**Investigation of the dissemination of microbiota between pressure ulcers and bed environment by culture-free bacterial identification using DNA analysis**

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The bacteria in the bed environment may contribute to the occurrence of pressure ulcer infection because most patients with pressure ulcers spend all of their time in bed. The aim of this study was to explore whether there is bacterial dissemination between pressure ulcers and bed environment. Ten pressure ulcers were recruited in this cross-sectional study. The microbiota of wounds, skin, and the bed environment were identified by 16S rRNA gene sequencing analysis. The zero-radius operational taxonomic units (zOTUs) was used for confirming the presence of dissemination. When the same zOTU is detected in the different microbiota, it can be determined that there is the dissemination between two sites because zOTUs indicate bacteria with identical sequence within V3/V4 region in 16S rRNA gene. The validity of zOTUs was confirmed by the clustering based on the UPGMA tree and PCoA. All ulcers had the common zOTUs among microbiota of wounds, skin, and the bed environment within every individual (the median number of zOTUs: 187, IQR: 61-266). Moreover, these microbiota were classified into the same cluster. This study suggested that there is bacterial dissemination between the bed environment and pressure ulcers. The bed environment might be an important target for infection control.