

Abstract

Cattle are the domestic animal reservoir for *Mycobacterium bovis* (*M. bovis*) which also affects other domestic animals, several wildlife species and humans leading to tuberculosis. The study area is in a resource-poor community that is surrounded by several game parks, where *M. bovis* infection has been previously diagnosed in wildlife. A cross-sectional study was carried out to determine the prevalence of *M. bovis* infection in 659 cattle from a total of 192 traditionally managed herds using the BOVIGAM® interferon gamma assay (IFN- γ). Infection was confirmed by post mortem examination and *M. bovis* isolation from three test-positive cattle. Genotyping of the *M. bovis* isolates was done using spoligotyping and VNTR (variable number of tandem repeats typing). The apparent *M. bovis* prevalence rate in cattle at animal level was 12% with a true population prevalence of 6% (95% Confidence interval (C.I) 3.8 to 8.1) and a herd prevalence of 28%. Spoligotyping analysis revealed that the *M. bovis* isolates belonged to spoligotype SB0130 and were shared with wildlife. Three VNTR profiles were identified among the SB0130 isolates from cattle, two of which had previously been detected in buffalo in a game reserve adjacent to the study area. The apparent widespread presence of *M. bovis* in the cattle population raises a serious public health concern and justifies further investigation into the risk factors for *M. bovis* transmission to cattle and humans. Moreover, there is an urgent need for effective bTB control measures to reduce infection in the communal cattle and prevent its spread to uninfected herds.