



SHORT COMMUNICATION

First Report of *Mycobacterium avium subspecies paratuberculosis* Infection in Yaks (*Bos mutus*) in Gansu Province, China

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ABSTRACT

Paratuberculosis (PTB) is an important bacterial disease in ruminants caused by *Mycobacterium avium subspecies paratuberculosis* (MAP). However, no information is available about MAP infection in yaks (*Bos mutus*) in China. Blood samples were collected from 1584 yaks, which consist of 610 black yaks and 974 white yaks from April 2013 through March 2014 from Gansu province, northwest China, and were tested for the antibodies against MAP using an indirect ELISA kit commercially available. The seroprevalence of MAP in yaks was 20.52% (325/1584), 22.13% (135/610) for black yaks and 19.51% (190/974) for white yaks. The MAP seroprevalences of yaks were detected in all three regions, 19.51, 19.86 and 22.84%, respectively. Logistic regression analysis suggested that abortion history was the risk factor concerning MAP infection in yaks ($P < 0.05$), breed, gender, age, geographic origin, and season were not considered as risk factors in this study. As far as we know, this is the first report of MAP infection in yaks in China, which provides information for controlling MAP infection in yaks.

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INTRODUCTION

Paratuberculosis (known as Johne's disease), an important bacterial disease in primarily domestic and wild ruminants, is caused by *Mycobacterium avium subsp. paratuberculosis* (MAP) (Sun *et al.*, 2015). Transmission of MAP is mainly through ingestion of milk and faeces contaminated with pathogens. MAP can cause chronic proliferative enteritis, refractory diarrhea and even death (Pieper *et al.*, 2015). Cattle are the most susceptible animals, it can cause significant damage to the cattle industry worldwide, it is listed as a notifiable disease by World Organization for Animal Health (OIE) (Correa-Valencia *et al.*, 2016). Moreover, PTB is associated with Crohn's disease in human (Correa-Valencia *et al.*, 2016).

Recently, a large number of surveys in various animals have been conducted in many countries like UK, France, Canada, Italy, Japan and Oman. However, no such data concerning MAP in yaks are available in China. Yaks are a unique semi-wild bovine species, which mainly live

in Tibetan Plateau. The white yak is a unique yak breed, and approximately 49,400 white yaks lived only in the Tianzhu Tibetan Autonomous County (TTAC), Gansu province, northwest China (Ma *et al.*, 2016). Therefore, we surveyed the MAP seroprevalence in yaks in Gansu province, and evaluated the risk factors that influenced MAP seroprevalence for the first time.

MATERIALS AND METHODS

Study design: A total of 1584 blood samples were collected between April 2013 and March 2014. 974 blood samples were obtained from white yaks (from TTAC) and 610 blood samples were obtained from black yaks (from Gannan Tibetan Autonomous Prefecture) in Gansu province, northwest China. Then blood samples were centrifuged to separate the serum as soon as possible. Detail information about breed, gender, age, geographic origin, abortion history and season were collected from local farmers and listed in Table 1.

Serological assay: The antibodies against MAP in serum were tested using a commercially available indirect ELISA kit (paratuberculosis, ID Screen® kit from ID-Vet, Montpellier, France) following the manufacturer's instructions (Meng *et al.*, 2015). Both the sensitivity (Se) and specificity (Sp) were 100% in the bovine, ovine and caprine sera as provided by the manufacturer. Moreover, the serum samples with doubtful or positive results were re-tested.

Data analysis: The variation in seroprevalence of MAP-infected yaks of different variables including breed, gender, age, geographic origin, abortion history and season were analyzed by SAS version 9.1 (SAS Institute Inc., USA). If Probability (P) value less than 0.05, this variable was considered as risk factor and calculated the odds ratios (ORs) with 95% confidence intervals (95% CIs).

RESULTS AND DISCUSSION

Three hundred and twenty-five (20.52%) out of 1584 serum samples were seropositive for MAP infection using the indirect ELISA kit. The MAP seropositive yaks were detected in all farms. The seroprevalences of MAP in Luqu, Maqu and Tianzhu were 19.86, 22.84 and 19.51%, respectively. MAP seroprevalence ranged from 17.32 to 23.03% in different age groups of yaks. Male yaks had a slightly higher seroprevalence (22.72%) compared to females (19.59%). Among yaks sampled in different seasons, MAP seroprevalence ranged from 16.12 to 22.70%. White yaks had a bit lower seroprevalence (19.51%) compared to black yaks (22.13%). Moreover, yaks with abortion history (22.60%) had a higher seroprevalence than that in yaks without abortion history (15.97%).

