



***Streptococcus massiliensis* in the human mouth: a phylogenetic approach for the inference of bacterial habitats**

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ABSTRACT. *Streptococcus* is a diverse bacterial lineage. Species of this genus occupy a myriad of environments inside humans and other animals. Despite the elucidation of several of these habitats, many remain to be identified. Here, we explore a methodological approach to reveal unknown bacterial environments. Specifically, we inferred the phylogeny of the Mitis group by analyzing the sequences of eight genes. In addition, information regarding habitat use of species belonging to this group was obtained from the scientific literature. The oral cavity emerged as a potential, previously unknown, environment of *Streptococcus massiliensis*. This phylogeny-based prediction was confirmed by species-specific polymerase chain reaction (PCR) amplification. We propose employing a similar approach, i.e., use of bibliographic data and molecular phylogenetics as predictive methods, and species-specific PCR as confirmation, in order to reveal other unknown habitats in further bacterial taxa.

Key words: *Streptococcus massiliensis*; Microbiome; Phylogeny; Mitis group, RecN