

## ABSTRACT

Tuberculosis caused by an obligate aerobic bacteria known as *Mycobacterium tuberculosis* is one of the most lifelong diseases that has been infecting humans worldwide; Indonesia is one of the countries that has the highest prevalence of tuberculosis. The bacteria itself possesses an atypical cell wall structure that protects them from harmful drugs. With the inconsistent, prolonged drug treatment, it initiates the presence of mutations in the bacterial genome causing drug-resistance. Up until today, there has been difficulties in detecting drug-resistant tuberculosis (DR-TB) as its gold-standard relies on methods that are time consuming, prone to contamination, and require high investments. With the advancement in technology, Oxford Nanopore Technology (ONT) offers real-time sequencing with rapid processing time for detection of DR-TB by detecting mutations associated with it; at the same time, there has not been any investigation on the most prevalent DR-TB present in Jakarta and West Java, few of the most populated areas in Indonesia. Using the undisclosed TB kit from ONT prevalence of DR-TB classifications was discovered, in which the majority of the samples were found to be RR-TB (48.8%), followed by MDR-TB (30.2%) and few XDR-TB (11.6%) samples. Drugs associated with the resistance include RIF, INH, EMB, PZA, ETH, STM, LEV, and MXF, which are the common drugs administered in treating TB. Each of the mutations responsible for drug-resistance was also discovered, conveying similar results with previous studies.

**Keyword:** Drug-resistant tuberculosis; *Mycobacterium tuberculosis*; Genetic profiling; Oxford Nanopore Technology