Immune evasion common in many viruses, bacteria and parasites is uncommon in M. tuberculosis

EurekAlert

(New York, NY, May 23, 2010): Scientists at NYU Langone Medical Center have discovered that the strategy of "immune evasion" common to many viruses, bacteria and parasites, is uncommon to M. tuberculosis where the antigens remain strikingly unchanged and homogenous. The study published in *Nature Genetics* on May 23, 2010, suggests that M. tuberculosis antigens do not mutate because they hope to be recognized by the body's immune system? perhaps because the host immune mechanism that leads to the typical lung destruction and cough can contribute to the spread of the disease. This finding has the potential to change the direction of vaccine research and could result in a new focus on different targets of immune response to the bacteria.

"The finding that the tuberculosis bacterium acts completely differently from other pathogens is quite surprising and unexpected," said Joel Ernst, MD, director of the division of Infectious Diseases and Immunology at NYU Langone Medical Center in NYC and lead author of the study. "If you get infected with the influenza virus, for example, the body's immune system recognizes it and tends to eliminate it. In tuberculosis, our immune response doesn't get rid of it ? it tends to hold on to it for a while ? keeping the bacteria under partial control."

The immune system plays a key role in protecting the human body from invading pathogens. These pathogens have molecules known as antigens that are recognized by the immune system. However, many pathogens can evade immune recognition by varying their antigens. This study found that rather than "suffering" from being recognized, recognition of tuberculosis antigens actually benefit the bacteria ? and it is this recognition that helps the bacteria to be transmitted from person to person.

Tuberculosis is a major cause of death and disability worldwide, killing someone every 15 minutes. TB in New York City, and in the United States as a whole, is being driven by the global TB epidemic. In 2008, despite very aggressive and expensive public health efforts, there were 895 cases of TB and 11 cases of multidrug-resistant TB. Over 70 percent of all cases of TB in NYC in 2008 were among individuals born outside the United States, although people with TB can transmit the infection to anyone.

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Of all the people who get the disease, 90 percent remain well while the immune system suppresses the disease. Approximately 10 percent of the people who get infected then transmit the disease. As a consequence of the emergence of drug resistance, the global epidemic of tuberculosis is worsening. Thus, new tools and strategies are urgently needed to combat this growing epidemic.

For this study, scientists used a novel high-throughput DNA sequencing method to analyze the whole genomes of 22 clinical strains of M. tuberculosis from different parts of the world. They then determined that the number of and type of mutations that occurred in antigens is much lower compared to other regions of the M. tuberculosis genome.

SOURCE [1]

Links:
[1] http://www.eurekalert.org/pub_releases/2010-05/nlmc-iec052010.php