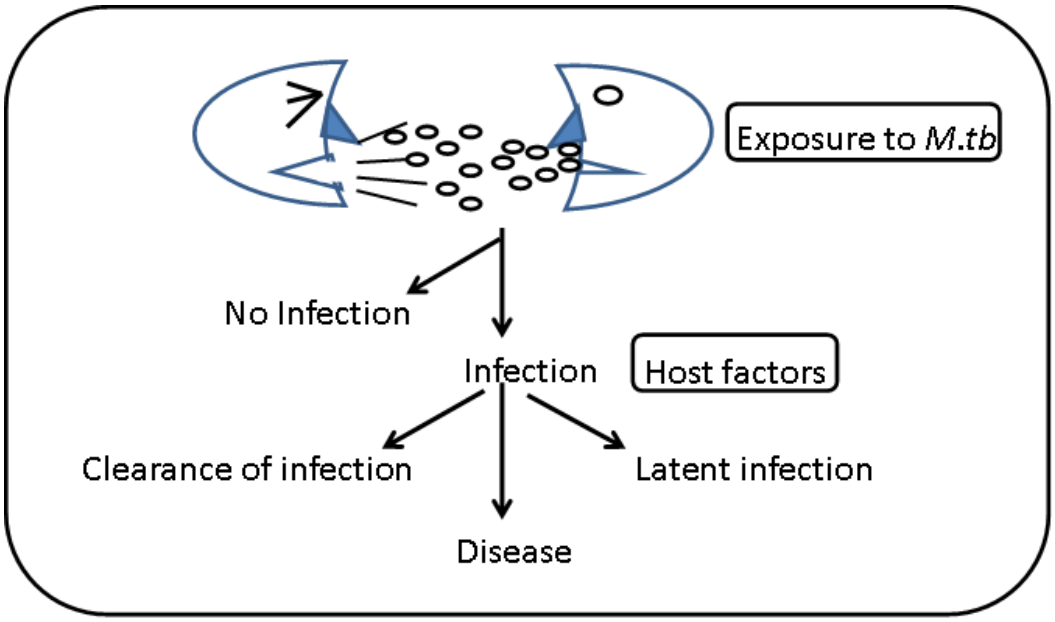
Scientists at NIBMG tried to explore the role of host genomics in understanding tuberculosis

To understand the contribution of genetic component of diverse response to *Mycobacterium tuberculosis* infection, studies on host genetics have been undertaken by researchers at DBT's National Institute of Biomedical Genomics (DBT-NIBMG), Kalyani. Twin studies suggest that the concordance of tuberculosis is higher among monozygotic twins than dizygotic twins. in this study. it was observed that difference in genetic background of animals results in a variable degree of severity when infected with *M. tuberculosis*. There are multiple approaches to identify the genetic region controlling response to infection. Screening and comparing genome of infected individuals in a family or the community to non-infected individuals will provide information on the genetic region. Comparing similar genetic regions identified in animals can give clue about new genes in infection. Genes with demonstrable role in infection or functionally linked to immunity are also considered to be candidates for such variability.



The studies undertaken unravelled the role of host genes in tuberculosis infection. Exomes are part of the genome that makes functional proteins. Study tested the variability in the exome to find any association with tuberculosis infection and identified the novel variants or polymorphic nucleotides in *SIGLEC15* and *HLA-DRA* genes. Exploration on the function of these variants may help us to understand the mechanism of conferring protection or risk to an individual. The

variants in the genome can differ from one population to other. Therefore, attempts to identify variants in the genome and its functional association with infection are essential to understand inter-individual variability in disease severity, treatment and response.

Tuberculosis is a deadly disease associated with human civilization from ancient times. *Mycobacterium tuberculosis* is the causative agent which is transmitted from an infected person in form of aerosol droplets. World Health Organization estimates worldwide approximately 10 million new infected cases every year. Exposure to *M. tuberculosis* does not ensure disease in every individual. It is the resultant output of complex interaction of two genomes, the host and pathogen with environmental factors. The genetic makeup of an individual plays major role in determining the fate of exposure. Only a minor group of people develop active tuberculosis. Many individuals are able to clear the infection whereas majority of infected individuals carry the infection in latent condition and serve as a reservoir. Why such variability? The answer lies in the genome of an individual.

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