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Paper Poster Session
Lessons from surveillance of resistance in Gram-negatives

Molecular characterization of beta-lactam resistant pathogens isolated from urinary infections in Lebanon and Jordan: An evaluation of SMART data 2010-2014

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Background: The Study for Monitoring Antimicrobial Resistance Trends (SMART) has been tracking resistance among gram-negative bacilli (GNB) since 2002. GNB resistance has been on the rise as shown by reports since then, with a parallel increase of number of acquired carbapenemases. This report summarizes the detection and molecular characterization of broad spectrum beta-lactamases isolated from five participating centers from Lebanon and Jordan during a 5 years period (from January 2010 to December 2014).

Material/methods: 733 isolates from urinary tract infections (UTI) were collected from five hospitals in Lebanon (n=2) and Jordan (n=3). The prevalence of the isolated GNB from 2010 to 2014 as well as the prevalence of broad-spectrum beta-lactamases pathogens was assessed. Extended spectrum beta-lactamases (ESBLs) and carbapenemases were characterized using the Check-Points microarray (Check-Points B.V., Wageningen, The Netherlands), followed by PCR and sequencing. We characterized all *Enterobacteriaceae* that were non-susceptible to ertapenem (using CLSI breakpoints), and 50% of the isolates that were phenotypically ESBL+ but ertapenem susceptible (due to cost constraints). Therefore, 160 isolates were candidates for molecular characterization.
Three major groups of broad-spectrum beta-lactamases were distinguished and confirmed by recommended methods: ESBLs, class C cephalosporinases (AmpC), and carbapenemases.

Results: One hundred sixty isolates (n=160) UTI isolates producing broad-spectrum beta-lactamases were detected. The distribution of the isolates was as follows: 127 *Escherichia coli* and 33 *Klebsiella pneumoniae.* Many isolates produced multiple beta-lactamases (coexistence of two to four beta-lactamases) and the molecular characterization showed an ESBL distribution as follows: i) CTX-M-type: **CTX-M-15** (n=141), **CTX-M-27** (n=7), **CTX-M-14** (n=5), **CTX-M3** (n=3), **CTX-M-8 (**n=1), **CTX-M-9** (n=1); ii) SHV-type **SHV-12** (n=3), **SHV-28** (n=2), **SHV-2** (n=1); iii) TEM-type β-lactamases: **TEM-169** (n=1). Only two isolates produced **CMY type AmpC:** one *E. coli* isolated in Lebanon and one *K. pneumoniae* isolated in Jordan. These isolates produced other types of beta-lactamases. Finally, ten isolates (6.3%) were non-susceptible to carbapenems with four producing **OXA-48**, one **OXA-181**, one **OXA-244** and four **NDM-1**. These carbapenemase-producing isolates also co-produced other beta-lactamases.

Conclusions: This study documented the molecular characterization of broad-spectrum beta-lactamases in clinical isolates from GNB in Lebanon and Jordan. The overall prevalence of carbapenem-non-susceptible *Enterobacteriaceae* from 2010 to 2015 was 6.3%, with OXA-48 and NDM-1 being the most commonly detected mechanisms of resistance. This result is slightly higher than the 4.2% reported by the Centers for Disease Control and Prevention (CDC) in 2011. This study confirms the urgent need to continue surveillance programs that monitor trends in antimicrobial

susceptibility and detection of new resistance mechanisms as well as spread of existing ones, develop antimicrobial stewardship initiatives, implement effective infection control programs, and measure effectiveness of such programs in reducing or halting the spread of resistance both regionally and globally.