DNA Fingerprinting of Mycoplasma bovis

The bovine pathogen, Mycoplasma bovis, has been shown to be genetically diverse, meaning that, within this single species, there are many genetic types.[1] This remarkable organism is able to alter the antigenic sites on the surface of its cell. This ability allows M. bovis to survive many different environments and most importantly, evade host immunity.[2] Preventing or treating disease due to such a pathogen is a challenge: its cellular structure limits antibiotic choice and with the variable antigenic sites, vaccination with commercial bacterins is often ineffective.

However, with the advent of DNA fingerprinting, we can monitor genetic variability of the isolates. This diagnostic method can be used to evaluate prominent strains in the herd, monitor for new genotypes, and provide a selection tool for vaccine strain selection. Clinical experience has indicated that using a bacterin with 3 or more genotypes can aid in the reduction of mortality due to M. bovis. [3]

What is DNA fingerprinting?

Every living organism is made up of DNA, the basic genetic code of life. The DNA of each living species is unique. M. bovis is very unique and a good candidate for fingerprinting since there is much genetic variation within the species. On the outside, or phenotypically, they all appear to be M. bovis, but on the inside, the "mechanics" or DNA is different, and it is these differences that can code for different antigenic expression.

The fingerprinting method is not difficult - it all starts with the extraction of total genomic DNA from a broth culture of M. bovis. From here, the polymerase chain reaction and agarose gel electrophoresis is used to generate the DNA fingerprint data. The data or result is in the form of a "banding" pattern. (See Figure 1 below.) The data is subsequently analyzed using a software program that determines "% similarity" and the results are depicted in a dendrogram or phylogenetic tree. (See Figure 2.)
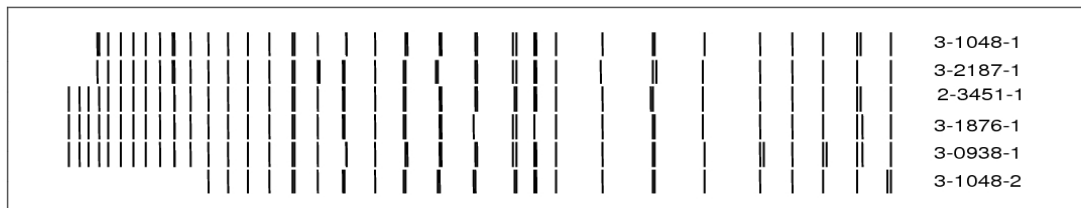

Figure 1

What is a dendrogram?

A dendrogram or phylogenetic tree is a diagram or chart used to show the relationship to, or similarity of two (or more) organisms. Isolates with similar DNA fingerprints will be grouped (or bracketed)