

# METAGENOMIC PROFILING OF POTENTIAL PATHOGENS ISOLATED FROM BLOOD SAMPLES AND TRACHEAL ASPIRATES OF CRITICALLY ILL CHILDREN WITH PERSISTENT FEVER UNRESPONSIVE TO BROAD-SPECTRUM ANTIBIOTICS

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**Abstract.** Critically ill children with refractory fever despite broad-spectrum antimicrobial therapy are common encountered in infectious disease. Causes of persistent fever in these cases are rarely identified by conventional diagnostic methods. Clinical metagenomics provides a promising approach to identify known and novel pathogens when currently available methods fail to yield diagnosis. Potential pathogens in blood and/or tracheal aspirates from critically ill were identified from 34 critically ill children <15 years of age with refractory fever despite receiving broad-spectrum antibiotics using a metagenomic shotgun sequencing platform. Multiple microorganisms were identified in 82% of blood samples, with *Stenotrophomonas maltophilia* and *Mycobacterium chelonae* being the two most common bacteria (62% each), followed by *Pseudomonas aeruginosa* (9%). The three most common viruses identified in blood were herpes simplex virus/HSV (26%), rhinovirus (20%), and human bocavirus (HBoV) (9%). Distribution of organisms in tracheal aspirates was comparable to that in blood samples. In conclusion, the metagenomic technique allowed identification of both potential pathogenic bacteria and viruses in blood and trachea of critically ill children with refractory fever and receiving broad-spectrum antibiotics; however, these findings should be interpreted with caution as no data from a case control group were available.

**Keywords:** *Mycobacterium chelonae*, *Stenotrophomonas maltophilia*, children, critically ill, fever, metagenomics, pneumonia, respiratory failure.

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