

Genes suggest who is most likely to get tuberculosis

Tuberculosis is caused by *Mycobacterium tuberculosis*. In 2016, this was the most common causative pathogen for death by infectious diseases. Therefore, investigating the biology of infection and disease development is important in the quest to end tuberculosis. In this study, the authors conducted an integrative analysis of human and pathogen genome variations in tuberculosis.

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Genome-wide association study (GWAS) is an analysis method in genetics which is used to identify disease-related genome variations by comparing the differences in genotype frequencies in a case and control group. There have been several GWAS regarding susceptibility to tuberculosis. However, previous GWAS have not been based on analysis that accounted for pathogen variations. [...] In this research the authors did a systematic exploration of host variations for their association with specific lineages of *Mycobacterium tuberculosis*, which share the same pathogen genome variations.

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“Nearly one third of the world’s population are infected by *Mycobacterium tuberculosis*, but only 10% of them show symptoms of TB throughout their life.” explains lead author Yosuke Omae. “This research lays the foundations for us to identify who will get TB.”

The GLP aggregated and excerpted this blog/article to reflect the diversity of news, opinion, and analysis. Read full, original post: [What role do genome variations play in tuberculosis?](#)