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16S rRNA SEQUENCING AND AMR GENOTYPING FOR INFECTION RISK ASSESSMENT IN ONCOHEMATOLOGY AND TRANSPLANT PATIENTS

Background. Antimicrobial resistance represents a significant global health challenge, resulting in over 1.27 million deaths annually. Immunocompromised individuals, including those undergoing chemotherapy or organ transplantation, are particularly susceptible. In these populations, hospital-acquired infections caused by multidrug-resistant bacteria frequently progress to sepsis, with mortality rates reaching up to 70%. Rapid molecular diagnostics are essential for effective infection management and treatment guidance in these groups. **Methods.** Gut microbiome profiling of 24 oncohematology patients was performed by 16S rRNA gene sequencing using the Ion AmpliSeq Pan-Bacterial Panel, the Ion Chef, and the Ion S5 Plus sequencer. The results were then analyzed using Torrent Suite Software. AMR genotyping was performed using the iAMP Drug Resistance Panel, covering 24 AMR genes across 8 antibiotic categories. Ethics approval and informed consent were obtained. **Results.** Sequencing identified 334 distinct microbial taxa. ESKAPEE pathogens were prevalent: *Escherichia coli* was detected in 69.6% of samples, *Klebsiella pneumoniae* in 43.5%, and *Enterobacter* species in 39.1%. 39 species were classified as potential opportunistic pathogens, including *Clostridium perfringens*. 28 taxa, such as *Blautia*, *Bifidobacterium*, *Faecalibacterium prausnitzii*, and *Roseburia*, were associated with favorable outcomes, including reduced rates of graft-versus-host disease (GvHD) and increased post-transplant survival. AMR analysis revealed that all samples harbored sulfonamide resistance genes (SUL1/2/3), 75% exhibited macrolide resistance, 46% contained CTX-M extended-spectrum beta-lactamase genes, and 25% had MRSA-related *MecA*. Carbapenemase genes (NDM/VIM/IMP and KPC/OXA-48) were detected in 8% of samples, indicating the presence of last-resort resistance mechanisms. **Conclusions.** Combining 16S rRNA microbiome analysis with detection of pathogens and resistance genes provides a rapid and comprehensive approach to assessing infection risk in oncology and transplant populations. This strategy facilitates expedited clinical decision-making alongside conventional microbiological methods. Additionally, microbiome profiling may predict patient responses to immunotherapy and the likelihood of developing GvHD. The broader implementation of molecular testing has the potential to improve outcomes in high-risk groups.

Keywords: AMR, immunocompromised individuals, microbiome, transplantology.

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