



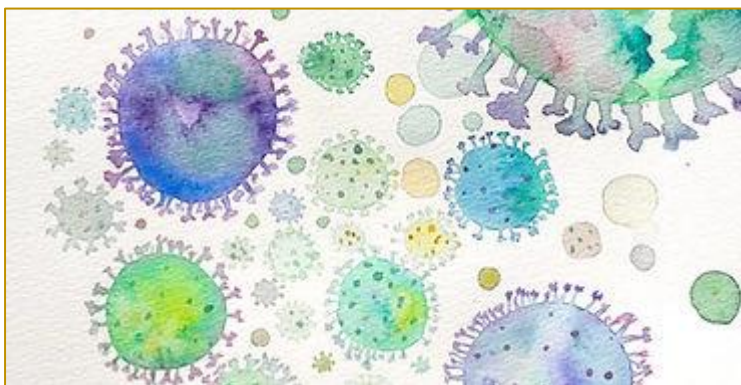
July 26, 2021

Why microbes?

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FindingPheno has taken on the challenging task of analyzing omics data from the holobiont, i.e., plant or animal hosts *and* their associated microbiome. This makes things challenging for our researchers, which leads one to ask ‘Why include microbiomes in our studies’?

The aim is to understand the biological mechanisms giving rise to phenotypic variance. Our researchers want to understand how processes inside plants or animals contribute to their physical outcomes. When this is understood, then changes can be made. To do this,



FindingPheno researchers are developing a new framework to analyze multi-omic data sets, *i.e.* information from various genetic and molecular processes in organisms, to find causal relationships. In recent years, it has become increasingly clear that researchers must also

consider the complex interactions between [organisms and their associated microbiome](#) to better understand this phenotypic variation. There is a multi-way flow of information and biological effects between the different players in the system, host, and microbiome, **meaning that the microbiome is a critical part of why a host is the way it is that should not be ignored.**

What is microbiome research?

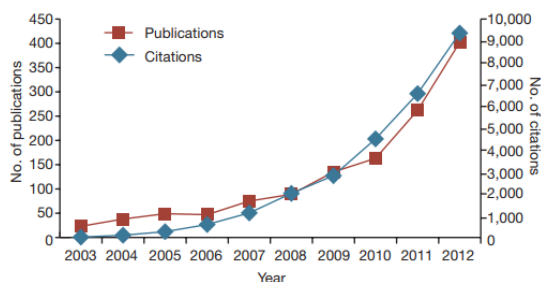
Microbiome research involves characterizing the genetic, species, or metabolic diversity of all microbes (*e.g.* bacteria, viruses, fungi, protozoa) present in a defined environment. FindingPheno researchers are particularly interested in microbes associated with a macrobiotic host, *e.g.* living in the gut of an animal or on the roots of a plant. The rise of microbiome research is driven by the ongoing development of [metagenomics sequencing](#)

tools like 16s profiling or shotgun sequencing, along with microbe-specific versions of other omics like metatranscriptomics, etc.

There are two main ways of looking at microbiomes. The first is cataloging species diversity, *i.e.* working out which microbes are in a given sample and in what proportions. This diversity influences and is influenced by host genetics and the environment, and can [give insights into the health or growth status](#) of the overall system. The second is to consider the metabolic capacity of the microbiome regardless of which exact microbes are providing this capacity, with a focus on the functional genes and proteins present rather than the exact species profile. While the latter approach is [more complex and computationally difficult](#), it [may be more informative](#) for understanding the phenotypic outcomes.

Application areas

The most researched model for microbiome-host interactions is the human, with studies dating as far back as the 1680s when Antonie van Leewenhoek [compared the diversity of his oral and faecal microbiota](#). The rise in metagenomic technology in the past 15 years has dramatically increased interest in human microbiome research, with [an exponential increase in publications and funding in this area](#) (see figure below). These studies provide increasing support for the importance of the microbiome in a wide array of human health phenotypes, with examples ranging from diseases like [obesity](#), [colitis](#), [diabetes](#), and [heart health](#) to more unexpected areas like [behavior](#), [antibiotic tolerance](#), and [response to chemotherapy](#).



Research publications listed in the Thomson Reuters Web of Science per year using the title search terms: human microbiota, human microbiome, microbiome, human microbial, human microbes or gut ecology.

Given that microbiomes are incorporated as a central part of human health-related studies, it is natural to expect that microbiome plays a [similarly significant role](#) in non-human-health-related fields, like [agriculture](#) and [aquaculture](#). Early successes in this area have included the use of probiotic interventions to [improve feed conversion efficiency](#) for animals or provide [germination or growth advantages](#) in crops. It is also likely that having a better understanding of the microbiome could be used to reduce antibiotic use or increase drought tolerance in food production systems. Although the role of the microbiome is now universally acknowledged to be important in these systems, there has been little research investigating interactions between the microbiome, host genome and host gut environment in food production species. **By including microbiome data in FindingPheno and working to analyse this web of hologenomic interactions, we can begin to see what is going on.**

Written: Shelley Edmunds

Updated: Marie Sorivelle