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Bacterial dissemination and molecular surveillance in public hospital in South Africa

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In South Africa it is estimated that approximately 1 in 7 patients entering South African hospitals are at high risk of acquiring a hospital-acquired infection (HAI). Quantitative cross-sectional studies were performed in four public hospitals in the eThekwini district of KwaZulu-Natal province, South Africa from September to November, 2017. Focus was on three wards viz. intensive care unit, paediatric ward and general male ward. Within each ward 5 sites were swapped viz. drip stand, patient files, patient bed, sink and ward reception. DNA was extracted using PureLink Microbiome DNA purification kit followed by amplification of the V3-V4 region of the 16S amplicon. Resulting PCR product was sequenced on an Illumina® MiSeq platform. Metagenomic data analysis revealed distinct diversity in the microbial populations associated with various hospital sites investigated. Bacteria made up more than 85% of the DNA reads compared to viruses or unclassified kingdom levels. Proteobacteria followed by Bacteroidetes and Firmicutes are the top phylums. The class mostly presented is Gammaproteobacteria, Flavobacteria and Baccili. The highest frequency of bacteria originated from the order Pseudomonadales and Enterobacteriales. The common families found was Moraxellaceae and Enteriobacteriaceae. As expected, Acinetobacter was found at genus level, but the variety of species was a surprise. Contact with contaminated surfaces in the health care setting attributes to cross infection. Variations was found within sites, wards and between hospitals. The information can assist IPC officers to deal with the hospital "microbiota" and a guideline to ascertain any shifts or variation in bacteria composition.

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