

P0914 **High prevalence of multidrug-resistant epidemic clonal group B2-ST131 ESBL *Escherichia coli* isolated from bloodstream infections in Ecuador**

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Background: Most Latin American countries have reported a rapid dissemination of extended-spectrum- β -lactamase (ESBL)-producing *Escherichia coli* in clinical settings. In Ecuador, ESBL *E. coli* isolation has increased from 2% in 1999 to 60% in 2017. Despite this issue, circulating clones of ESBL *E. coli* from bloodstream infections have not been characterized in our country. This study aimed to (i) characterize ESBL *E. coli* and (ii) identify possible associations between STs and ESBL variants.

Materials/methods: 57 ESBL-producing *E. coli* isolates from bloodstream infections were recovered from three hospitals in Quito (June 2013 to September 2014). Bacterial species identification and antimicrobial susceptibility profiles were performed using VITEK2 system according to CLSI. All the isolates were screened for *bla*_{CTX-M}, *bla*_{TEM} and *bla*_{SHV} genes by PCR and amplicons were sequenced. Phylogenetic groups were determined by PCR-multiplex. MLST was performed using the Warwick scheme (<http://mlst.warwick.ac.uk/mlst/dbs/Ecoli>) and the Center for Genomic Epidemiology database (<https://cge.cbs.dtu.dk/services/MLST/>).

Results: Urinary tract was the most frequent source of bloodstream infection. CTX-M-15 variant were the most prevalent (47/57 isolates). Phylogenetic group B2 was predominant (59.6%) and exhibited high association with CTX-M-15 variant ($p < 0.05$). The multidrug-resistant epidemic clonal group B2-ST131-CTX-M-15 was the most frequent (27/57) (Table 1).

Conclusions: Clonal group B2-ST131-CTX-M-15 is related to fluoroquinolone and aminoglycoside resistance, several virulence factors for extraintestinal infections and it is hospital and community associated. Our results reveal the necessity to alert about the high prevalence of this clone group B2-ST131-CTX-M-15 in bloodstream infections in Ecuador and to track down the origin of these strains to tackle its dissemination.

Table 1.- Sequence types, phylogenetic groups and *bla*_{CTX-M} variants.

Genotype ESBL <i>E. coli</i> (n)	Phylogenetic Group/ST (n)			
	A	B1	B2	D
CTX-M-15 (47)	ST10 (4)	ST10 (1)	ST 131 (27)	ST131 (3)
	ST131 (1)	ST 168 (1)	ST 405 (1)	ST354 (1)
	ST 46 (1)		ST 23 (1)	ST648 (1)
	Unknown (1)			ST405 (1)
			Unknown (3)	
CTX-M-14 (5)	ST 23 (1)		ST14 (2)	ST 405 (1)
			ST 131 (1)	
CTX-M-2 (1)	ST131 (1)			

CTX-M-27 (1)			ST 131 (1)	
CTX-M-3 (1)	Unknown (1)			
CTX-M-15/14 (1)			ST131 (1)	
CTX-M-15/27 (1)				ST131 (1)
TOTAL	10	2	34	11