Decoding the human microbiome: Bioinformatics insights into its impact on health and disease.

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Introduction

The interaction between the human microbiome and immune system has an effect on several human metabolic functions and impacts our well-being. Additionally, the interaction between humans and microbes can also play a key role in determining the wellness or disease status of the human body. Dysbiosis is related to a plethora of diseases, including skin, inflammatory, metabolic, and neurological disorders. A better understanding of the host-microbe interaction is essential for determining the diagnosis and appropriate treatment of these ailments. The significance of the microbiome on host health has led to the emergence of new therapeutic approaches focused on the prescribed manipulation of the host microbiome, either by removing harmful taxa or reinstating missing beneficial taxa and the functional roles they perform [1].

Culturing large numbers of microbial taxa in the laboratory is problematic at best, if not impossible. Consequently, this makes it very difficult to comprehensively catalog the individual members comprising a specific microbiome, as well as understanding how microbial communities function and influence host-pathogen interactions. Recent advances in sequencing technologies and computational tools have allowed an increasing number of metagenomic studies to be performed. These studies have provided key insights into the human microbiome and a host of other microbial communities in other environments. In the present review, the role of the microbiome as a therapeutic agent and its significance in human health and disease is discussed. Advances in high-throughput sequencing technologies for surveying host-microbe interactions are also discussed. Additionally, the correlation between the composition of the microbiome and infectious diseases as described in previously reported studies is covered as well. Lastly, recent advances in state-of-the-art bioinformatics software, workflows, and applications for analysing metagenomic data are summarized [2].

As the microbiome field continues to grow, a multitude of researchers are learning how to conduct proper microbiome experiments. We outline here a streamlined and custom approach to processing samples from detailed sequencing library construction to step-by-step bioinformatic standard operating procedures. This allows for rapid and reliable microbiome analysis, allowing researchers to focus more on their experiment design and results. Our sequencing protocols, bioinformatic tutorials, and bundled software are freely available through Microbiome Helper. As the microbiome research field continues to evolve, Microbiome Helper will be updated with new protocols, scripts, and training materials [3].

Viruses are dependent biological entities that interact with the genetic material of most cells on the planet, including the trillions within the human microbiome. Their tremendous diversity renders analysis of human viral communities ("viromes") to be highly complex. Because many of the viruses in humans are bacteriophage, their dynamic interactions with their cellular hosts add greatly to the complexities observed in examining human microbial ecosystems. We are only beginning to be able to study human viral communities on a large scale, mostly as a result of recent and continued advancements in sequencing and bioinformatic technologies. Bacteriophage community diversity in humans not only is inexorably linked to the diversity of their cellular hosts but also is due to their rapid evolution, horizontal gene transfers, and intimate interactions with host nucleic acids [4, 5].

Conclusion

There are vast numbers of observed viral genotypes on many body surfaces studied, including the oral, gastrointestinal, and respiratory tracts, and even in the human bloodstream, which previously was considered a purely sterile environment. The presence of viruses in blood suggests that virome members can traverse mucosal barriers, as indeed these communities are substantially altered when mucosal defenses are weakened. Perhaps the most interesting aspect of human viral communities is the extent to which they can carry gene functions involved in the pathogenesis of their hosts, particularly antibiotic resistance. Persons in close contact with each other have been shown to share a fraction of oral virobiota, which could potentially have important implications for the spread of antibiotic resistance to healthy individuals. Because viruses can have a large impact on ecosystem dynamics through mechanisms such as the transfers of beneficial gene functions or the lysis of certain populations of cellular hosts, they may have both beneficial and detrimental roles that affect human health, including improvements in microbial resilience to disturbances, immune evasion, maintenance of physiologic processes, and altering the microbial community in ways that promote or prevent pathogen colonization.

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References

1. Qian XB, Chen T, Xu YP et al. A guide to human microbiome research: study design, sample collection, and bioinformatics analysis. Chin Med J. 2020 ;133(15):1844-55.
2. Kuczynski J, Lauber CL, Walters WA et al. Experimental and analytical tools for studying the human microbiome. Nat Rev Genet. 2012;13(1):47-58.
3. Chu J, Vila-Farres X, Inoyama D et al. Discovery of MRSA active antibiotics using primary sequence from the human microbiome. Nat Chem Biol. 2016;12(12):1004-6.
4. Zheng J, Gänzle MG, Lin XB et al. Diversity and dynamics of bacteriocins from human microbiome. Environ Microbiol. 2015;17(6):2133-43.
5. Ghosh A, Firdous S, Saha S. Bioinformatics for Human Microbiome. Adv Bioinform. 2021:333-50.

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