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Defining the normal bacterial flora of the oral cavity.

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Source

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Abstract

More than 700 bacterial species or phylotypes, of which over 50% have not been cultivated, have been detected in the oral cavity. Our purposes were (i) to utilize culture-independent molecular techniques to extend our knowledge on the breadth of bacterial diversity in the healthy human oral cavity, including not-yet-cultivated bacteria species, and (ii) to determine the site and subject specificity of bacterial colonization. Nine sites from five clinically healthy subjects were analyzed. Sites included tongue dorsum, lateral sides of tongue, buccal epithelium, hard palate, soft palate, supragingival plaque of tooth surfaces, subgingival plaque, maxillary anterior vestibule, and tonsils. 16S rRNA genes from sample DNA were amplified, cloned, and transformed into *Escherichia coli*. Sequences of 16S rRNA genes were used to determine species identity or closest relatives. In 2,589 clones, 141 predominant species were detected, of which over 60% have not been cultivated. Thirteen new phylotypes were identified. Species common to all sites belonged to the genera *Gemella*, *Granulicatella*, *Streptococcus*, and *Veillonella*. While some species were subject specific and detected in most sites, other species were site specific. Most sites possessed 20 to 30 different predominant species, and the number of predominant species from all nine sites per individual ranged from 34 to 72. Species typically associated with periodontitis and caries were not detected. There is a distinctive predominant bacterial flora of the healthy oral cavity that is highly diverse and site and subject specific. It is important to fully define the human microflora of the healthy oral cavity before we can understand the role of bacteria in oral disease.