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Commentary

Metagenomics: An Unbiased Tool for Understanding and Preventing Pandemics

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ABSTRACT

Metagenomics is a branch of genomics that involves sequencing genetic material directly from environmental samples. These data could facilitate evidence-based decisions by providing a more complete view of the microbial ecosystem in a pandemic setting. It would provide essential knowledge for future pandemic preparedness programs.

Metagenomics is a branch of genomics that involves sequencing genetic material directly from environmental samples. By focusing on single organisms and studying the combined genomes of all microorganisms within a sample (1). It offers a holistic view of the microbial community in an environment. Metagenomics has revolutionized our understanding of microbial communities by enabling the assessment of genetic diversity and functional capacity of entire microbiomes, obviating the need to pure culture single bacteria strains in the laboratory (2). One well-documented example is the role of metagenomics in responding to a pandemic, tracking microbial communities through culture-independent techniques that are holistic and can study all microbes at once. We explored the role of metagenomics in pandemic understanding and prevention in this short article.

We can apply metagenomics as a tool of epidemiological surveillance to characterize strains genetic diversity and relatedness in different environments, enhancing the understanding inherited or adapted equilibria of traits governing dynamics transmission within-population (within-host) and between-population (between-host) level processes. It also elucidates the source of an outbreak (wildlife, location, or host species) (3). Scientists can utilize metagenomics — the direct sequencing of genetic material from clinical samples such as blood, saliva or respiratory secretions — to identify and characterise new infections. It also helps determining if the outbreak was due to new or modified viruses (1). The quasispecies genetic diversity of a virus population can also be characterized by metagenomics, which is important to track the evolution of the virus and potentially anticipate changes in transmissibility or virulence (1).

Additionally, it helps in detecting potential zoonotic disease reservoirs and spillover events before they occur, as metagenomics can be performed on environmental specimens. (3). Metagenomics can also be used for the detection of antimicrobial resistance genes from microbial communities, providing insights into the prevalence and spread of resistance in both pathogenic as well as non-pathogenic bacteria (5). Conserved regions of pathogen genomes are targeted for metagenomic vaccine development and since antigens that elicit immune responses can sometimes indicate promising vaccine targets, that helps determine what they might use to build a vaccine. (6).

In conclusion, these metagenomic data facilitates evidence-based decisions by providing a more complete view of the microbial ecosystem in a pandemic setting. It is a powerful weapon in the pandemic response arsenal with information on pathogen identification, epidemiology, antibiotic resistance, diagnostics, vaccine development, and environmental monitoring as well as public health policy in general. Further, metagenomic studies would provide critical knowledge for future pandemic preparedness programs.

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