RESEARCH INSTITUTE FOR MICROBIAL DISEASES
OSAKA UNIVERSITY

RIMD
Research Institute for Microbial Diseases
大阪大学微生物病研究所

SEMINAR INFORMATION

2024.10.28.16:00 @ BIKEN HALL

TITLE:

AI-enabled identification of Antibiotic Resistance Bacteria (ARB) and Antibiotic Resistance Genes (ARGs) from the sputum at the genome and metagenome levels.

SPEAKER:

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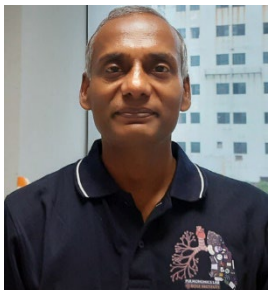

ABSTRACT:

Sputum is the most prevalent clinical sample used for diagnosing respiratory diseases, including tuberculosis (TB) and chronic obstructive pulmonary diseases (COPD). In TB, the emergence of Bedaquiline (BDQ) resistance strains of Mycobacterium Tuberculosis (MTB) poses a severe threat to the End TB Strategy proposed by WHO. The absence of any defined resistance locus and the wide variation in the drug targets across BDQ-resistant clinical isolates have put a big question on our understanding of the molecular basis of BDQ resistance acquisition. We have applied deep learning-based machine learning (ML) to whole genome sequencing (WGS) data of MTB clinical strains available in the public domain and were able to predict BDQ resistance in MTB with an accuracy of 84%. We also can predict the BDQ-resistant genes. BDQR-MTB web server (http://bicresources.jcbose.ac.in/ssaha4/bdqr-mtb), and a standalone application, named BDQR- MTB-standalone, were developed for end-users to perform the BDQ resistance predictions on FASTQ and VCF format files for the WGS sequences of MTB clinical isolates. In another study, we used the Random Forest model in metagenomics data obtained from sputum samples of COPD patients. Acute exacerbations in COPD accelerate lung function deterioration and are associated with dysbiosis in the sputum microbiome. Genus Streptococcus and Moraxella were enriched in exacerbation, while Veillonella and Haemophilus were upregulated in the stable stage. The resistome profile of the COPD sputum indicates the presence of antimicrobial resistance genes, providing resistance to a wide range of antibiotics such as fluoroquinolone, tetracyclines, macrolide, and amminoglycosides. In summary, AI was first applied to the genome of MTB to predict BDQ-resistant strains and to the microbiome sputum metagenome to predict the acute exacerbations of COPD and its resistome profile.

No registration required.

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