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Molecular epidemiology of Tuberculosis in animals and man in Bangladesh

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Abstract

Tuberculosis (TB) is a progressive granulomatous infectious disease caused by the gram positive, acid fast bacilli classified under the genus Mycobacterium. Tuberculosis in human is mostly by Mycobacterium tuberculosis and primarily affects lungs causing pulmonary tuberculosis (PTB). It can also affect intestine, meninges, bones, joints, lymph nodes, skin and other tissues of the body causing extra-pulmonary tuberculosis (ETB). Tuberculosis also affects animal like cattle, buffalo etc. known as bovine tuberculosis (BTB) caused by Mycobacterium bovis, a member of Mycobacterium tuberculosis complex (MTBC). The MTBC consists of closely related species that cause TB in both human and animal. From the total population of Bangladesh, about 85% of the people are engaged in agriculture and are at risk of bovine TB. Bovine TB has great economic importance disease as well as public health significant. The study is designed to determine the prevalence of tuberculosis (Mycobacterium species) in human and animals by conventional and molecular techniques. The cross-sectional descriptive study is being conducted in Mymensingh, Sirajganj and Dhaka district during the period of January 2018 to December 2019. Data is being collected by history taking from the TB suspects (calculated minimum sample size is 369 in case of human and 1530 for animals especially dairy cows) and from the findings of laboratory investigations of relevant specimens especially sputum from human and milk, blood, lymph node aspirate and tissue from animals. A total of 444 TB suspects were interviewed. Sputum from 443 patients were examined under LED microscope after auramin staining and 46 was found positive for tubercle bacilli. A case of extra-pulmonary TB was detected by Fine Needle Aspiration Cytology (FNAC) of cervical lymph node. Culture in liquid media was done with 42 Specimens of sputum. Thirty seven (37) of those showed growth while 5 did not. DNA was extracted from growth in liquid media by boiling method and was preserved accordingly in -200C. GeneXpert/RIF was done with 37 samples of sputum and 29 was found MTB positive and RIF sensitive while 4 were found MTB positive but RIF resistant. Conventional PCR showed 17 positive cases for Mycobacterium species. Multiplex PCR and gel electrophoresis were done and 10 were found positive for Mycobacterium tuberculosis. These Multiplex PCR products were used for DNA Sequencing. Results of DNA sequencing was submitted to GeneBank and the accession numbers were received. Strains of Mycobacterium Tuberculosis were isolated & showed similarity with the strains which are reported from other parts of the world. Overall incidence of TB in TB suspects was found 10.36%. A total of 470 BTB suspected animals were screened by CFT (Caudal Fold Tuberculin) test using bPPD (Bovine purified protein derivatives) where 101 (21.49%) were shown sensitive. CFT sensitive animals were tested by CCT (Comparative Cervical Tuberculin) using bPPD and aPPD (Avium purified protein derivatives) where 36 (7.66%) were shown BTB sensitive. On the other hand, a total of 570 BTB suspected animals were tested with Bovine antibody rapid test kid where 0.88% found positives for Mycobacterium bovis. One thirty eight samples (Milk, blood and tissue) were tested by Zeihl-Neelsen staining and light and inverted microscopy where 7 (7.97%) were positive. Conventional PCR was done for 214 samples (Milk, blood and tissue) and 06 (2.91%) found Mycobacterium spp positive from bovine tissue sample. Ending the TB epidemic by 2030 is one of the health targets of the newly adopted Sustainable Development Goals (SDGs). Understanding of

Molecular epidemiology of tuberculosis is essential for its effective control in human as well as in animal.

Biography

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