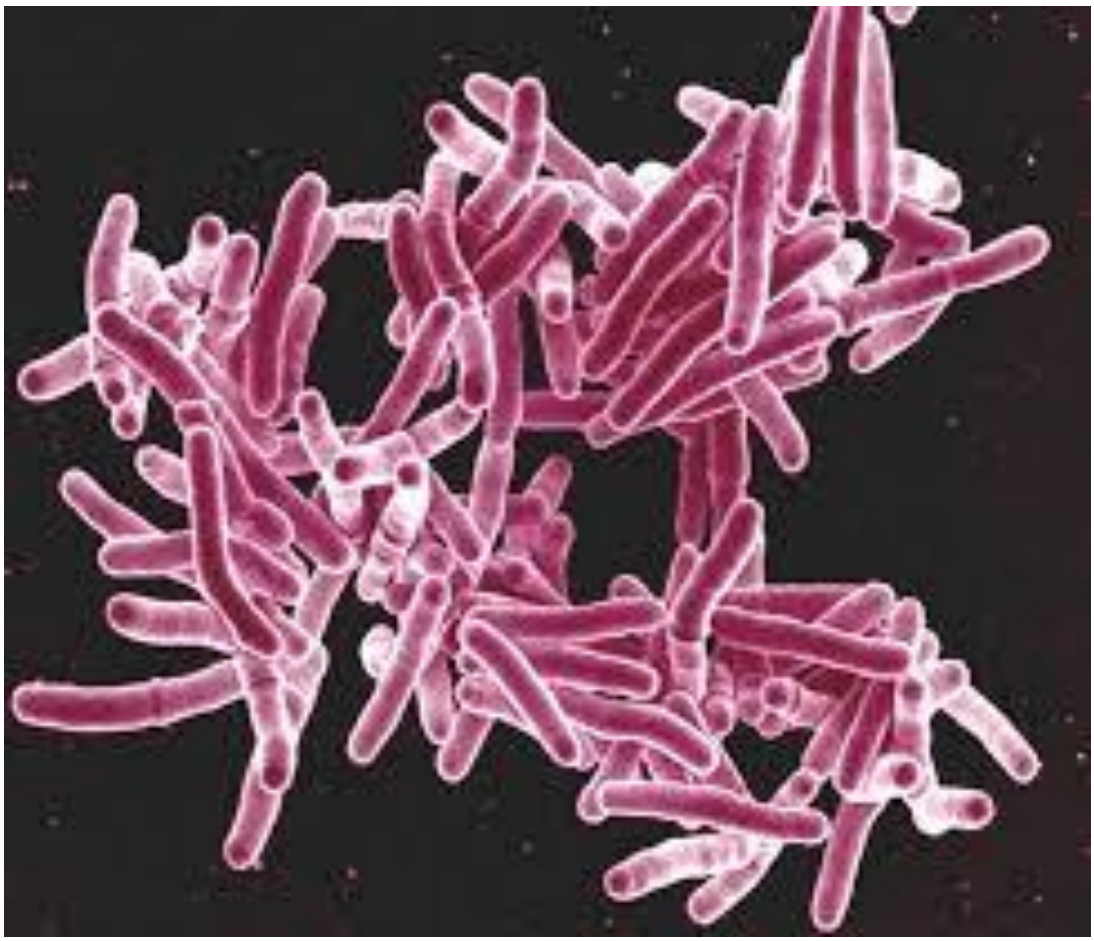
Study at DBT-THSTI may pave way for new TB drugs and vaccines



New Delhi, June 08: Tuberculosis (TB) is a highly infectious disease caused by a bacterial pathogen called *Mycobacterium tuberculosis* (MTB) that predominantly attacks the lungs. It is a leading cause of death worldwide, and many people are affected by it without showing any symptoms. The bacterium has co-evolved with humans and learned to replicate and survive inside the macrophages that are supposed to kill it. The infection of macrophages by the bacterium alters the proteins responsible for killing bacterial pathogens.

To understand these protein modifications better, researchers at the Department of Biotechnology's Translational Health Science and Technology Institute (DBT-THSTI), Faridabad did a comparative study of the complete set of phosphorylated proteins of macrophages on being infected by TB and a non-pathogenic bacterium called *Mycobacterium bovis* (BCG).

Phosphorylation is one of the most crucial protein modifications which helps in regulating the cellular response in our body. In this study, researchers determined the differences in the macrophage response on being infected by a pathogenic and non-pathogenic bacterium. This is done by studying the entire set of proteins of macrophages undergoing phosphorylation.

The technique used is mass spectrometry, which is considered the best method to compare pairs of protein samples efficiently.

A macrophage protein, cytosolic RIG-1, is known to play an essential role in immune response during viral infection. It releases various kinds of chemical mediators triggering immune response to fight the pathogens. But in response to MTB infection, these proteins are found to perform a contradictory role: they help in the survival of MTB in macrophages.

This research study is the first one to provide comprehensive information on relative and quantitative protein modifications in the complete set of proteins of macrophages. It gives new information on the differential sites where protein modifications occur in macrophagic proteins. This would help understand unexplored pathways useful in controlling tuberculosis, and protection through prospective vaccine candidates. It could also be useful in future for designing new drug targets for treating tuberculosis. The protein modification sites can target macrophagic proteins for drug designing.

The article on the study can be accessed at:
https://pubs.acs.org/doi/abs/10.1021/acs.jproteome.9b00895

Contact person: Dr. Siuli Mitra (smitra@thsti.res.in)

DBT-THSTI website: https://thsti.res.in/

Phone: Reception: 0129-2876300/350