Performing human whole genome sequencing from saliva samples provides highly reliable information about the salivary microbiome

This manuscript (permalink) was automatically generated from lvelosuarez/gazel-article@4e1d651 on April 11, 2024.

Authors

- **Lourdes velo Suarez**
  XXXX-XXXX-XXXX-XXXX · lvelosuarez · johndoe · @johndoe@mastodon.social
  Department of Something, University of Whatever · Funded by Grant XXXXXXXX

- **Jane Roe** ✉
  XXXX-XXXX-XXXX-XXXX · janeroe
  Department of Something, University of Whatever; Department of Whatever, University of Something

✉ — Correspondence possible via GitHub Issues or email to Jane Roe <jane.roe@whatever.edu>.

Abstract

The past two decades have seen tremendous advances in understanding human genetic variation and its implications for disease. Similarly, the microbiome was also shown to play a significant role in human health and disease. However, the relationship between host genetic variation and microbiome composition is largely unknown, mainly because of the elevated cost of processing both samples with high throughput sequencing. This study explores how well an individual salivary microbiome can be characterized using whole-genome sequencing (WGS) data from DNA saliva kits designed to study human genome variation. WGS was performed on saliva samples from 35 healthy individuals who received saliva kits at home. The relative abundance distributions obtained from the analysis of non-human reads were compared against those obtained by specific 16S rRNA gene resequencing of the same DNA samples. The results showed that 16S sequencing detects only part of the salivary microbiome revealed by WGS analysis. Low-abundant taxa were identified on the WGS data that could not be captured by 16S sequencing. Interestingly, some of these taxa could be linked to oral diseases such as periodontitis.

Our microbiome communities were similar to those described in the Human Microbiome Project (HMP) and core salivary microbiome studies, showing that accurate microbiome profiles can be obtained from read data generated for human whole-genome sequencing. Furthermore, our metagenomic approach also provides additional insights into microbiome characterization such as the analysis of antimicrobial resistance in our samples.

Introduction

Background information on the importance of studying the salivary microbiome and its relevance to human health. Overview of previous research on microbiome profiling methods and their limitations. Rationale for conducting whole genome sequencing (WGS) of human DNA from saliva samples to assess the reliability of salivary microbiome information.

References