

01471 Unexpected high prevalence of fosfomicin resistance mediated by *fosA3* in *Escherichia coli* ESBL isolated from poultry farms, broiler carcasses, and humans Quito, Ecuador

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INTRODUCTION

In Ecuador, community-onset urinary tract infection (co-ITU) caused by ESBL *E. coli* is increasing in the last few years. Additionally, ESBL *E. coli* co-resistant to fosfomicin (FOS) is more frequently isolated from these cases in our location. One possible answer for the origin and dissemination of this co-resistance is the use of FOS as prophylactic in poultry production, the selection of plasmids codifying *bla*_{CTX-M} and *fos* genes in poultry farms, and the dissemination of these strains through the raw chicken carcasses to our community. Therefore, this study aimed to establish the prevalence of FOS resistance in 3GC-ECO isolated from three components: broiler farms, broiler carcasses at retail, and human co-UTI, to characterize ESBL and *fosA3* genes and plasmids carrying the resistance to 3GC and FOS at the replicon type level.

METHODS

A total of 605 isolates of *E. coli* ESBL were analyzed (farms n=124, carcasses n=266, and co-UTI n=215, as the animal, food, and human components, respectively). Isolates were obtained from previous prevalence studies in Quito, Ecuador. The antimicrobial susceptibility test was performed using Vitek®2 and the results were confirmed by agar dilution. *fosA3* and ESBL genes from positive isolates were characterized by PCR and Sanger Sequencing. Clonality was analyzed by MLST. Co-resistant isolates were conjugated with a J53 strain using a double selection agar. Transconjugants' plasmids were characterized by replicon typing.

RESULTS

FOS resistance was detected in 50% (n=62), 47,7% (n=127), and 21,4% (n=46) of the isolates from animal, food and human components, respectively. *fosA3* gene was detected in 89,8% (59/62), 91,9% (123/127), and 82,9% (41/46) of animal, food, and human components, respectively. Of the FOS resistant isolates, a variety of Clonal Complexes (Cplx) were identified. A clon from Cplx10 was identified in all three components and one ST131 was detected in the human component (Figure 1). The most prevalent ESBL/AmpC genes were *bla*_{CTX-M-55}, *bla*_{CTX-M-65} and *bla*_{CMY-2} (table 1). Two-thirds of isolates showed a successful conjugation. Transconjugants presented Inc11 (n=33), IncN (n=31), IncB/O (n=1), Inc11+IncN (n=1) and Inc11+IncFIC (n=2) plasmids.

