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The Effects of Common Oral Hygiene Routines on the Oral Microbiota

The oral cavity consists of hundreds of species of bacteria which form communities that potentially change in composition and diversity as a result of different influences. The object of this study was to determine the effects of common oral hygiene routines on the oral bacterial communities and the community reassembly that occurs approximately twelve hours afterward. Subjects were asked to perform three different treatments before sleep on three alternating nights to prevent any potential carry-over effect. Samples were then taken before treatment, after treatment, and in the morning from the dorsal tongue and the surfaces of the molars. Bacterial DNA was extracted from the samples and was analyzed by sequencing the 16S ribosomal gene using 454 sequencing techniques. Statistical analyses of the phylogenetic and species diversity showed that toothpaste and mouthwash had an impact on the oral microbial composition which lasted overnight. The diversity of bacteria increased after treatment, which could be caused by the removal of inhibitory predominant bacteria or the displacement of bacteria from other locations in the oral cavity. The diversity of bacteria decreased overnight, suggesting that the microbial community began reverting to its composition before treatment. Further studies would be necessary to ascertain whether either hypothesis is correct, as well as whether or not the change is beneficial. It is clear that using toothpaste and mouthwash disturb the oral microbial community and that although these disturbances last overnight, the bacterial community may begin to reassemble to its original configuration by morning.