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ANTIBIOTIC RESISTANCE GENE PROFILES AND THEIR ASSOCIATION WITH DISEASE SEVERITY, PATHOPHYSIOLOGICAL PARAMETERS, AND CLINICAL OUTCOMES

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Objective: To characterize antimicrobial resistance gene profiles in bacterial isolates from patients with sepsis and/or pneumonia and explore their associations with inflammatory biomarkers.

Materials and Methods: The study included 32 patients of both sexes with sepsis and/or pneumonia treated at the First University Clinic. The mean age was 70.2 years, with an age range of 29-93. Bacterial isolates predominantly comprised Acinetobacter and Klebsiella. DNA microarray analysis targeting 57 antimicrobial resistance-associated genes was performed at the Walter Reed Army Institute of Research. Resistance gene profiles were visualized using a custom MATLAB program, and isolates were grouped according to their genetic profiles. Associations between major cluster membership and bacterial group were evaluated using Fisher's exact test. Differences in C-reactive protein (CRP), ferritin, procalcitonin (PCT), white blood cell count (WBC), and recorded clinical severity measures were assessed using the Mann–Whitney U test. Analyses were exploratory.

Results: Visual inspection of the resistance gene clustergram identified two major clusters, A and B, with distinct resistance gene patterns. Cluster A predominantly comprised Acinetobacter isolates, whereas Cluster B predominantly comprised Klebsiella isolates.

Cluster membership was significantly associated with bacterial group (Fisher's exact $p < 0.001$). No statistically significant differences in the recorded clinical severity measures were detected between the major clusters.

Further examination identified within-cluster genetic heterogeneity, permitting subdivision into A0 and A1, and B0 and B1. CRP levels differed between A0 and A1 ($p = 0.0233$).

Ferritin levels differed between both A0 and A1 ($p = 0.043$) and B0 and B1 ($p = 0.047$). CRP did not differ significantly between B0 and B1, and no significant within-cluster differences were identified in PCT or WBC.

Conclusion: Antimicrobial resistance gene profiles identified distinct genetic clusters associated with bacterial group. Within-cluster differences in selected inflammatory biomarkers suggest preliminary associations between resistance gene patterns and inflammatory characteristics. These exploratory findings do not establish independent associations with disease severity or clinical outcomes. Larger studies are required to evaluate their clinical significance.

Keywords: Antimicrobial resistance, resistance genes, sepsis, inflammatory biomarkers