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Next generation sequencing: How useful is it in TB diagnosis and research in resource limited settings

Mandira Varma Basil
University of Delhi, India

Tuberculosis (TB), though curable and preventable, is still a major cause of illness and death in most developing countries. TB is one of the top most among highly infectious diseases in the world. Globally, of the 10 million cases of active TB, 1.3 million deaths were reported in 2017. The World Health Organization (WHO) has stated that of the incident TB cases missed from the TB surveillance system, two thirds were not reported and remaining one third were not detected. This underscores the importance of rapid and effective methods of TB diagnosis. Traditional laboratory techniques are time consuming and cumbersome and not sufficiently sensitive or specific to fight this menace, especially in the face of increasingly prevalent drug-resistant TB. Though rapid molecular methods such as GeneXpert and line probe assays are vital tools in the fight against TB, major advances in Next Generation Sequencing (NGS) technology are allowing increasingly rapid and accurate sequencing of entire bacterial genomes, providing unprecedented depth of information. NGS has the ability to cause a revolutionary paradigm shift in the diagnosis and epidemiological study of Mycobacterium tuberculosis infection. Current applications of NGS for TB diagnosis include sequencing cultured isolates to predict drug resistance and even direct diagnostic sequencing from clinical samples. The recent increase in cost effectiveness of NGS for Whole Genome Sequencing (WGS) analyses has also rapidly increased the utility of this method for outbreak detection and surveillance. However, certain challenges need to be overcome to enable the use of this promising technology in routine diagnosis and research, especially in resource limited regions of the world.

mandirav@rediffmail.com