

Small RNA datasets of drug-susceptible *Mycobacterium tuberculosis* strains from Sabah, Malaysia

ABSTRACT

These datasets present a list of small RNAs from three drug-susceptible *Mycobacterium tuberculosis* strains isolated from Sabah, Malaysia. Sputum samples were obtained from three tuberculosis patients belonging to different districts. The bacteria were detected using GeneXpert MTB/RIF, isolated and cultured in BACTECTM MGITTM 320, and tested for their drug susceptibility. Total RNAs were extracted, sequenced, and analyzed using bioinformatic tools to filter out small RNA present in the *Mycobacterium tuberculosis* strains. Small RNA sequencing generated total raw reads of 63,252,209, 63,636,812, and 61,148,224 and total trimmed reads (15-30 nucleotides) of 51,533,188, 53,520,197, and 51,363,772 for *Mycobacterium tuberculosis* strain SBH49, SBH149, and SBH372, respectively. The raw data were submitted to the Sequence Read Archive (SRA) database of the National Center for Biotechnology Information (NCBI) under the accession numbers of SRX16744291 (SBH49), SRX16744292 (SBH149), and SRX16744293 (SBH372). Small RNAs play important roles in cellular processes such as cell differentiation, cell signaling, development of resistance to antibiotics and immune response, and metabolism regulation. The small RNAs determined here could provide further insights into various cellular processes crucial for *Mycobacterium tuberculosis* survivability and a better understanding of their gene regulation which ultimately opens a new pathway for combating tuberculosis infection.