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Molecular epidemiology of extensively drug-resistant mcr encoded colistin-resistant bacterial strains co-expressing multifarious β-lactamases

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Plasmid-mediated colistin resistance (Col-R) conferred by mcr genes endangers the last therapeutic option for multifarious β-lactamase-producing bacteria. The current study aimed to explore the mcr gene molecular epidemiology in extensively drug-resistant (XDR) bacteria. Col-R gram-negative bacterial strains were screened using a minimum inhibitory concentration (MIC) breakpoint ≥4 µg/mL. Resistant isolates were examined for mcr variants, extended spectrum βlactamase, AmpC, and carbapenemase genes using polymerase chain reaction (PCR). The MIC breakpoints for mcr-positive strains were determined using broth microdilution and E-test strips. Overall, 19/718 (2.6%) gram-negative rods (GNRs) harboring mcr were identified, particularly in pus ($p = 0.01$) and tracheal secretions ($p = 0.03$). Molecular epidemiology data confirmed 18/19 (95%) mcr-1 and 1/19 (5%) mcr-2 genes. Integron detection revealed 15/17 (88%) Int-1 and 2/17 (12%) Int-2. Common co-expressing drug-resistant β-lactamase genes included 8/16 (50%) blaCTM-1, 3/16 (19%) blaCTM-15, 3/3 (100%) blaCMY-2, 2/8 (25%) blaNDM-1, and 2/8 (25%) blaNDM-5. The MIC50 and MIC90 values (µg/mL) were as follows: Escherichia coli, 12 and 24; Klebsiella pneumoniae, 12 and 32; Acinetobacter baumannii, 8 and 12; and Pseudomonas aeruginosa, 32 and 64, respectively. Treatment of XDR strains has become challenging owing to the co-expression of mcr-1, mcr-2, multifarious β-lactamase genes, and integrons.

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