

The 'MIP-MAP' game: Indian bug is the ancestor of Crohn's disease pathogen

October 3 2007

An Indian team of researchers led by Seyed E. Hasnain of the Institute of Life Sciences (ILS), University of Hyderabad, India has found that a seemingly unknown mycobacterial organism *Mycobacterium indicus pranii* (MIP) could be the earliest ancestor of the 'generalist' branch of mycobacterial pathogens.

The 'generalist' bacteria infect anything from cockroaches to human and are capable of surviving in soil and water as against human adapted 'specialists' such as tubercle and leprosy bacilli. TB, a disease that killed about 1.7 million humans last year alone, is caused by a member of the Mycobacterial family of pathogens.

The finding further suggests that the prominent 'generalist' pathogen *M. avium* which seriously haunts AIDS patients, together with its close associate *M. avium paratuberculosis* (MAP), the agent of Crohn's disease in humans and Johne's disease in cattle descended from the MIP. It was also found that the MIP and the MAP bacilli initially inhabited water bodies and infected marine organisms predated by fishes finally arriving on soil through bird-droppings.

The MIP bacilli, also called as *Mycobacterium w* (Mw) were first isolated in India by G. P. Talwar at the All India Institute of Medical Sciences, New Delhi, in eighties and it is currently used, after an extensive and perhaps the largest clinical trial in the world, as an immunotherapeutic against leprosy in India. The success with MIP based leprosy vaccine has led to human clinical evaluations of MIP in

interventions against HIV-AIDS, psoriasis and bladder cancer in India. MIP, commercially available as 'Immuvac', is currently the focus of advanced multi-centric phase III clinical trials for its antituberculosis efficacy.

The comparative genomics study based on complete sequence of the MIP organism published in October 2, 2007 release of the prestigious open access journal PLoS ONE reports observations based on the first ever whole genome sequencing project from India, carried out jointly by the ILS, the Centre for DNA fingerprinting and Diagnostics also at Hyderabad and the University of Delhi.

The study provides an important evolutionary basis for the acquisition and optimization of virulence in mycobacteria and determinants of boundaries therein. Similarly these efforts constitute a step forward in understanding the role of non-pathogenic and saprophytic mycobacteria in immunomodulation and in triggering innate immune responses. The study advocates exploitation of genetic similarity between MIP and MAP as a plausible advantage for therapeutic intervention against Crohn's and Johne's diseases.

Source: Public Library of Science

Citation: The 'MIP-MAP' game: Indian bug is the ancestor of Crohn's disease pathogen (2007, October 3) retrieved 26 April 2024 from <https://phys.org/news/2007-10-mip-map-game-indian-bug-ancestor.html>

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