Evaluation of pre-treated healthcare wastes during COVID-19 pandemic reveals pathogenic microbiota, antibiotics residues, and antibiotic resistance genes against beta-lactams

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ABSTRACT

The disposal of healthcare waste without prior elimination of pathogens and hazardous contaminants has negative effects on the environment and public health. This study aimed to profile the complete microbial community and correlate it with the antibiotic compounds identified in microwave pre-treated healthcare wastes collected from three different waste operators in Peninsular Malaysia. The bacterial and fungal compositions were determined via amplicon sequencing by targeting the full-length 16S rRNA gene and partial 18S with full-length ITS1–ITS2 regions, respectively. The antibiotic compounds were characterized using high-throughput spectrometry. There was significant variation in bacterial and fungal composition in three groups of samples, with alpha- (p-value = 0.04) and beta-diversity (p-values <0.006 and < 0.002), respectively. FC samples were found to acquire more pathogenic microorganisms than FA and FV samples. Paenibacillus and unclassified Bacilli genera were shared among three groups of samples, meanwhile, antibiotic-resistant bacteria Proteus mirabilis, Enterococcus faecium, and Enterococcus faecalis were found in modest quantities. A total of 19 antibiotic compounds were discovered and linked with the microbial abundance detected in the healthcare waste samples. The principal component analysis demonstrated a positive antibiotic-bacteria correlation for genera Pseudomonas, Aerococcus, Comamonas, and Vagococcus, while the other bacteria were negatively linked with antibiotics. Nevertheless, deep bioinformatic analysis confirmed the presence of *bla*_{TEM-1} and *penP* which are associated with the production of class A beta-lactamase and beta-lactam resistance pathways. Microorganisms and contaminants, which serve as putative indicators in healthcare waste treatment evaluation revealed the ineffectiveness of microbial inactivation using the microwave sterilization method. Our findings suggested that the occurrence of clinically relevant microorganisms, antibiotic contaminants, and associated antibiotic resistance genes (ARGs) represent environmental and human health hazards when released into landfills via ARGs transmission.

KEYWORDS

Healthcare; Waste management; Pathogenic microbe; Antibiotic resistance; Beta-lactam; Microwave

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