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A New Paradigm for Genus *Mycobacterium* Population Structure

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Abstract

BACKGROUND The genus *Mycobacterium* contains 150 currently recognized rapidly (RGM) or slowly (SGM) growing species. The SGM *Mycobacterium tuberculosis*, is a major cause of human infection and mortality. Non-tuberculosis mycobacteria (NTM) are increasingly recognized as wide-spread opportunistic human pathogens. Demands for quicker and more accurate identification of species spur usage of genomic polymorphism to facilitate identification of *Mycobacterium* species. However, obtaining from this molecular data a robust phylogeny or population structure for the genus *Mycobacterium* remains elusive.

RESULTS *rpoB* 342 bp gene fragment sequences for 47 *Mycobacterium* species and 3 related species *Corynebacterium diphtheria*, *Nocardia nova*, and *Rhodococcus equi*, were obtained from GenBank. *In silico* restriction using Javascript with Perl regular expressions, was performed for 5 restriction enzymes. 30 restriction sites were identified and used to generate a minimum spanning tree (MST) which was highly polarized and could be empirically divided into 3 regions. Certain restriction site alleles were in linkage disequilibrium with the MST regions. MST-region 1 contained all the RGM and a halo of SGM which for certain alleles were similar to RGM, and significantly different from MST-region 3 SGM. *Mycobacterium* genotypes, such as number of *rrn* rRNA operons and promoters, were consistent with the model. *Rhodococcus equi* was associated with MST-region 1 RGM as expected from genomic studies.

CONCLUSION The MST-regions model of genus *Mycobacterium* population structure was robust, unambiguous, transparent for alleles, consistent with genotypes and phenotypes, and statistically testable. Genomic comparisons based on the model should provide information that will yield new therapeutics and vaccines.

Biography

Paul Jeffrey Freidlin. Born 9 March 1951, Washington, D.C.; married plus children, grandchildren. 1972 BSc with honors University of Maryland, College Park; 1976 MS and 1979 PhD Department of Microbiology and Public Health, Michigan State University, East Lansing. Postdoctoral: Tel-Aviv University. Research and advanced studies in molecular and population genetics, DNA markers: 1998 Hebrew University of Jerusalem, Faculty of Agriculture, Rehovot, rank of lecturer. Bioinformatics and Net Programming: Weizmann Institute of Science. 2001 Israel National Mycobacterium Reference Laboratory, Tel Aviv: currently coordinator for molecular biology. Area specialization: molecular epidemiology of tuberculosis. General research interest: understanding biodiversity at the molecular level.