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Host specific transmission study on *Mycobacterium avium* subsp. *Paratuberculosis* in ruminants

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Abstract
Mycobacterium avium subsp. *paratuberculosis*is one of the major disease in ruminants in India, since both treatments and vaccination programs are not still in practice. In this contest regular screening program for MAP is recommended by GOI in organized farms in India in order to eliminate the infected MAP animals from the healthy animal population. This study was carried out in an organized livestock farm having an animal population of 80 which includes 26 cattle, 23 buffaloes and 31 goats. Screening of the animals were carried out for *Mycobacterium avium* subsp. *paratuberculosis* during the years 2019, 2020 & 2022 using Johnin by SID test. The prevalence of MAP in these farm animal s analyzed and discussed. In this study no cattle were tested positive and 9.3% (4 numbers) buffaloes and 13.1% (10 numbers) goats were tested positive for the years 2019, 2020 & 2022. The study revealed johnin reactors both in buffaloes and in goats where the cattle population remained intact for *Mycobacterium avium* subsp. *paratuberculosis* infection, and these observations suggests the variations among MAP isolates affecting ruminant species. A detailed overall molecular study needed to rule out the prevalence of different ruminant MAP strain in both buffaloes and goats and involvement of a host specific strain in goat population.

Keywords: Mycobacterium, ruminants, host specific

Introduction
India is a tropical country with varying animal husbandry rearing systems in comparison to other countries. Therefore the epidemiology of M*ycobacterium avium* subsp. *paratuberculosis* (MAP) infection in India is different from other countries. There are lot of opportunities for interspecies transmission of infection between species and breeds of animals in India. The risk factors associated for herd and animal-level infection for MAP transmission are not known. Assessment of variations among MAP isolates affecting different ruminant species is an essential requirement for MAP control measures (G.C. Sonawane, *et al*. 2019). Small numbers of MAP isolates characterized in previous studies suggested that a different strain could infect ruminant population in India. (Sevilla I, *et al*. 2005; Tripathi B.N, *et al*. 2007) [11, 14]. G.C. Sonawane, *et al*. (2016) [13] reported that sheep population from the semi-arid region of Rajasthan were endemic for MAP, while the disease was not detected in goat populations despite the goat farm being situated in the vicinity of sheep farms and the facts that these animals share common grazing areas. Some studies indicated that MAP strains are host specific and infect their respective host species only. (Collins DM, *et al*. 1990a) [3].
It is important to understand the role of cross-species transmission in causing MAP outbreaks and in maintaining infection cycles. Epidemiologic evidence suggested that natural transmission of MAP between cattle and sheep was uncommon. (Allworth and Kennedy 1999; Fridriksdottir, *et al*. 2000; Kennedy and Allworth, 1999) [1, 7, 8]. This suggested that cattle and sheep harbor different strains of the same organisms, and these strains were somewhat host adopted.
At least two strains of MAP, designated as C (Cattle) and S (Sheep) are now documented. (Bauerfeind, *et al*. 1996; Collins, *et al*. 1990a; Cousins, *et al*.., 2000; Pavlik, *et al*. 1995; Whittington, *et al*. 1998a, 2001c) [2, 3, 5, 10, 15]. There also is endemic of a goat specific strain in Norway (Collins, *et al*. 1990a) [3].
Seven (3.4%) out of 203 buffaloes had clinic-pathological findings characteristic of MAP. Although buffaloes are considered less susceptible to MAP than cattle (Sivakumar, *et al*. 2006) [12] a high prevalence of disease was observed in this buffalo herd compared with previous reports (Sivakumar, *et al*. 2006; Mota, *et al*. 2010) [12, 9] and with cattle managed under very intensive farming (Driemeierer, *et al*. 1999) [6]. The reason for the high infection rate in this

buffalo herd has not been definitely established.

