BP-06: Metagenomics: A strategy to study complex microbiota

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Abstract

The development of genome-sequencing technologies, especially the application of next-generation sequencing (NGS), has accelerated the study of complex microbiota.

Metagenomics plays a crucial role in expanding our knowledge of the microbial world, has numerous applications across various fields, and holds the potential to address pressing global challenges in health, the environment, and biotechnology.

This new approach has the potential to uncover novel enzymes, pathways, and molecules with industrial applications. Furthermore, by analyzing metagenomic data, researchers can identify new natural products with therapeutic potential. Many antibiotics, antivirals, and other pharmaceuticals have been discovered through metagenomic approaches.

This work is intended to introduce different research methods to study complex microbiota, with a specific focus on the current progress and application of metagenomics.

We discuss here computer programs used in metagenomics such as MEGAN, Kraken and MePIC that allow analysis of large data sets by a single scientist.

We also highlight the necessity to begin studying complex infections using metagenomics approach, which is essential for better understand the host–bacterial interactions.

Keywords: Metagenomics, microbiota, next-generation, bioinformatic