Why “missing heritability” may not be found in microbiomes

Gavin M. Douglas
Joseph P. Bielawski
Morgan G. I. Langille

Video Byte

Keywords: Microbiome, missing heritability, heritable traits, disease, genomes, genome-wide association studies, GWASs, human microbiome, genomic sequence, environmental factors, sequencing data

Posted Date: October 28th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-99203/v1>

License: This work is licensed under a Creative Commons Attribution 4.0 International License.
[Read Full License](#)

Abstract

Heritable traits such as height or disease vary from person to person. One way to explain these variations is by looking at the genomes of large populations. That's the aim of genome-wide association studies, or GWASs. Unfortunately, GWASs often come up short – explaining only a small fraction of trait heritability. That has many researchers looking to the human microbiome for this “missing heritability”. But according to a new perspective piece, there could be a few problems with that approach. While individuals have only one genomic sequence, they're host to numerous microbiomes that evolve over time. That means that it would likely be incorrect to consider the microbiome as an extension of the human genome. Additionally, microbiomes may be strongly shaped by environmental factors, making them irrelevant to the genetic component of human heritability. Microbiome sequencing data could still have a place in heritability studies. But the feasibility and benefits of this data in GWASs remain to be determined.