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Clinical Proteomics and Bioinformatics: Exploring Drug Resistant Tuberculosis

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Editorial

Tuberculosis (TB) is a major public health problem across the globe. As per WHO, 10.4 million new TB cases and 1.8 million deaths occur annually [1]. In developing countries, TB burden among the healthcare workers is a serious issue [2] and spreading of drug-resistant Mycobacterium tuberculosis strains further worsened the situation which leads to the emergence of multidrug-resistant tuberculosis (MDR-TB), extensively drug-resistant tuberculosis (XDR-TB) and totally drug-resistant tuberculosis (TDR-TB). Use of effective diagnostics and therapeutics strategies are the only valid options to combat the situation of global antibiotic resistance [3,4]. Researchers have paid attention in this direction and trying to develop alternative strategies against global antibiotic resistance. Repurposing of the drugs against the antibiotics resistant M. tuberculosis infection has been considered as an effective strategy and might be shown the positive outcomes in the treatment of MDR-TB, XDR-TB and TDR-TB [4]. Still, our current therapeutic strategies are unable to give complete protection against antibiotics resistant TB infections. Therefore, an urgent need is required for developing the possible diagnostics and therapeutic strategies against the antibiotics resistance.

Proteomics and Bioinformatics: Possible Diagnostics and Therapeutic Strategies against Drug Resistance

Since the last decade, mass spectrometric-based proteomics and bioinformatics emerged as advanced approaches to understand the biology of M. tuberculosis pathogenesis and drug resistance [5-15]. Clinical proteomics related to the first and second line drug-resistant M. tuberculosis isolates have been accumulated which lighten the pathobiology and resistance biology of these strains [5-15]. Differential expressions of known and hypothetical proteins (functionally unknown) have reported in drug-resistant strains of M. tuberculosis. In-silico analysis (Molecular Docking, KEGG Pathways, Pupylome, and Interactome) of these proteomes explored the possible pathways as well as subsequent targets involved in the drug resistance [16-21]. Selected proteins and subsequent targets of the affiliated pathways might serve as the possible diagnostics and therapeutic targets for the development of alternative strategies against the drug resistance. In-depth study of these proteins may lead to biomarkers and drug targets discovery which contribute to the quick diagnosis of the drug resistance and effective therapeutics against the bad bugs.

Conflict of Interest

There is no conflict of interest between the authors.

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