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Popular Article

Zoonotic Threat of *Mycobacterium orygis* Associated Tuberculosis in Animals

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Abstract:

Bovine Tuberculosis (bTB) is a zoonotic disease that can infect humans, animals, and wildlife. It is primarily transmitted through the respiratory tract and is the most common infectious disease that causes death. The incidence of zoonotic tuberculosis is still unknown, despite India having the largest number of human tuberculosis cases worldwide and the largest number of cattle populations, where bovine tuberculosis is endemic. Over the past few decades, bovine tuberculosis has emerged as a significant global public health concern. Achieving the goals of the bTB strategy requires considerable effort. Therefore, innovations are essential to accelerate the transition toward a world free of bovine tuberculosis, and immediate global actions are required to restore the One Health system.

Key words: Bovine tuberculosis, animals, human, zoonotic

Introduction:

Bovine tuberculosis (bTB) is a major infectious disease that causes chronic wasting, has a global distribution, and possesses significant zoonotic potential. Based on of genomic analysis, it has been previously found that *Mycobacterium tuberculosis complex* (MTBC) can be classified into over eight distinct subgroups: including *M. tuberculosis, M. caprae, M. bovis, M. africanum, M. canettii, M. pinnipedii, M. microti* and *M. mungi* (Olsen *et al.,* 2011). *Mycobacterium orygis* belong to the members of the *Mycobacterium tuberculosis complex*, which has the potential to cause tuberculosis in both humans and animals. *Mycobacterium orygis*, often referred to as the oryx bacillus, is a bacteria that causes tuberculosis and has been related to both animal and human tuberculosis (Van Ingen *et al.,* 2012). It has been isolated from a variety of species in South Asian, including zoos, cattle

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farms, and wild animals who move freely (Thapa *et al.,* 2015).

M. orygis is believed to be endemic in Southeast Asia, particularly in countries such as India, Pakistan, and Nepal. (Marcos *et al.,* 2017). MTBC infections could be misdiagnosed, potentially leading to underreporting of *M. orygis* infections in the scientific literature (Brites *et al.,* 2018). Therefore, it can be assumed that *M. orygis* may have historically existed in the sub-continent but was mistaken for other MTBC members. *M. orygis* was originally identified in 2012 Africa and South Asia, following the examination of isolates for their polymorphism in the length of the *IS6110* restriction fragment patterns' closeness to previously recognized oryx bacilli (Rahim *et al.,* 2017). A whole-genome sequencing test verified that RD9 and RD12 are absent, leading to the detection of the strain as *M. orygis*. India has the largest cattle population in the world, with nearly 300 million cattle, more than any other country. Bovine tuberculosis is both uncontrolled and endemic in India, with an estimated 21.8 million infected cows as of 2017 (Srinivasan *et al.,* 2018). The *M orygis* found in South Asia's livestock, wildlife, and humans indicates that it is endemic and a cause of zoonotic and animal tuberculosis. To fully understand the distinct epidemiological, ecological, and pathogenomic drivers of distribution, risk factors, and transmission dynamics of *M orygis* in south Asia, comprehensive epidemiological surveillance should to be carried out across humans, and animals.

Transmission of Bovine Tuberculosis:

The potential risk of zoonotic tuberculosis to public health is increasingly being recognized. The majority of zoonoses occur in areas where humans come into close contact with commonly encountered animal species (Johnson *et al.,* 2020). In MTBC, airborne transmission is likely the primary mode of transmission for these bacteria. Also, other routes of human transmission are inhalation, consuming unpasteurised milk, and having close contact with animals that are infected or that were not properly treated (Teppawar *et al.,* 2018). *M. orygis* can be transmitted from humans to bovine and has been reported in New Zealand (Dawson *et al.,* 2012). A zoonotic cause of human tuberculosis has been identified as an infection with *M. orygis* (Lipworth *et al.,* 2019). Although ruminants, particularly antelopes, maybe the main host of *M. orygis*, mounting evidence of the disease in people and other animals implies it may also have a diverse host range.

