

Microbiome and its role in shaping planetary health

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Understanding the relationship between host and microbes is crucial for maintaining human health, and it is imperative to investigate this intricate association in greater depth. Microbes that reside within the human body can have both positive and negative effects, making it vital to differentiate between pathogenic and beneficial microbes in disease conditions. With the advancement of high-throughput technologies, our understanding of host-microbe interactions is improving each day. By analysing the vast amounts of data generated from microbial genomics research, we can better comprehend these interactions, manage diseases and infections, create vaccines and therapeutic targets, and promote the health of both host and microbes.

The main objective of this thesis was to delve into the intricate dynamics of the host-microbe relationship and shed light on the significance of the human microbiome. In Chapter 2, a comprehensive examination is conducted to examine the diverse microbial signatures and compositions observed among individuals. It becomes evident that these microbial profiles are susceptible to various influencing factors, including age, diet, lifestyle, stress, and environment. By studying these fluctuations, it is possible to identify microbial signatures that hold great potential as biomarkers for personalized health management and the overall well-being of communities. These insights pave the way for a deeper understanding of the intricate interplay between the human body and its microbial inhabitants, opening up new avenues for personalized healthcare approaches.

Chapters 4 and 5 of this thesis focus on the use of comparative genomics to assess the virulence potential of sequenced strains. Utilizing genomics data and computational resources, these chapters identify factors that contribute to virulence and antimicrobial resistance. Comparative genomic studies are a valuable tool in the fight against antibiotic resistance, as they can detect emerging pathogens and help determine the pathogenicity of closely related strains within a species. The evolution of emerging pathogens is a significant global health concern, and monitoring this evolution allows for the identification of potential molecular drug targets to combat future infections. Furthermore, comparative genomic studies can reveal novel regions encoded in microbial genomes that allow them to adapt and survive in exposed environment.

Chapter 6 of this thesis lists all major computational tools and resources that play a crucial role in the field of microbial genomics, aiding researchers in the analysis and interpretation of genomics data. This chapter compile most important tools together to provide a resource guide for key steps involved in microbial research. In this chapter tools and databases are listed for genome assembly, genome annotation, metagenomics, antibiotic resistance prediction, virulence factor and potential drug target identification. The purpose of this chapter is to function as a valuable reference guide for researchers facing challenges in finding and selecting the most suitable tools for their analysis.

Chapter 7 of the thesis emphasizes on the significance of genomic surveillance, using the COVID-19 pandemic as a prime example of why monitoring emerging pathogens is crucial. Outbreaks of infectious diseases lead to significant losses in human life and cause socio-economic damages. Modern technologies can produce copious amounts of data that enable us to prepare for and control such outbreaks. However, merely generating data is insufficient; it is vital to store this data in global repositories to facilitate research and report new scientific findings.

Chapter 8 of the thesis provides an exemplary instance of a global cloud repository for storing and sharing health data worldwide. The model proposed in this chapter is founded on a health data cooperative ecosystem that is primarily citizen-oriented ("For the people by the people"). This model represents an exceptional platform for predictive studies in various scientific fields. The availability of data enables its usability, which, in turn, provides significance to the raw data. The platform aims to integrate data from existing science clouds to facilitate global scientific collaboration and provide solutions for planetary health concerns.

Using the research discussed above, I have endeavoured to contribute novel information to the realm of human microbiome. However, additional experimental validations are necessary to make definitive assertions regarding the host-microbe interactions, as the *in-silico* studies are limited in their scope. It is crucial to investigate the molecular level of human microbiome relationships beyond the microbial abundance to gain a deeper understanding of this complex system. While the comparative genomic analysis conducted in this thesis provides valuable insights, experimental validation is still required to ensure that the phenotypic characteristics of the sequenced strains align with the genomic data. It is important to note that the mere presence of antimicrobial resistance genes or virulence factors does not necessarily indicate a pathogenic phenotype of a particular strain.

Like any other scientific work, it is impossible to fully encapsulate the complexity of a topic within a limited number of pages. Nonetheless, I believe the results of my research, which was carried out as part of this dissertation, have made a valuable contribution to the scientific community.