A Library of a Large Collection of Genotypically Defined Mutants

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Technology description

Value Proposition:
Tuberculosis is a serious and lethal infectious disease that exists worldwide. There is a recognized need to understand the infectivity mechanisms used by mycobacterium to identify useful therapeutic and prophylactic targets. JHU researchers have generated a near-comprehensive library of over a thousand genotypically defined M. tuberculosis mutants. The library was made using high throughput transposon-mediated random insertion mutagenesis. This collection of mycobacterium mutants provides a vast resource of defined mutants that has not been previously available. Mutation sites have been genetically mapped and defined to provide a valuable resource for clinical, pharmaceutical and basic science research. JHU scientists have also developed custom microarrays to probe to track the presence or absence of the mutants during experimentation.
Technical Details:
JHU researchers have generated a library of 1,183 genotypically defined Mycobacterium tuberculosis mutants using transposon-mediated random insertion mutagenesis. The transposon used to generate the library, Himar1, has a small but defined target site allowing the disruption of nearly all open reading frames, and a genetic map of the exact mutation sites has been compiled. In addition, custom microarrays have been developed to probe for the presence or absence of each mutant.

Advantages

- Availability of a large collection of mutants allows a broader selection of potentially appropriate strains and increases versatility for experimental design and therapeutic agent screens.
- Library provides an available source of many mutant M. tuberculosis organisms and eliminates extensive time and expense required to produce and characterize mutants before experimental use.
- Mutant organisms of interest do not require genetic mapping because the molecular identities have already been compiled for the entire library to reduce time from data collection to data interpretation.
- Custom DNA microarray designed for the library allows high- throughput tracking of mutants.

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