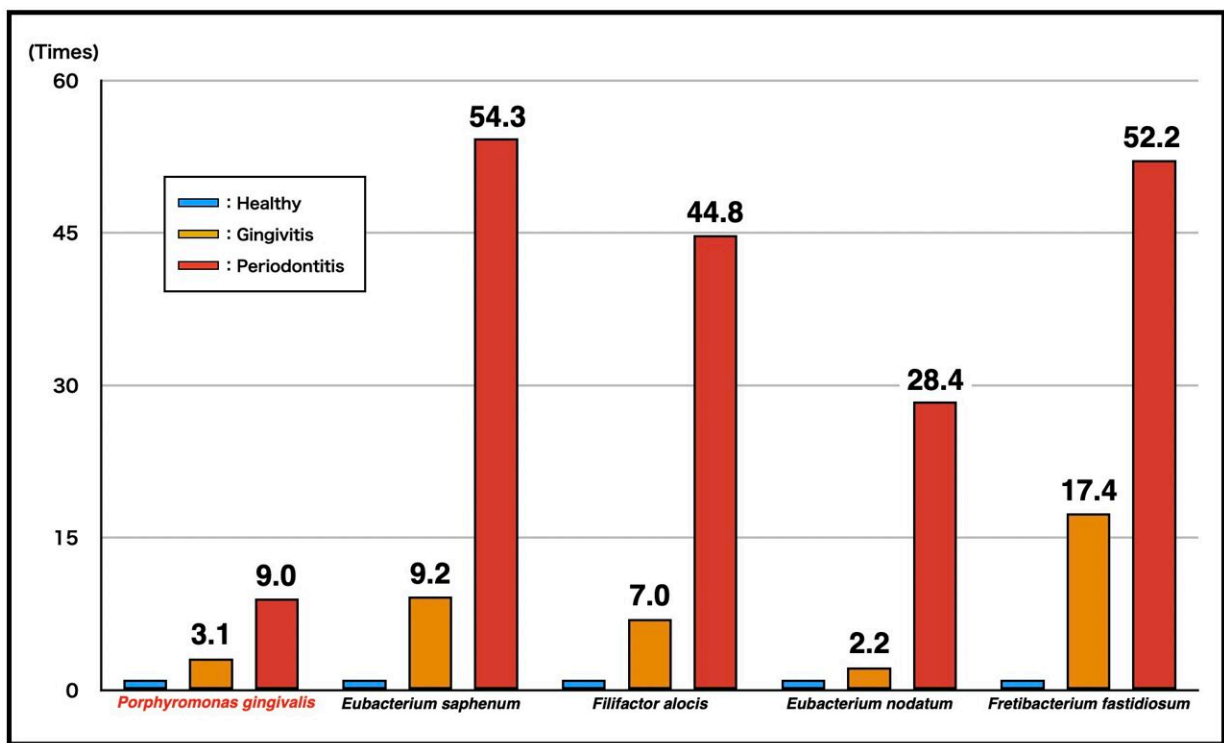


That's so meta(transcriptomics): Distinctive bacterial taxonomic and functional profiles in mouth disease

December 7 2021



The bacterial activity of a healthy site was defined as 1. The activities of several taxa were higher than that of red complex bacteria (e.g., *Porphyromonas gingivalis*). Credit: Department of Periodontology, TMDU

When you're smiling, the whole world smiles with you; but what happens

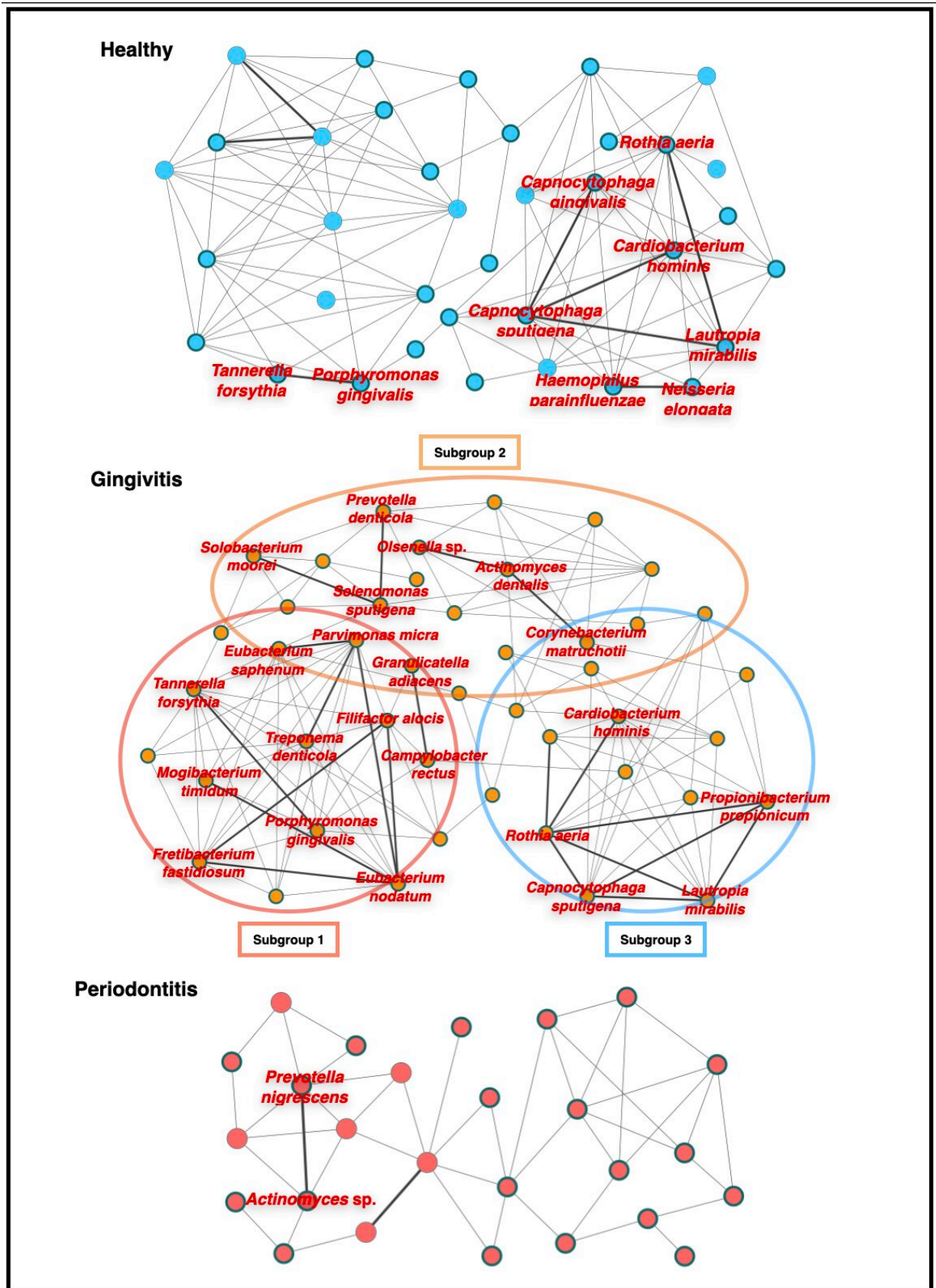
when gum or tooth disease starts to dim your pearly whites? Now, researchers from Japan have found a bacterial signature that marks the shift from healthy teeth and gums to periodontitis.

