

7th World Congress on

Mass Spectrometry

June 20-22, 2018 | Rome, Italy

Exploring aminoglycosides resistance in *Mycobacterium tuberculosis* isolates by proteomics and mass spectrometry

Deepa Bisht

National JALMA Institute for Leprosy & Other Mycobacterial Diseases (ICMR), India

Tuberculosis (TB) caused by the pathogen *Mycobacterium tuberculosis* (MTB) still remains a major global public health issue. India is a country burdened with high TB. Increasing incidences of multidrug-resistant strains and of co-infection with HIV, urgently demands better control measures. Aminoglycosides are broad spectrum antibiotics and are an important component of any antituberculosis therapy regimen and drugs of choice especially for category II patients. Streptomycin (SM), kanamycin (KM) and amikacin (AK) are the key aminoglycosides drugs against TB and resistance to these severely affects the options for treatment. They inhibit protein synthesis by interacting with steps of translation. Several explanations have been put forward for aminoglycosides resistance but still our understanding is fragmentary. As proteins manifest most of the biological processes, these are attractive targets for developing drugs, immunodiagnostics or therapeutics. Two-dimensional gel electrophoresis is an extremely powerful tool to dissect multiprotein complexes. Whole proteome analysis of aminoglycosides susceptible and resistant isolates by two-dimensional gel electrophoresis and their identification by mass spectrometry and bioinformatics tools have been carried out. Some proteins were found to be overexpressed in resistant isolates. Few of these were identified as hypothetical proteins. *In silico* docking analysis showed significant interactions of these drugs with hypothetical proteins. Characterization of hypothetical proteins may provide information about new targets against resistant TB or some new more effective vaccine candidates.

Biography

Deepa Bisht completed her PhD in Biotechnology from the Institute of Microbial Technology, Chandigarh, India. Presently she is working as Scientist E at National JALMA Institute for Leprosy & Other Mycobacterial Diseases (ICMR), India. Her research areas are mycobacterial proteomics and drug delivery systems and she is involved in understanding the resistance mechanism of aminoglycosides resistant *Mycobacterium tuberculosis* clinical isolates by proteomics approaches.

abd1109@rediffmail.com

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