Colistin-resistant Escherichia coli harbouring mcr-1 isolated from food animals in Hanoi, Vietnam

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Colistin-resistant *E. coli* harboring *mcr-1* isolated from food animals in Hanoi, Vietnam

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In the November 18, 2015 issue, Liu *et al* reported, for the first time, plasmid-mediated colistin resistance in *Escherichia coli* isolated from animals, food and patients in China.[1] Here, we screened 24 extended-spectrum beta-lactamase (ESBL, $bla_{\text{CTX-M}}$) harboring *E. coli* isolated during 2014-15 from rectal swabs taken from chickens on 2 farms (n = 11) in the Van Lam district of the Hung Yen province, and from a pig farm (n = 7) and a pig slaughterhouse (n = 4) located in the Hoai Duc region of the Hanoi province, Vietnam. All strains were screened for the presence of *mcr-1* using PCR and Sanger sequencing. The *mcr-1* gene was detected in 9/24 *E. coli* strains (37.5%), of which 6 were isolated from the rectal swabs of pigs on the farm, one from a rectal swab from a pig about to be slaughtered, and 2 strains from swabs collected from the lairage area of the slaughterhouse. All 9 isolates exhibited phenotypic colistin resistance (macrobroth dilution MICs 4 and 8 mg/L). The *mcr-1* sequence showed 100% sequence similarity to the gene reported in China.[1] Plasmid sequencing (MiSeq, Illumina) from one *mcr-1* positive strain isolated multiple genes encoding resistance to trimethoprim (*dfrA12*), tetracycline (*tetA*), aminoglycoside (*aadA3*, *aph(3')-IA*), phenicol (*cmlA1*), quinolone (*qnrS1*, *oqxA*), lincosamide (*lnu(F)*) and sulphonamide (*sul2*, *sul3*), and beta-lactam (extended-spectrum beta-lactamase $bla_{\text{CTX-M55}}$) antibiotics. Blast comparison with the plasmid, pHNSHP45,[1] showed 100% similarity in a 3677 bp region that included *mcr-1* (1626 bp) and a complete IS*ApI1* mobile element including the transposase-encoding *tnpA*

gene. Incompatibility typing using Plasmid Finder[2] identified IncFII, IncF1A(H1), and IncF1B(K), and IncX1 replicons, however, none of these could be directly linked to the *mcr-1* harboring contig. Of note, the sequence coverage of the *mcr-1* harboring contig was ~100-fold lower than the adjoining regions indicating either carriage on a low-copy plasmid or a chromosomal origin of the gene. Next, we screened 112 ESBL-harboring *E. coli* isolated during 2014-2015 from urines of out- and in-patients with symptomatic urinary tract infections collected at the National Pediatric, 103 General Military, and Cuba hospitals in Hanoi. *mcr-1* was not detected in any of the urinary isolates.

Our findings highlight a high prevalence of the *mcr-1* gene among ESBL-harboring *E. coli* isolated from rectal screenings of pigs in Vietnam; however, we did not find any evidence of transfer or emergence of the gene among ESBL-harboring pathogenic *E. coli* of human origin. These data add to recent studies showing a global emergence of the *mcr-1* harboring mobile genetic element linked to different plasmids,[3,4] underscoring the importance of active surveillance in both animal and human populations.

References

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