

Cultivable Oral Microbiota of Domestic Dogs

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Bacteria were isolated from the dental plaques of nine dogs and a sample of pooled saliva from five other dogs and were then identified by comparative 16S rRNA gene sequencing. Among 339 isolates, 84 different phylotypes belonging to 37 genera were identified. Approximately half of the phylotypes were identified to the species level, and 28% of these were considered members of the indigenous oral microbiota of humans. The 16S rRNA gene sequences of the remaining 44 phylotypes were not represented in GenBank, and most of these phylotypes were tentatively identified as candidate new species. The genera most frequently isolated from saliva were *Actinomyces* (26%), *Streptococcus* (18%), and *Granulicatella* (17%). The genera most frequently isolated from plaque were *Porphyromonas* (20%), *Actinomyces* (12%), and *Neisseria* (10%). A comparison of the DNA sequences from this study with sequences of the human microbiota available in GenBank showed that, on average, canine and human microbiotas differed by almost 7% in the 16S rRNA gene. In conclusion, this study has shown that the cultivable oral microbiotas of dogs and humans show significant differences.