Materials and Methods

This study was conducted in an organized livestock farm in Jamdoli, Rajasthan state (during the years 2019, 2020 & 2022) having an animal population of 50-65 which includes 21 cattle, 9-22 buffaloes and 22-31 goats. The bovine i.e. the cattle and the buffaloes reared in the same vicinity, where the goat population is being maintained in a nearby vicinity of 30 meters inside the farm. Cattle and buffaloes were stall fed and the goats allowed for indoor grazing in addition. All the animals maintained under normal conditions. Screening of the animals above 6 months were carried out for J.D using Johnin by single intradermal test (SID), during the above mentioned periods. The prevalence of MAP in these animals are analyzed and discussed.

Results

Status of MAP in the livestock farm

Livestock species	Total animals tested 2019	Animals positive & %	Total animals tested 2020	Animals positive & %	Total animals tested 2022	Animals positive & %	Total animals/ positives & %
Cattle	21	Nil	10	Nil	21	Nil	52 (Nil %)
Buffaloes	22	1 (4.5%)	9	2 (22.2%)	12	1 (8.33%)	43 (4) 9.3%
Goats	22	4 (18.1%)	31	3 (9.67%)	23	3 (8.69%)	76 (10) 13.1%
Total	65	5 (7.69%)	50	5 (10%)	56	3 (5.35%)	171 (13) 7.6%

Johnin reactors in this farm animals

Cattle

A total number of 21, 10 & 21 cattle were tested for J.D in the years 2019, 2020 & 2022 respectively and all cattle were found negative.

Buffaloes

Among 22 buffaloes tested one animal (4.5%) was positive in the year 2019, followed by 2 buffaloes (22.2%) in the year 2020 and one buffalo (8.33%) in the year 2022.Out of 43 buffaloes tested 4 (9.3%) animals were found positives during these period of time.

Goats

In goats out of 22 tested, 4 goats (18.1%) were positive in the year 2019, followed by 3 positives out of 31(9.67%) and 3 positives, out of 23 goats (8.69%) in the years 2020 & 2022 respectively. The overall positive percentage of MAP infected animals in cattle is nil and it was 9.3% and 13.1%.in buffaloes & goats respectively. The overall positive percentage of MAP reactors in the farm was 7.6% in buffaloes and goats. The study revealed that the buffaloes and the goat population in this farm were continuously in infection status of MAP, while the cattle population remained intact for MAP infection.

Discussion

In this study it was observed that the cattle population remained intact for MAP infection, while the buffalo population suffers with JD even though both populations maintained in the same yard. Sivakumar, *et al*. (2006) [12] and Driemeier, D, *et al*. (1999) [6] reported low level of J.D infection in cattle population and high level infection in buffaloes even though both populations maintained in the same farm premises. The authors were not able to attribute the reasons for this observation. However Sevilla I, *et al*. 2005; Tripathi B.N, *et al*. (2007) [11, 14] reported that different MAP strains could infect ruminant population in India. In this farm also cattle were not infected, while 9.3% (4 animals) buffaloes got infected with J.D pathogen which is in concurrence with the observation of the mentioned authors.

Out of 76 goats tested, (10 goats) 13.1% were found positive for J.D infection. A detailed study needed to rule out the involvement of goat strain in this MAP infection as suggested by Collins, *et al*. (1990a) or if it could be due to a different ruminant strain as suggested by Sevilla I, *et al*. 2005; Tripathi B.N, *et al*. (2007) [11, 14].

A detailed overall molecular study needed to rule out the prevalence of different ruminant MAP strain both in buffaloes and goats and involvement of a host specific strain in case of goat population.

Conclusions

Studies on the prevalence of M*ycobacterium avium* subsp. *paratuberculosis* in cattle, buffaloes & goats was carried out in an organized livestock farm in Jamdoli, Rajasthan state. In this study the prevalence of M*ycobacterium avium* subsp. *paratuberculosis* reactors were confirmed in buffaloes and goat population, while the cattle population remained intact for M*ycobacterium avium* subsp. *paratuberculosis* infection. The study suggests that the infection in buffaloes and goats could be due to the prevalence of different ruminant strain or it could be due to a host specific goat strain in case of goat population. Detailed molecular studies needed to rule out the MAP strain causing infection in ruminants and then to confirm a host specific goat strain.

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