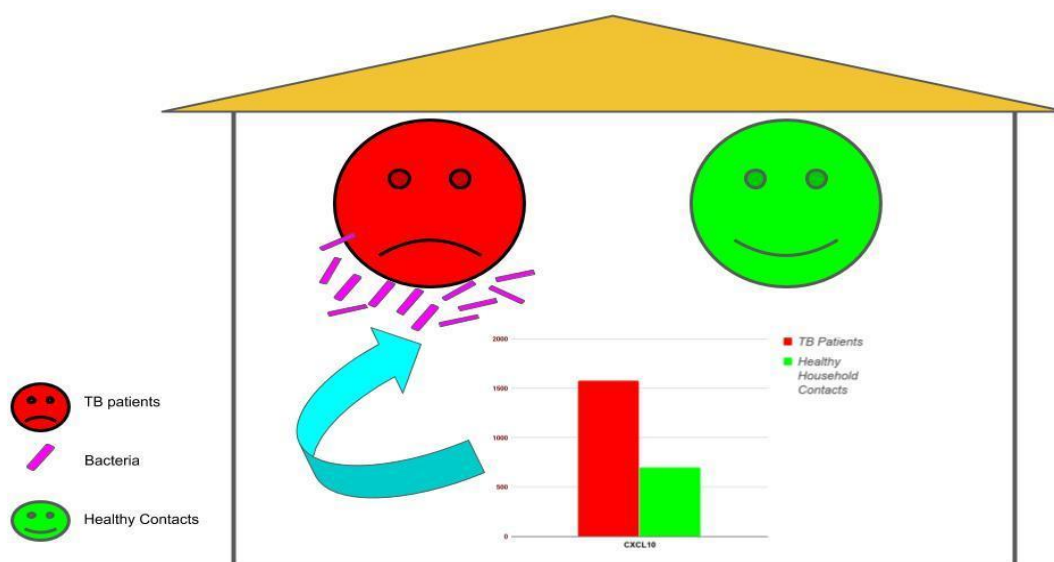


DBT-NIBGM researchers identify a potential biomarker for TB

New Delhi, Aug 05: Though an ancient disease, Tuberculosis (TB) is still among the top ten causes of death. In 2019 alone, the nationwide death toll due to TB was 0.4 million and 2.69 million people were infected. Upon exposure to the causal pathogen *Mycobacterium tuberculosis*, some people develop active disease with clinical symptoms like fever, weight loss, and coughing up of blood, requiring treatment, while many other individuals do not develop active disease in spite of harboring the pathogen. Many people can clear off the infection spontaneously. Investigation on critical host factors that act as weapons against the *Mycobacterium* is the main theme of a study conducted by the Department of Biotechnology's National Institute of Biomedical Genomics (DBT-NIBGM).



Variable clinical outcome is essentially a result of various human and bacterial factors, playing together. To underpin the plausible host factors, a team of researchers at the Institute designed a study with a bunch of TB patients and their healthy household contacts, preferably spouses. The healthy contacts did not develop any diseases in spite of sharing the same environment even for a long period of time.

They hypothesized that cytokines/chemokines, a type of secretory proteins from immune cells, are one of the first lines of defense against the invading bacteria. Consequently, the levels of these cytokines/chemokines would be altered among TB patients compared to their asymptomatic household contacts.

To accomplish their aim, the researchers enrolled the clinically and microbiologically confirmed TB patients on the very first day of their visit to the clinic before treatment starts. Next, they enrolled their spouses, if they remained disease free for at least next ninety days. They performed a comparative study on twenty two cytokines, relevant in mycobacterium infection, from plasma samples of enrolled TB patients and their household contacts. After

doing all the statistical analysis, they found that one chemokine named CXCL10 was significantly high among the TB patients. Interestingly, the level of CXCL10 protein also showed a positive trend with the severity of the disease.

Next, they checked whether this altered expression of CXCL10 protein was due to the underlying variations in the CXCL10 gene of the individuals, instead of being due to the TB infection. To further strengthen their finding, CXCL10 protein was higher in TB patients irrespective of their sequence variation at CXCL10 gene, compared to healthy individuals. Active phase TB antigens were able to stimulate CXCL10 in-vitro, but not others.

The finding of the researchers raises a possibility of considering this protein as a marker for active phase of infection. However, further community-based large scale studies are warranted to evaluate its potential as a candidate biomarker of tuberculosis infection.

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