Prevalence and Some Possible Mechanisms of Colistin-Resistance Among Multidrug-Resistant and Extensively Drug Resistant Pseudomonas aeruginosa

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Abstract:

Background and Aim: The emergence of colistin-resistant strains is considered a great threat for patients with severe infections. Here, we investigate the prevalence and some possible mechanisms of colistin resistance among multidrug-resistant (MDR) and extensively drug-resistant (XDR) Pseudomonas aeruginosa (P. aeruginosa). Methods: Antimicrobial susceptibility was performed using disc diffusion methods while colistin resistance was detected by agar dilution method. Possible mechanisms for colistin resistance were studied by detection of mcr-1 and mcr-2 genes by conventional PCR, detection of efflux mechanisms using Carbonyl Cyanide 3-Chlorophenylhydrazone (CCCP), studying outer membrane protein profile and Lipopolysaccharide (LPS) profile of resistant isolates. Results: It was found that MDR and XDR represented 96% and 87% of the isolated P. aeruginosa, respectively, and colistin resistance represented 21.3%. No isolates were positive for mcr-2 gene while 50% of colistin-resistant isolates were positive for mcr-1. Efflux mechanisms were detected in 3 isolates. Protein profile showed the presence of a band of 21.4 KDa in the resistant strains which may represent OprH while LPS profile showed differences among colistin-resistant mcr-1 negative strains, colistin-resistant mcr-1 positive strains and susceptible strains. Conclusion: The current study reports a high prevalence of colistin resistance and mcr-1 gene in P. aeruginosa strains isolated from Egypt that may result in untreatable infections. Our finding makes it urgent to avoid unnecessary clinical use of colistin.

Keywords:

Pseudomonas aeruginosa, colistin resistance, mcr-1, mcr-2, toxA gene, XDR, MDR

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