

EV0087

ePoster Viewing

Antimicrobials: epidemiology of MDR Gram-negatives

Virulence of carbapenem-resistant *Escherichia coli* isolated in the Arabian Peninsula

R. Al-Marzooqi¹, M. Al-Dhuhoori¹, D. Darwish¹, T. Pal¹, A.M. Sonnevend¹

¹College of Medicine UAE University, Al Ain, United Arab Emirates

Objectives

To understand the relationship, if any, between virulence and multi-drug resistance in pathogenic bacteria is of particular importance. However, little is known about the virulence traits of carbapenem-resistant *Escherichia coli*, increasingly common not only in the hospitals, but also in the community. Our aim was to reveal the frequency and distribution of virulence factor-coding genes and the presence of some virulence-related phenotypes of carbapenem resistant extraintestinal pathogenic *E. coli* isolated in the Arabian Peninsula.

Materials & Methods

Thirty independent carbapenem resistant *E. coli* were collected between 2009 and 2013 from the Kingdom of Saudi Arabia (KSA) (n=3), Kuwait (n=5), Sultanate of Oman (n=7) and the United Arab Emirates (UAE) (n=15). Carbapenemase production was confirmed by the carba-NP test. Genes of KPC, NDM, OXA-48-like, VIM, IMP carbapenemases, the LPS core types and the phylogenetic types were identified by PCR. Clonal relations were established by PFGE using an 80% similarity threshold. Thirty-one virulence-factor-encoding genes were detected by multiplex PCRs. Biofilm production in aerobic as well as in anaerobic condition was assessed in a stationary model.

Results

Of the 30 isolates 11 produced OXA-48-like, 7 NDM-1 and one VIM-4 carbapenemase, and 11 of them did not produce carbapenemases. The strains exhibited 27 different PFGE patterns with only 3 pairs of strains exhibiting clustering. Although strains belonged to all four phylogenetic groups and all five core types were detected, remarkably all OXA-48-like positive isolates belonged to phylogenetic group D and carried core type R4. The virulence factor score for the carbapenemase producers did not differ substantially from that of the carbapenemase non-producer strains (4.58 vs 5.27). However, members of the former group were significantly more likely to carry theyersiniabactin siderophore gene ($p=0.01$) and to possess the virulence associated K5 capsular type ($p=0.02$).

Conclusions

Carbapenem resistant *E. coli* strains exhibit a variety of virulence factors. In our strain collection K5 capsular type, promoting intestinal colonization, showed significant association with carbapenemase production.