Molecular Diagnostics:

M. orygis is likely an emerging pathogen in Indian cattle that has not been previously recognized (Brites *et al.,* 2018). The isolation of *M. orygis* from humans, along with its

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apparent prevalence in South Asian cattle, raises the question of whether this recently identified pathogen should be included as a causative agent of zoonotic tuberculosis (zTB). Bovine TB is primarily diagnosed through post-mortem examination, single intradermal and comparative intradermal cervical tuberculin test, as well as interferon-gamma release assay. The intradermal tuberculin skin test is the primary method used to diagnose TB in live animals to detect a delayed hypersensitivity reaction to the tuberculin. The TB-causing agent is confirmed microbiologically using culture or molecular methods (PCR and WGS). Diagnosis of *M. bovis* infection also involves the use of blood assays based on host immune responses, such as the Differentiating Infected from Vaccinated Animal [DIVA] test, ELISA, and IFN-ɣ release assay (Vordermeier *et al.,* 2011). In clinical and research labs, whole genome sequencing (WGS) technologies are being used in increasing numbers to study TB monitoring, outbreak detection, antibiotic resistance prediction, characterisation, and MTBC species diversification (Brites *et al.,* 2018). *M. orygis* was clearly distinguished from members of other MTBC species by molecular marker characterisation on their genomes. Whole genome analysis was carried out to enhance precisely identify *M. orygis* and other species within MTBC. Additionally, the diversity and worldwide distribution of the recently sequenced *M. orygis* isolates was determined using phylogenetically based analysis.

Prevention and Control of Zoonotic Tuberculosis:

Effective prevention and control of zoonotic tuberculosis (zTB) require a comprehensive approach that addresses both animal and human health. Recent data suggests that *M. orygis* and other mycobacterial species may also be associated with zoonotic tuberculosis (zTB) (Duffy *et al.,* 2020). According to a recent study, *M. orygis*-associated zoonotic tuberculosis is becoming increasingly prevalent as an infectious disease. The emphasis is on tuberculosis diagnosis and management, with a focus on multidrug-resistant tuberculosis. Considering the WHO's End TB Strategy, which aims to identify and treat every case of tuberculosis in order to eradicate the epidemic by 2030, it is crucial to recognize the threat posed by *M. orygis* and implement the necessary control measures both nationally and globally. Globally, zoonotic tuberculosis continues to be a significant, underreported burden that remains largely untreated and poorly monitored. Adopt a One Health strategy that fosters collaboration between veterinary, medical, and environmental sectors to manage the shared risks between humans and animals. Implement biosecurity measures on farms to prevent the introduction and transmission of *M. tuberculosis* or *M. orygis*. The use of unpasteurised milk and milk products, close

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and frequent physical contact with infected animals, high human-animal density, and insufficient disease management measures are among of the region's many zTB risk factors. Rapid testing could help farmers and veterinarians to diagnose TB in animals so that they can be isolated from the rest of the herd. The Bacillus Calmette Guérin vaccination should be widely given to animals in addition to conventional management methods in order to reduce host reservoirs and induce protection against TB. BCG vaccination may offer some protection against various *MTBC* species, including *M. orygis*, but it is important to recognize that this protection is not absolute. It should be used in combination with traditional management practices for optimal effectiveness.

Future Prospects:

Due to the endemic nature of tuberculosis and its zoonotic potential, routine screening should be carried out, and farms must adopt appropriate preventive and control measures. Early detection of tuberculosis can facilitate the prompt isolation of infected animals, help limit the spread of the disease, and contribute to the eradication of bovine TB from the country. The growing evidence of *M. orygis* endemicity in cattle highlights the importance of a comprehensive One Health strategy, which includes multisectoral coordination between the veterinary and clinical sectors, for the prevention and treatment of tuberculosis in India.

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