

# Genetic study reveals the origins of cavity-causing bacteria

December 23 2009

---

Researchers have uncovered the complete genetic make-up of the cavity-causing bacterium *Bifidobacterium dentium* Bd1, revealing the genetic adaptations that allow this microorganism to live and cause decay in the human oral cavity. The study, led by Marco Ventura's Probiogenomics laboratory at the University of Parma, and Prof. Douwe van Sinderen and Dr Paul O'Toole of the Alimentary Pharmabiotic Centre at University College Cork, is published December 24 in the open-access journal *PLoS Genetics*.

Bifidobacteria, largely known as long-term beneficial [gut bacteria](#), are often included as probiotic components of food to aid digestion and boost the immune system. However, not all species within the genus *Bifidobacterium* provide beneficial effects to the host's health. In fact, the *Bifidobacterium dentium* species is an opportunistic pathogen since it has been linked to the development of tooth decay. The [genome sequence](#) of *B. dentium* Bd1 reveals how this microorganism has adapted to the oral environment through specialized nutrient acquisition features, acid tolerance, defences against antimicrobial substances and other gene products that increase fitness and competitiveness within the oral niche.

This report identifies, through various genomic approaches, specific adaptations of a *Bifidobacterium* taxon to a lifestyle as a tooth decay-causing [bacterium](#). The data in this study indicate that the genome of this opportunistic pathogen has evolved through only a small number of horizontal gene acquisition events, highlighting the narrow boundary that separates bacteria that are long-term residents on or in the human body

from opportunistic pathogens.

Provided by Public Library of Science

Citation: Genetic study reveals the origins of cavity-causing bacteria (2009, December 23)  
retrieved 18 April 2024 from

<https://medicalxpress.com/news/2009-12-genetic-reveals-cavity-causing-bacteria.html>

This document is subject to copyright. Apart from any fair dealing for the purpose of private study or research, no part may be reproduced without the written permission. The content is provided for information purposes only.