

Point of view

Usefulness of metagenomics for management of problematic paediatric infection

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Infection is an important problem in paediatrics. Clinically, an infectious disease is a condition where the pathogen causes pathological changes in a host. In clinical epidemiology, there is a triad (host, agent, and environment) for occurrence of an infection. Environment is the surrounding space for host and pathogen inter-relationship. The host and pathogen must interact in an appropriate period at the same time and same place in the same environment. Therefore, the environmental factor is a very important determinant of an infection.

Based on modern computational technology, genomics is a useful biomedical technology at present for both clarification and prediction purposes¹. Genomics is the study of whole genomes of organisms, and incorporates elements from genetics². Genomics uses a combination of recombinant DNA, DNA sequencing methods, and bioinformatics to sequence, assemble, and analyse the structure and function of genomes². The data from genomic studies are helpful for early prediction of disease outbreaks and can predict the course of endemic diseases that might vary by season and region. In addition to a genomic study on clinical specimens, genomic application to environmental specimens or metagenomics is a very useful tool at present. Metagenomics is based on the genomic study of specimens collected from environmental sources³.

In general, the pathogen usually exists in the host or resides as a contaminant in the environment. The existence of pathogens in the environment is an important consideration in clinical medicine. The

metagenomic approach is the present modern standard technology to assess contamination in the environment. Metagenomic study can determine the environmental contamination rate that can represent risk or causal relationship to the infectious disease. The role of metagenomics is clearly seen in the case of an outbreak. The metagenomic tool can provide data on the exact kind of problematic contaminant and can be useful for prediction of the pattern of contamination and the course of an infectious disease. Therefore, there is no doubt that metagenomics is very helpful in clinical infectious medicine⁴. For a new emerging infection, metagenomics can help clarify the environmental contamination of a new emerging pathogen and can also give scientific evidence that the new emerging disease is transmittable due to contamination. Additionally, environmental surveillance by the metagenomic technique can give useful information for public health policy planning against the problematic infection. Finally, metagenomics is helpful for tracing genomic diversity of pathogens in an evolutionary view. The phylogenetic pattern of the studied sample can help identify the root of a new pathogen⁵.

In clinical paediatrics, there are many good examples of applied metagenomics. Mosquito borne infections and respiratory virus infections are the two groups of paediatric infections that show clear advantages from applied metagenomics. The studies on metagenomes of mosquito-borne viruses are useful for clarifying the diversity of viruses with mosquito species and the geographical locations. The region-specific pathogen origin can be shown by micro-biodata marker, such as predominant bacterial population change due to arbovirus, derived from metagenomic study⁶. Regarding respiratory infections, metagenomics can help identify the infectious surfaces. In the present COVID-19 pandemic, many contaminations at several surfaces, such as lockers, are confirmed as sources for disease spreading. A metagenomic study can also provide concrete scientific evidence for confirmation of the risk contamination that might be a possible transmission vector of the virus. For example, during the COVID-19 outbreak, there is evidence of metagenomic identification of

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pathogenic virus in sewage⁷. It is also proposed that metagenomic monitoring of contamination in waste water might be useful for surveillance of disease⁸. There is no doubt that the metagenomic tool is useful for management of problematic paediatric infection but it might not be widely used due to a possible resource limitation in the poorer developing settings where infectious diseases are usually common.

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