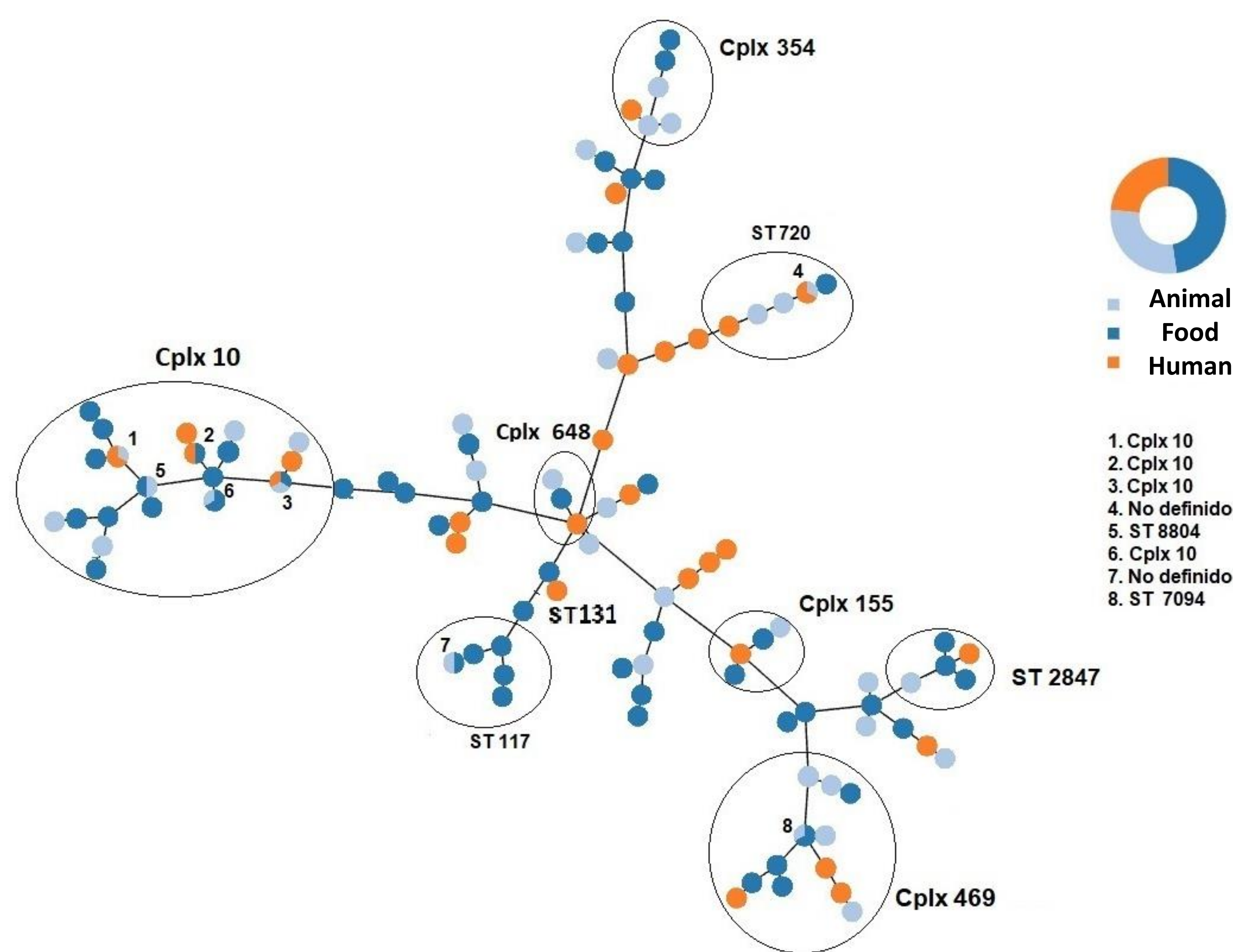


Figure 1. Minimum spanning tree of phylogenetic relationship.

Table 1. Prevalence of ESBL/AmpC genes and their alleles.

	Animal (%)	Food (%)	Humans (%)
Group 1	<i>bla</i> _{CTX-M-55} (51,2%)	<i>bla</i> _{CTX-M-55} (46,8%)	<i>bla</i> _{CTX-M-55} (29%)
	<i>bla</i> _{CTX-M-3} (12,2%)	<i>bla</i> _{CTX-M-3} (15,9%)	<i>bla</i> _{CTX-M-3} (29%)
Group 9		<i>bla</i> _{CTX-M-123} (1%)	<i>bla</i> _{CTX-M-15} (4,3%)
	<i>bla</i> _{CTX-M-65} (29,3%)	<i>bla</i> _{CTX-M-65} (36,2%)	<i>bla</i> _{CTX-M-65} (19,4%)
CMY			<i>bla</i> _{CTX-M-21} (6,5%)
Others	<i>bla</i> _{CMY-2} (2,4%)		
	<i>bla</i> _{CTX-M-65} <i>bla</i> _{CTX-M-24} (4,9%)		<i>bla</i> _{CTX-M-3} <i>bla</i> _{CTX-M-127} (3,2%)

Table 2. Conjugation rate

Component	Conjugation rate
Animal	62.5%
Food	65.2%
Human	75.86%

CONCLUSIONS

The prevalence of FOS resistance is higher than other countries (>10%).

The co-resistance to FOS and 3GC can be transmitted to other bacteria by conjugation of one plasmid.

MLST suggest the existence of various lineages moving among the three studied components (poultry, carcasses and humans).

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