

Establishment and clinical application of rapid and highly accurate identification method for nontuberculous mycobacteriosis by real-time core genome analysis

Principal Investigator

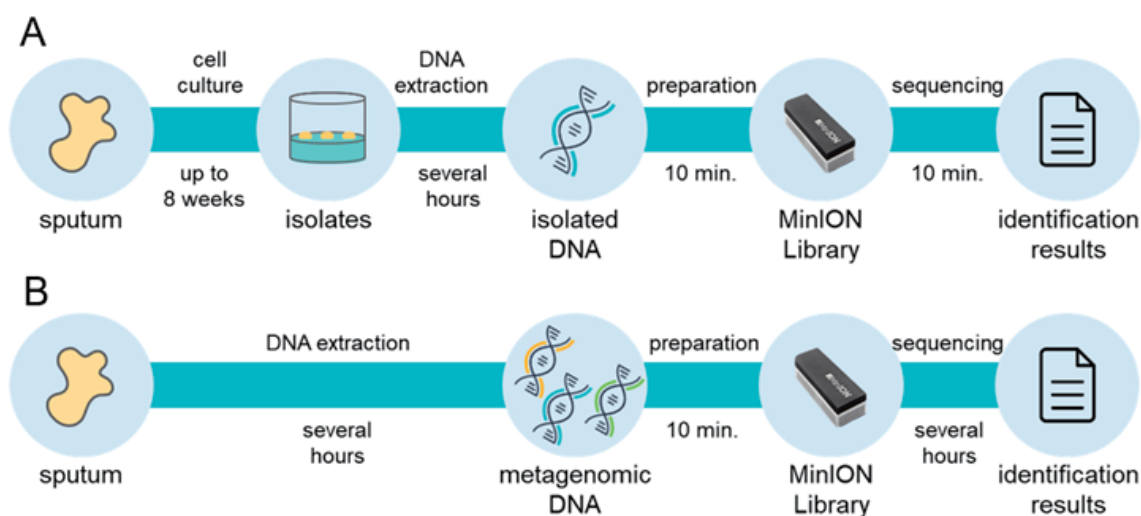
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Project Outline

Nontuberculous mycobacteriosis (NTM disease) has been increasing in recent years, and rapid identification of causative organism is required, but conventional test methods using culture tests require weeks to identify the causative bacteria. The applicants have established a method that enables subspecies identification in cultured samples in about 10 minutes by nanopore sequencing method and core genome analysis using an original NTM database and software. It has already been confirmed that direct identification from sputum specimens is possible using mycobacteriosis patient specimens. Therefore, the time schedule from diagnosis to treatment in clinical practice can be significantly shortened.

Real-time identification of NTM bacteria by direct sequencing technology



Although nontuberculous mycobacteriosis has been increasing in recent years, it takes weeks to identify the causative bacterium by the conventional test method using the culture test, and the identifiable bacterial species are limited. We will establish a method that enables rapid and comprehensive identification of bacterial species and accurate identification of drug resistance, and verify the effectiveness of real-time analysis in prospective clinical trials.