

***Streptococcus sanguis* genome sequencing and comparative genomics**

Todd Kitten

Dept. of Oral & Craniofacial Molecular Biology

A collaborative group here at VCU is determining the DNA sequence of the entire genome of the bacterium *Streptococcus sanguis*. We have finished the random sequencing phase and are now in the process of closing gaps in the sequence. One approach to gap closure is to compare the sequences we have to those of finished sequences available for other streptococci. There are a few streptococci that are available, but which should be used? *S. sanguis* lives in the human mouth and attaches to teeth as part of dental plaque. It also causes a disease of heart tissue called infective endocarditis. *Streptococcus mutans*, which causes dental cavities, is also a component of dental plaque and also causes infective endocarditis. Yet, by analysis of 16S ribosomal RNA, which is a traditional method for determining relatedness among organisms, *S. sanguis* is more closely related to *Streptococcus pneumoniae* (which causes pneumonia) than it is to *S. mutans*. Apart from the utility of exploring the relationship between *S. sanguis* and other species for gap closure, we can also ask other questions concerning their relationships. For instance, if *S. sanguis* is more closely related to *S. pneumoniae*, why does it appear phenotypically to be more similar to *S. mutans*? Also, what genes may be responsible for the shared properties of *S. sanguis* and *S. mutans* and which may be responsible for the unique properties of each?