

struggle with microbes—an “us-versus-them” mentality that focused on the necessity of eradicating bacteria—to the more recent understanding that we live in a carefully negotiated state of détente with our commensal organisms. Instead of holding a simple view of microbes as enemies to be eliminated with antibiotics, scientists are increasingly recognizing the critical role these organisms play in maintaining human health; loss of these host–microbe interactions in the increasingly sterile environment typical of Western civilization may have predisposed to the increased incidence of autoimmune and inflammatory diseases. The field of microbiome research has made great strides over the past decade in cataloguing the normal microbiota and is now on the cusp of being able to identify clinically actionable microbe–host relationships.

The recent explosion of “–omics” technologies (e.g., metagenomics, metatranscriptomics, metabolomics) has enabled the generation of vast amounts of data, but it is not yet clear how best to integrate data sets in order to gain useful insights into host–microbe relationships. The use of FMT has demonstrated that modulation of an individual’s microbiota can effectively treat certain diseases; however, models with which to predict specifically how a microbiota will change after modulation—and what potentially untoward effects these changes might have—are still lacking. Implicit in this limitation is our ignorance about what microbial configuration is optimal and how a given microbiota should be rationally altered to obtain an ideal outcome.

Despite initial hyperbolic hype and a few false starts, microbiome research now stands at the forefront of an ability to treat the fundamental basis of many diseases. As the field continues to mature, it will need to move beyond correlations and address causation. The identification of causal microbes and their mechanisms of action will create a “microbial toolbox” from which relevant bioactive strains can be chosen on a per-patient basis to correct specific underlying microbial dysbioses. In the near future, our knowledge base regarding the microbiome and its relationship to health and disease will be robust enough that this information can be applied in making important treatment decisions.