In a study published in *mSystems*, researchers from Tokyo Medical and Dental University (TMDU) have revealed that specific bacterial signatures differentiate healthy mouths from those with gingivitis and periodontitis.

Periodontal disease is inflammation of the gums caused by infection with many different kinds of bacteria. The infection begins at the gum line and then makes its way down into the bones of the jaw, where it can cause permanent damage and tooth loss.

"Previous studies have explored the differences in bacterial communities in healthy mouths or those affected by gingivitis or periodontitis," says lead author of the study Takashi Nemoto. "However, it was unclear how the metabolic activities of these communities changed during the progression from health to periodontitis, so we wanted to investigate the functional profiles of these communities."

To do this, the researchers took plaque samples from three sites within the mouths of 21 patients with periodontal disease: from a healthy site, from a site showing gingivitis, and from a [site](#) with periodontitis. They then performed a specialized analysis called metatranscriptomic analysis to determine what functional substances the bacteria at these sites were producing, as well as a lineage analysis to determine what types of bacteria were present at these sites.



Each bacterial species and co-occurrence relationship are indicated by a node and an edge, respectively. Bacterial species with significant-high activity are indicated with bold circles, and interactions with significant co-occurrence are indicated with bold lines. Core bacterial species that are shown significant-high activity and significant co-occurrence interactions with other bacteria are indicated in red letters. The gingivitis co-occurrence network appeared to comprise three subnetworks. Subgroup 1 included the species mainly exhibited co-occurrence relationships with red complex bacteria; these species were detected in both gingivitis and periodontitis sites. Subgroup 2 included the species detected mainly in gingivitis sites. Subgroup 3 included mainly the species detected mainly in both healthy and gingivitis sites. Credit: Department of Periodontology, TMDU

"The results showed clear differences in both bacterial community composition and functional profiles between health and diseased sites," explains Takanori Iwata, senior author. "Importantly, we found that the transcriptional activity of taxa including *Eubacterium nodatum*, *Eubacterium saphenum*, *Filifactor alocis*, and *Fretibacterium fastidiosum* was higher than that of well-known periodontopathic bacteria (red complex; *Porphyromonas gingivalis*, *Tannerella forsythia*, and *Treponema denticola*) at diseased sites than at healthy sites, and as gingivitis progressed to periodontitis."

These changes indicate that these taxa are associated with the progression of periodontal disease, and that [dynamic changes](#) occur in the oral microbiome as [periodontal disease](#) worsens.

"The changes that we observed in the transcriptional activity of these taxa with [disease](#) progression show that the shift from health to periodontitis is accompanied by changes in both the structure and the complexity of the bacterial network," says Nemoto.

Given that gingivitis is reversible, but periodontitis is not, the identification of key bacterial species and functions involved in the progression from a healthier state to a diseased state could help prevent permanent damage.

More information: Takashi Nemoto et al, Discrimination of Bacterial Community Structures among Healthy, Gingivitis, and Periodontitis Statuses through Integrated Metatranscriptomic and Network Analyses, *mSystems* (2021). [DOI: 10.1128/mSystems.00886-21](https://doi.org/10.1128/mSystems.00886-21)

Provided by Tokyo Medical and Dental University

Citation: That's so meta(transcriptomics): Distinctive bacterial taxonomic and functional profiles in mouth disease (2021, December 7) retrieved 2 July 2023 from <https://medicalxpress.com/news/2021-12-metatranscriptomics-distinctive-bacterial-taxonomic-functional.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.