Molecular identification of *Mycobacterium tuberculosis* in cattle

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**Abstract**

Bovine tuberculosis continued to be a re-emerging problem in some countries especially in endemic areas due to the fact that human and animal health surveillance system is not adopted to diagnose the infection. This crisis can be attributed due to sharing of the same habitat especially in rural areas. In the present study, a total of 148 samples were collected from cattle for isolation over a period of 3 years from cattle with and without lesions, of which 67 isolates were obtained by culture. Fifty one isolates were identified as *Mycobacterium tuberculosis* complex (MTBC) by IS6110 PCR of which 43 (84.3%) were identified as *M. tuberculosis* and 08 (15.6%) were identified as *M. bovis* by using 12.7 kb fragment multiplex PCR. Among this, 31 isolates which were positive for IS6110 PCR were subjected to spoligotyping and revealed 28 isolates belonging to MANU1 strain of *M. tuberculosis*. This study clearly indicates that high prevalence of *M. tuberculosis* than *M. bovis* in bovine was identified by means of culture and by molecular methods *M. tuberculosis* can affect cattle producing lesion in contradiction to the earlier thoughts. This study speculate that *M. tuberculosis* MANU1 strain infection in cattle can be due to spoligotype pattern and it is considered a serious threat worldwide, in countries where human TB is endemic. *M. tuberculosis* infection of cattle needs to be considered.

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**1. Introduction**

Bovine tuberculosis (BTB) caused by *Mycobacterium tuberculosis* (*M. tuberculosis*) and *Mycobacterium bovis* (*M. bovis*) is a highly prevalent infectious disease affecting cattle and human globally and India is one of the 22 high-burden countries (Mukhopadhyay and Ganguly, 2013). Over 50 million cattle are estimated to be infected with *M. bovis* worldwide resulting in economic loss of about $3 billion (Grange and Yates, 1994). Recent reports indicate an increase in the prevalence of tuberculosis among cattle. Several research works carried out in Tamil Nadu (India) indicate as high as 13.4% prevalence of BTB among cattle (Yesuf, 2012). Though *M. tuberculosis* and *M. bovis* are primarily considered as host specific pathogens, the bacteria’s ability to infect a wide range of hosts and its capacity to cross species barriers has led to spread of transmission of the disease among human and animals. In India the prevailing cultural and religious taboos have resulted in the endemic nature of the disease which is of public health importance. Hence the safety of the food animal of origin especially tuberculosis is worth giving consideration, taking into cognizance not only the endemcity of tuberculosis and its association with immunosuppressive diseases but also the emergence of drug resistance among *M. tuberculosis*. Close association of humans and animals has resulted not only in zoonosis but also suspected for possible reverse zoonosis. Bovine tuberculosis continued to be a major problem in countries where test and slaughter principles are not affordable and these programs are partially effective due to the fact that wild life act as reservoir host and it maintains the infection (Sechi et al., 2001). Due to the involvement of human, domesticated animals and wild animals, only a well conducted study involving all these will provide the exact magnitude of the problem (Srivastava et al., 2008). This is posing a formidable challenge in controlling and eradicating mycobacterial diseases. Several studies (Prasad et al., 2005; Mishra et al., 2005; Ocepek et al., 2005; Chen et al., 2009; Du et al., 2011; Romero et al., 2011; Spicic et al., 2012; Thakur et al., 2012) have reported isolation and characterization of *M. tuberculosis* and *M. bovis* among cattle whereas the transmission of disease among