Bovine tuberculosis in India: potential basis for zoonosis.

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Abstract

Our laboratory has designed a specific nested-PCR (N-PCR) assay, based on the hupB gene of Mycobacterium tuberculosis (Rv2986c) and Mycobacterium bovis (Mb3010c) as a method to differentiate these closely related species. The present paper deciphers the utility of this assay for identification of pathogenic Mycobacteria in clinical samples. Extra-pulmonary clinical samples obtained from cattle and humans were investigated. Pre-dominance of M. tuberculosis (15.7%) and M. bovis (26.8%) was seen in humans and cattle, respectively. However, more importantly, both mycobacterial pathogens (mixed infection) were identified in a number of samples. In humans 8.7% of the samples and 35.7% in cattle were classified as mixed infection. The detection of mixed infection with the mycobacterial pathogenic duo in humans and bovines denotes the prospect of potential transmission of these pathogens from humans to cattle (zoonosis) and vice versa (reverse zoonosis).