Genetics and Resistance to Tuberculosis: Could Resistance Be Enhanced by Genetic Engineering?

Abstract

Recent observations strongly suggest a significant role for genetic factors in innate resistance to infection by *Mycobacterium tuberculosis*. This relation was discovered in a study of tuberculosis in Arkansas nursing homes and was supported by data from three outbreaks of tuberculosis in two prisons. A person's resistance level was found to correlate with the region of his or her ancestry. Ancestors of person's in the more resistant group tended to derive from densely populated areas and cities rife with tuberculosis, whereas the ancestors of person's in the more susceptible group tended to derive from areas once free of tuberculosis. In accordance with current genetic theory, those persons who are less resistant to tuberculosis would be expected to be more resistant to infections endemic to the region once inhabited by their ancestors. Isolation of the gene previously shown to confer specific innate (nonimmune) resistance to tuberculosis should result in the creation of a more rational approach to increasing the capacity of human macrophages to kill tubercle bacilli without producing a positive tuberculin skin test.
A model was sensitive but not specific for screening for tuberculosis in contact patients

*Annals of Internal Medicine;* 149 (8): JC4-15

**View More**

---

**RELATED POINT OF CARE**

**Tuberculosis**

*Annals of Internal Medicine;* 166 (3): ITC17-ITC32

**Tuberculosis**

*Annals of Internal Medicine;* 150 (11): ITC6-1

**View More**

---

**RELATED TOPICS**

**Infectious Disease**

**Mycobacterial Infections**

---

**PUBMED ARTICLES**

**Spontaneous spondylodiscitis: review, incidence, management, and clinical outcome in 44 patients.**

*Neurosurg Focus* 2019;46(1):E10.

**Genetic variation in the conjugative plasmidome of a hospital effluent multidrug resistant Escherichia coli strain.**

*Chemosphere* 2018;

**View More**

Results provided by: PubMed
A new TB-Profiler tool analyses and interprets genome sequence data to predict resistance to 11 drugs used for the treatment of TB. This rapid tool means that sequence data can now be used without delay, so that finding which drugs to use for a patient with TB can be sped up by days or even weeks, increasing the likelihood of a cure. Share: FULL STORY. Finding out what drugs can be used to treat a patient with tuberculosis (TB) can be sped up by days or weeks, thanks to a new free online tool. The new TB-Profiler tool, developed by a team of scientists led by Dr Taane Clark, means that sequence data can now be used without delay, so that finding which drugs to use for a patient with TB can be sped up by days or weeks, increasing the likelihood of a cure.