

Emerging Threats of Multidrug-Resistant Nosocomial Pathogen *Enterobacter Aerogenes*

Tahir Hussain, Muhsin Jamal, Saadia Andleeb

Atta-ur-Rahman School of Applied Biosciences, National University of Sciences and Technology,
Islamabad, Pakistan

tahirhussainmdn@gmail.com; muhsinkhan08@gmail.com; saadiaamarwat@yahoo.com;

Maria Zubair

Peshawar Medical and Dental College, Warsak Road Peshawar, Pakistan

mariazubair@live.com

Extended Abstract

Enterobacter aerogenes is a nosocomial pathogen causing urinary tract, gastrointestinal and respiratory tract infections. Multidrug resistant variants of *E. aerogenes* increase not only severity of infections but also the costs of hospitalization. *E. aerogenes* isolates have been found resistant to variety of antimicrobial agents commonly used in empirical therapy. CTX-M type Extended Spectrum Beta-lactamases (ESBLs) have been found responsible for this overwhelming resistance, which are the most commonly encountered Beta-lactamases in *Enterobacteriaceae* (Bonnet, 2004). And since genes for ESBLs are present on plasmids, which also co-carry the genes for other antibiotics such as aminoglycosides, quinolones, chloramphenicol and tetracycline (Al-Zahrani *et al.*, 2005; Bradford, 2001), so ESBL plasmids often disseminate resistance to several classes of antibiotics. The aim of this study was to investigate the increasing prevalence of CTX-M type beta-lactamases in clinical isolates of *E. aerogenes* and identify the emerging threats to human population. Fifty three *E. aerogenes* isolates (already identified) were collected from Pakistan Railway General Hospital, Rawalpindi, in the summer 2012, and tested against several classes of antibiotics using the Kirby- Bauer disk diffusion tests to check their multidrug resistance phenotype. Presence and identification of CTX-M type beta-lactamases was confirmed on PCR using the primers for CTX-M group (Monstein *et al.*, 2007). Overall resistance pattern of *E. aerogenes* to the tested antibiotics was amoxicillin (90%), cefazolin (60%), cefotaxime (53%), ceftazidime (47%), gentamycin (58%), ciprofloxacin (82%), levofloxacin (37%), chloramphenicol (42%), erythromycin (79%), amoxicillin/clavulanic acid (34%) and trimethoprim/sulfamethoxazole (88%). The prevalence CTX-M type beta-lactamases was (57%) in the tested *E. aerogenes* isolates. There could be other mechanisms for this overwhelming resistance, but most pre-dominant mechanism seems to be the production of CTX-M type beta-lactamases. Since genes for these enzymes are present on plasmids, which can readily be exchanged between diverse bacterial communities and can potentially lead this resistance to epidemic level. Over 50% of population live below the poverty line in Pakistan and cannot afford or have excess to expensive treatments such increasing resistance to modern antimicrobials is challenging the very health care system of the country.

This study was supported in part by a research grant from the Higher Education Commission of Pakistan. We are grateful to the Lab staff of Pakistan Railway General Hospital for their technical support.

Al-Zahrani, A.J., & Akhtar, N. (2005). Susceptibility Patterns Of Extended Spectrum β - Lactamase (ESBL)-Producing *Escherichia Coli* and *Klebsiella Pneumoniae* Isolated in a Teaching Hospital. *Pak J Med Res.*, 44, 2.

- Bradford, P.A. (2001). Extended-Spectrum B-Lactamases in the 21st Century: Characterization, Epidemiology, and Detection of This Important Resistance Threat. *Clin Microbiol Rev.*, 14, 933-51.
- Bonnet, R. (2004). Growing Group of Extended-Spectrum Beta-Lactamases: The CTX-M Enzymes. *Antimicrob. Agents Chemother.*, 48, 1–14.
- Monstein, H. J., Ostholm-Balkhed, A., Nilsson, M.V., Nilsson, M., Dornbusch, K., & Nilsson, L.E. (2007). Multiplex PCR Amplification Assay For The Detection Of Blashv, Blatem And Blactx-M Genes In Enterobacteriaceae. *Apmis.*, 115, 1400-1408.