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Gum disease genome on line

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The genome of *Porphyromonas gingivalis*, the bacterium that causes periodontitis or gum disease, has been fully sequenced by a team from The Institute for Genomic Research (TIGR) in Rockville, Maryland in collaboration with The Forsyth Institute in Boston, Massachusetts. Dennis Mangan and colleagues who completed the work decided to make the genome freely available to researchers worldwide by releasing it on TIGR's Comprehensive Microbial Resource website. The site allows researchers to access all bacterial genome sequences completed to date.

The P. gingivalis genome contains 2.3 million base pairs and 2226 genes, many of which are involved in protein synthesis and energy metabolism. The sequence provides the first genomic information on an organism from a major group of bacteria not previously genotyped: the bacteroides group of Gramnegative anaerobes. Mangan *et al.* said that with the genetic blueprint for *P. gingivalis* in hand, dental researchers will be able "to identify the genetic mechanisms for the organism's virulence and to develop better approaches for preventing or eradicating periodontitis."

Currently the primary treatments for periodontitis are deep cleaning and surgery. In America alone more than 35 million people suffer from periodontitis, which if left untreated can destroy the gum and result in tooth loss.

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