

Spatial and Temporal Relationships of *Mycobacterium bovis* in Animals of the United States

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A cooperative state and federal effort to eradicate bovine tuberculosis (TB) from the United States has made significant progress toward eradication. However, between 4 and 12 infected cattle herds are detected annually and the goal of eradication has been elusive. Remaining challenges include infected wildlife, large affected dairies, off-site calf raising facilities, and imported cattle. Continued reintroduction combined with a low prevalence of *Mycobacterium bovis* (*M. bovis*) in livestock necessitates new methods to assist program eradication efforts. Molecular techniques are promising new tools to enhance epidemiologic investigations through identification of potential associations between infected animals.

A total of 645 *M. bovis* isolates obtained from TB cases occurring between 1991 and 2008, were evaluated by spoligotyping, a molecular method of genotyping *Mycobacterium tuberculosis* complex organisms. A spatial cluster statistic was used to assess the spatial and temporal patterns of *M. bovis* and to determine the number of geographically isolated clusters of *M. bovis* spoligotypes occurring in animals in the United States. In addition, phylogenetic trees were created to identify the molecular clustering of isolates. This information was compared with known cases in cattle and cervids to describe potential epidemiologic characteristics of the clusters.

A total of 497 (77.1%) isolates were from beef and dairy cattle and 147 (22.8%) were from wildlife; one isolate was from cheese. Of the 70 spoligotypes identified, fourteen genetic clusters were identified. One cluster consisted of *M. bovis* isolates from a Michigan outbreak; however, this cluster also included cases from Hawaii that are not epidemiologically linked to Michigan. A second cluster consisted of Minnesota outbreak isolates. Several clusters consisted of isolates from Mexican origin and domestic cattle, suggesting disease transmission between these groups. Spoligotyping provides valuable information regarding the epidemiology of *M. bovis* in the United States cattle herd.

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