

## ***Streptococcus sanguis* Genome Sequencing Project**

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*Streptococcus sanguis* is important in bacterial colonization of the mouth, acting as a tether for other microorganisms that can cause dental plaque and periodontal disease. The sequencing of its genome has been undertaken by the Philips Institute and the Nucleic Acids Core Facility at VCU. The genome is close to being finished, but requires a certain amount of gap closure. Gaps are unsequenced regions which inhibit the ability to align contigs and complete the genome. We used comparative alignment and genome walking as strategies for gap closure. In all, nearly half of the remaining gaps were closed. We also began the process of comparative genomics. Many *Streptococcus* genomes have already been sequenced, and just as many are in the process of being sequenced. The large number of *Streptococcus* genomes available increases the resolving power of genome comparison. Our analysis will hopefully lead both to a better understanding of the *Streptococcus* family and to a better understanding of *S. sanguis*, resulting in the identification of peptide targets for drugs.