Report on Lecture

Topic: "Cloning, Expression, Purification and Structural Studies of Adenosine Deaminase from *Mycobacterium tuberculosis (MtbADA)*"

Speaker: Dr. Sanjit Kumar

Date: 17/05/23

Time: 11.45 AM and 1.15 PM

Venue: Department of Biotechnology, DAVV Indore

The welcome address was given by Professor Anjana Jajooin which she introduced Dr. Sanjit Kumar, Associate Professor, Guru Ghasidas University (A Central University), Bilaspur. He talked on antibiotic resistance as well as the complications associated with Mycobacterium tuberculosis. Mycobacterium tuberculosis is highly pathogenic bacteria. M. tuberculosiscauses causes highly communicable pulmonary infections called tuberculosis (TB). World health organization in its report has declared tuberculosis as one of the most infectious diseases with high fatality rate across the world. In present times, multidrug resistant (MDR) strains of tuberculosis have raised a concern among medical professionals with respect to management of patients infected with MDR strains of M. tuberculosis . Adenosine Eeaminase (ADA) is one of the several enzymes of Salvage pathway of purine synthesis which maintains adenosine homeostasis in the cell and protects the cells from toxic concentrations of adenosine. Adenosine deaminase from mycobacterium tuberculosis has not been characterized. Moreover, no inhibition studies by various ADA inhibitors on mycobacterial ADA (MtbADA) have been carried out to date. In his lab, they have expressed and purified MtbADA. Molecular modeling and sequence analysis has shown that the molecule has stable three dimensional structure. Insilico and kinetic studies have shown that taxifolin binds to the active site and could be a potential therapeutic molecule against MtbADA.

He discussed the benefits of using a variety of structural biology techniques, such as X-ray crystallography, nuclear magnetic resonance, and cryoelectron microscopy. He also covered hands-on training on homology modeling and docking studies for drug design. In between talk he mentioned about several bioinformatics programs like Open Babel, SWISS ADME, AUTODOC, YASARA, and GROMACS.

The talked concluded with many questions and clarifications from faculty members and students present in the audience. After this, there were conversations taking on offstage between the speaker and the audience.