Phenotypic and Genotypic Characterization of Macrolide, Lincosamide and Streptogramin Resistance among Nosocomial Staphylococci Isolated from Intensive Care Units

Omania H.B. El-Badawy, Mona H. Abdel-Rahim, Asmaa M Zahran, Nahla M Elsherbiny

Abstract:

Background: The extensive misuse of antibiotics has increased cross-resistance to macrolide–lincosamide–streptogramin B (MLSB) antibiotics among Staphylococci. Objectives: The study aimed to investigate the distribution of MLSB resistance phenotypes and their encoding genes among Staphylococci isolated from the Intensive Care Units of Assiut University Hospitals. Methodology: A total of 243 nosocomial staphylococcal isolates were collected. MLSB phenotypes were assessed by double disc diffusion method (D test) and the encoding genes (ermA, ermB, ermC, msrA, mphC and ImuA) were detected by PCR. Results: Of all isolates, 93.8% were resistant to erythromycin. MLSB resistance phenotypes detected were the constitutive phenotype (cMLSB) (56.8%), macrolide/macrolide–streptogramin B resistance (M/MSB) (24.7%) and the inducible resistance (iMLSB) (12.3%). The most prevalent MLSB resistance genes were ermC in the cMLSB, msrA in the M/MSB and ermC and msrA in the iMLSB phenotype isolates. The most common gene combinations were either the msrA with erm genes or with both erm and mphC genes. Most of the strains harboring these combinations were of the cMLSB phenotype. The coexistence of the 4 gene groups was detected in 3.8% of the isolates; all of them were of the constitutive phenotype. Conclusion: A high percentage of erythromycin resistance and an alarming percentage of iMLSB phenotype were detected among our isolates. Routine D- test is mandatory to discover the inducible phenotype prone to acquire clindamycin resistance especially in patients with life threatening infections.

Keywords:

Staphylococci, clindamycin, MLSB resistance genes, cMLSB, iMLSB, M/MSB

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