in farming sectors/food chain was conducted to understand the true breadth and depth of the environmental and animal resistome. Whole genome sequencing (WGS) were performed on all bla_{NDM}-positive *E. coli* isolates and additional carbapenem-susceptible *E. coli* isolates.

Results: We show that mcr-1 but not bla_{NDM} is prevalent in hatcheries yet bla_{NDM} quickly contaminates chicken flocks through dogs/flyes/wild birds. DST for bla_{NDM} and mcr-1 on commercial farms, slaughterhouse and supermarkets revealed considerably higher levels of positive samples than the

*bla*_{NDM}- and *mcr-1*-positive *E. coli* indicating a substantial segment of the unseen resistome - a phenomenon we have termed “phantom resistome”. WGS identified common *bla*_{NDM}-positive *E. coli* shared among farms, flies/dogs/farmers, providing direct evidence of carbapenem-resistant *E. coli* transmission and environmental contamination.

Conclusions: Until now, reports on *bla*_{NDM} in the Chinese poultry sector are rare and there has been no systematic analysis of carbapenem-resistant Enterobacteriaceae in China. Furthermore, there has been little contextualization of carbapenem-resistant *E. coli* and *mcr-1*-positive *E. coli* isolates at a global level. It is evident from our data that NDM is the dominant mechanism of CRE in both animals and humans in China. Comparison between resistomes from DST and resistance phenotypes indicates that the Chinese farming environment contains a considerable phantom resistome carrying *bla*_{NDM} and/or *mcr-1* genes, suggesting that the level of environmental contamination is underestimated. In particular, flies showed the biggest difference between *bla*_{NDM} detection by DST (62/120) and *bla*_{NDM}-positive strains (31/120). This is the first published study linking flies to the spread of carbapenem resistance. Given that they carry a “phantom” *bla*_{NDM} and *mcr-1* gene pool, their ability to contaminate the environment has immense public health concerns. Furthermore, local *bla*_{NDM} dissemination (flies/dogs) increases the phantom resistome and thereby increases the probabilities of carriage by migratory birds such as swallows, the migratory winter destinations of which are usually South East Asia.