International Research Journal of Microbiology (ISSN: 2141-5463)
Vol. 10(6) pp. 1-1, November, 2021
Available online @ https://www.interesjournals.org/microbiology.html

Editorial

Clinical Microbiology and Metagenomic Studies

Riyan Diaz*

Department of Medical Microbiology, Jomo Kenyatta University of Agriculture and Technology, Kenya

E-mail: riyandiaz@fsc.jkuat.ac.ke

EDITORIAL

Metagenomic investigations have grown more common as a result of Next Generation Sequencing techniques. Metagenomics, which was first used to describe microbiomes, is now being proposed as a diagnostic tool in clinical microbiology, however this application is still in its early stages. In this overview, we'll look at how metagenomics may be used to detect bacterial pathogens and show how the interpretation of metagenomic results varies depending on the sample type. We do, however, give a perspective on metagenomic applications in antimicrobial resistance testing, epidemic investigations, and forensic medicine. Second, we discuss the significant limitations of metagenomic analysis and application in clinical microbiology. Metagenomics is not yet reliable enough for general application in clinical microbiology, in our opinion.

With the introduction of OMICS technology at the turn of the century, clinical microbiology has changed considerably. The proliferation of molecular techniques has permitted quick diagnosis without the need for a culture step and has transformed how some infections (such as Chlamydia trachomatis-related infectious sexual disorders) are discovered. At the same time, MALDI-TOF mass spectrometry and its application to clinical microbiology have made it easier to identify cultivated microbes. Microbial antibiotic sensitivity testing is now the most time-consuming aspect of the diagnosing process. The Koch postulate emphasises the importance of a pure culture of a microbe to prove pathogenicity in traditional clinical microbiology approaches. However, culture appears to have been abandoned since the development of molecular techniques and metagenomic investigations. Nonetheless, some scientists' predictions that molecular technologies will eventually supplant pure culture were quickly dismissed.

The premise of metagenomics is based on the genomic analysis of a sample from a complex environment comprising several microorganisms, which gives a view of the sample's composition. With the advent of Next Generation Sequencing, metagenomic research has become more accessible (NGS). NGS can be used for metagenomic analysis in two ways: focused metagenomics (which focuses on a single amplified region, such as the 16S region) or shotgun metagenomics (which entails amplification of all sequences in a sample without making any assumptions about its composition). We recommended reviewing the present applications of metagenomics in clinical microbiology in this review, with an emphasis on the hazards of these approaches and the difficulty in interpreting them. We propose testing if metagenomics can be employed as a diagnostic tool right now.

Pathogens have been detected using metagenomics in clinical samples. We'll go through how it's used in bacterial microbiology. The majority of studies compare metagenomics to the classic culture approach. However, in other circumstances, metagenomic analysis has been used to make diagnoses that could not be made using culture or traditional molecular methods. Metagenomics has been used as a method for prospective diagnosis in only a few researches. Wilson et al. were the first to report an encephalitis case that was solved by shotgun metagenomics. Despite significant research, which included 16S rRNA amplification and cerebrospinal fluid sequencing, no cause had been identified. Metagenomics revealed that leptospirosis was present in the Cerebrospinal Fluid (CSF), but not in a control sample. Specific molecular techniques and serology were also used to validate the diagnosis. In clinical microbiology, metagenomics is still uncommon.

Despite the fact that this technology has been used to discover bacterial infections in clinical samples in roughly fifteen researches, metagenomics appears to have been the only instrument used in only two of them. Although the use of metagenomics to detect ARGs appears to be promising, it has yet to be put to the test as a routine technique for changing antibiotic treatment. Other applications, such as epidemiology and forensic medicine, are yet hypothetical. Due to many biases in its interpretation, lack of standardisation and availability in only a few large laboratories, democratisation of this technology is impossible at this time. Using standard culture methods or simpler molecular technologies like real-time PCR, we were able to diagnose the majority of cases in our study. To summarise, we believe that metagenomics is now insufficiently reliable for widespread application in clinical microbiology.