

Locational effects on oral microbiota among long-term care patients F.T. Tsai¹*, D.H. Wang²*, C.C. Yang^{2,3}, Y.C. Lin², L.J. Huang⁴, W.Y. Tsai⁴, C.W. Li⁵, W.E. Hsu⁶, H.F. Tu^{2,4} and M.L. Hsu²



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Introduction

Oral dysbiosis is the cause of many diseases related to oral and general health. However, few Asia-based studies have evaluated the role of oral microbiota specifically in patients receiving long-term care. As the understanding of oral microbiota in long-term care patients is insufficient, there is a need to inform new criteria and indications for early prevention and risk management based on information derived from the oral microbiota.

Methods

We used next-generation sequencing (NGS) to identify the oral bacterial composition and abundance in 40 patients receiving long-term care: 20 from the dental outpatient department (OPD) of special needs and 20 community-dwelling, home-care patients. Their basic clinical-demographic information was obtained, and NGS was used to characterize the microbiota composition in each patient's tongue plaque sample. We then analyzed various alpha and beta diversity indices to assess within-group and between-group diversity.

Long-term care patients (N=40)

	OPD	Home care
of patients	20	20

Result

study flowchart (Figure 1) The and patients characteristics and the result of oral examination (Table 1)were presented. Specifically, species diversity and homogeneity was higher in the OPD group than in the home-care group (Figure 2), suggesting that bacterial species were more balanced and stable in the OPD group than in the home-care group. Taxonomic analysis showed that the five most abundant phyla of the two group (Figure 3). Further, within-group comparisons revealed that the microbiota of home-care patients were more divergent than that of OPD patients (Figure 4). The two groups showed significantly different bacterial diversity and homogeneity, as well as distinct dominant bacterial species (Figure 5). These findings indicated that home-care patients have a higher risk of oral or general disease due to the existence of specific dominant species as well as a less stable microbial community.



Number o

Conclusion

Despite the limitation of scale in this study, we conclude that a significant difference exists in the oral microbiota between long-term care patients receiving treatment at OPD and those receiving home-care. The oral microbiota of home-care patients was less diverse than that of OPD patients, and specific pathogenic species were dominant, leading to dysbiosis.





	Mild	2	0
	Moderate	0	1
	Severe	5	16
Moveable denture			
	Partial	2	0
	Full mouth	3	0
Crown / Bridge		3	10

Figure 5. Comparison of the difference bacteria biomarker between OPD group and home care group. (A) LefSe analysis. (B) The LDA score. O, OPD group; H, home care group.

Figure 4. Comparison of the differences in microbiota composition between OPD and home care groups. (A) Principal coordinates analysis (PCoA) (B) principal components analysis (PCA) (C) Nonmetric multidimensional scaling (NMDS) (D) analysis of similarities (ANOSIM). O, OPD group; H, home care group.