Overall, the results showed the gender, age, breed, season and region of yaks were not significant risk factors for MAP ($P > 0.05$) analyzed by logistic regression model. A significant difference has been found between yaks with abortion history or not ($P < 0.05$), for which the OR was 1.456 (95% CI 1.012- 2.094) (Table 2). In this study, the overall MAP seroprevalence in the tested yaks was 20.52%, with 22.13% in black yaks and 19.51% in white yaks. This prevalence (20.52%) was slightly lower than the 22% seroprevalence among dromedary camels in the Canary Islands, Spain (Mentaberre *et al.*, 2013), but higher than that in sika deer (17.64%) in China (Meng *et al.*, 2015). The MAP seroprevalence in this study was much higher than the 11.79% reported dairy and beef cattle in northern and northeastern China, 4.8% in dairy cattle in China (Sun *et al.*, 2015; Liu *et al.*, 2017), 3.3% in cattle in Korea (Lee and Jung, 2009), 0.84% in Mongolian cattle in Mongolia (Ochirkhuu *et al.*, 2015), and 0.3% in saiga antelope in Kazakhstan (Orynbayev *et al.*, 2016). Transmission of MAP is mainly through ingestion of milk and faeces contaminated with pathogens. The free-ranging herds of yaks have a better chance to eat the grass contaminated with faeces. Moreover, other factors may be contributable to such differences, including the species, sample size, geographical conditions and farm management.

Table 1: Seroprevalence of *Mycobacterium avium* subspecies *paratuberculosis* (MAP) infection in yaks in Gansu province, northwestern China by enzyme-linked immunosorbent assay (ELISA)

Factor	Category	No. tested	No. positive	% (95 % CI)
Breed	White yaks	974	190	19.51 (17.02-22.00)
	Black yaks	610	135	22.13 (18.84-25.43)
Gender	Male	471	107	22.72 (18.93-26.50)
	Female	1113	218	19.59 (17.26-21.92)
Age (years)	0<years ≤2	578	121	20.93 (17.62-24.25)
	2<years ≤4	521	120	23.03 (19.42-26.65)
	4<years	485	84	17.32 (13.95-20.69)
Season	Spring	428	91	21.26 (17.39-25.14)
	Summer	354	74	20.90 (16.67-25.14)
	Autumn	467	106	22.70 (18.90-26.50)
	Winter	335	54	16.12 (12.18-20.06)
Region	Tianzhu	974	190	19.51 (17.02-22.00)
	Luqu	146	29	19.86 (13.39-26.34)
	Maqu	464	106	22.84 (19.03-26.67)
Abortion history	Yes	323	73	22.60 (18.04-27.16)
	No	431	72	16.71 (13.18-20.23)
Total		1584	325	21.09

Table 2: Odds ratios for abortion history as risk factor for *Mycobacterium avium* subspecies *paratuberculosis* (MAP) seroprevalence in yaks (n=1584)

Factor	Group	Prevalence (%)	OR	95%CI	P-value
Abortion history	Yes	22.60	1.46	1.01-2.09	0.042
	No	16.71	Reference		

The present study has shown that the adult yaks with abortion history had a 1.46 times higher risk of infecting MAP compared with those without abortion history (OR= 1.46, 95% CI=1.012-2.094). This result is similar to the previous study, which found that the cattle with abortion history have a significantly higher seroprevalence than those without abortion history (Sun *et al.*, 2015).

Conclusions: This study revealed that MAP prevalence (20.52%, 325/1584) is widely distributed in white (19.51%) and black (22.13%) yaks in Gansu province, northwest China. Abortion history of yak is considered as the risk factor to affect the MAP seroprevalence significantly. Moreover, the findings of this study provided base-line information to prevent and control MAP infection in yaks.

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Authors contribution: JGM designed the study, performed the test and write the paper. DHZ collected the blood samples. WBZ, XXZ and YZ performed the test and revised the manuscript. GXH and RD designed the study and revised the manuscript. All authors read the manuscript and approved the contents.

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