# Comparative Genomics of *Mycobacterium Tuberculosis*

# My Questions

- What is TB
  - What are the characteristics of the disease?
  - What is the global outlook?
  - How is it treated?
- How is bioinformatics used in TB research?

# Goals for the talk

- Teach you about the applications I have discovered in the literature.
- Emphasize that genomics techniques are not limited to hereditary diseases.

# Methods

- Massive PubMED search of the literature
- Read many papers
- Interview with Katherine Skillern from Peter Small’s lab

# Assumptions

- You are familiar with the characteristics of infectious diseases.
- You have a basic understanding of TB
- You are familiar with technology of microarrays and gene chips.

# Papers of interest

- The Epidemiology of Tuberculosis in San Francisco, Peter M. Small et. Al

- Deciphering the biology of Mycobacterium Tuberculosis from the complete genome sequence, Stuart Cole et al.

# Papers continued

- Comparative Genomics of BCG Vaccines by Whole-Genome DNA microarray, M.A. Behr et al.

- Comparing Genomes within the Species *Mycobacterium Tuberculosis*, Midori Kato-Maeda et al.

# TB in San Francisco

- Interesting because:
  - There was a large outbreak of TB signifying future outbreaks
  - Small et al. Successfully identified the index case. Using RFLP’s as markers
  - They collected TB samples and clinical profiles for 4000 cases

# Complete Sequence of TB Genome

- Interesting because:
    - It was the first sequence of the TB genome
    - They sequenced the well characterized lab strain H37Rv
    - Given the complete sequence , Affymetrix produced a gene chip containing every TB gene

# Comparison of BCG vaccines using microarrays

- Interesting because:
  - Used Affymetrix gene chips containing the H37Rv strain of TB to compare BCG vaccine. (The vaccine is produced in many different locations)
  - Research verified variation in the BCG vaccine.

# Comparing TB Genomes using microarrays

- Interesting because:
  - Midori Kato Maeda et al. used Peter Small’s data from the TB outbreak in San Francisco.
  - Of the 19 TB isolates compared, 16 were different

# Conclusions

- Researchers held to the dogma that the various manifestations of TB were due to different host conditions
- Recent research has proved the genome of TB varies a great deal.
- Comparisons between genomes should illuminate the mechanisms of virulence and immunity.
- Finally we have the big picture

# Sources

- Small PM et al. The Epidemiology of Tuberculosis in San Francisco -- A Population-Based Study Using Conventional and Molecular Methods. New England J Med 1994; 330: 1703-09.
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- Behr MA, Wilson MA, Gill WP, Salamon H, Schoolnik GK, Rane S, Small PM. Comparative genomics of BCG vaccines by whole-genome DNA microarray. Science. 1999 May 28;284(5419):1520-3.