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# Accuracy of three diagnostic tests for diagnosis of *Mycobacterium avium* subsp. *paratuberculosis* in domestic ruminants using Bayesian latent class models

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## INTRODUCTION

- Paratuberculosis, is a chronic wasting disease affecting domestic and wild ruminants globally, caused by *Mycobacterium avium* subsp. *paratuberculosis* (MAP).
- The primary route of MAP transmission is faecal-oral.
- Infected animals can shed MAP in faeces and milk for up to two years before clinical signs appear, leading to environmental contamination and persistence.
- MAP infections often go undetected; however, in late stages, symptoms such as intermittent or persistent diarrhea, weight loss, decreased milk production, and mortality may develop.
- Various diagnostic tests exist for detecting MAP, though none possess perfect accuracy as a reference standard, largely due to low sensitivity.
- Commonly used MAP diagnostic tests include direct tests (e.g., faecal smear, culture, PCR) and indirect tests (e.g., ELISA, interferon- $\gamma$ ).
- Assessing the accuracy of diagnostic tests traditionally requires knowledge of the true infection status. However, a definitive gold standard for MAP detection in animals is currently lacking.
- Latent class models (LCMs) offer a valuable approach to estimate sensitivity (Se) and specificity (Sp) of multiple diagnostic tests in the absence of a reference standard.

## Objectives:

1. Estimate the Se and Sp of faecal smear (FS), faecal PCR, and serum ELISA for detecting MAP infections in sheep, goats, cattle, and camels in flocks/herds with a previous history of MAP infection using LCM.
2. Estimate the prevalence of MAP infection in each ruminant species in this context.



## MATERIALS AND METHODS

**Study design:** A cross-sectional study was conducted in the Eastern province of Saudi Arabia to collect faecal and blood samples from animals over 2 years old including 240 camels, 220 sheep, 123 goats, and 66 cattle.

**Diagnostic tests:** three tests were performed including:

- **Faecal smears (FS):** Faecal sample was decontaminated with 0.9% hexadecylpyridinium chloride, and the supernatant was smeared, stained with Ziehl-Neelsen, and examined microscopically. A sample was considered positive if at least 10 acid-fast bacilli were observed across 100 fields.
- **Faecal IS900-PCR:** MAP DNA extraction was performed using QIAamp® PowerFecal® kit (QIAGEN, Courtaboeuf, France). Amplification of the IS900 gene was carried out using an iCycler PCR machine (BIO-RAD, Hercules, CA, USA). A sample was deemed positive if the IS900-PCR yielded positive results.
- **Serum antibody-ELISA:** IDEXX ELISA kit (*Mycobacterium paratuberculosis* antibody test kit, IDEXX, Hoofddorp, Netherlands) was used. A sample was deemed positive if the S/P ratio was  $\geq 55\%$ .

**Statistical analyses:**

**Model and assumptions:** A three-tests-one-population BLCM was fitted and FS and PCR to be dependent conditionally on the true MAP health status of animals.

**Prior information:** Prior information about the accuracy of FS, PCR and ELISA for each ruminant species was obtained from the literature where available (**Table 1**).

**Table 1.** Prior information and corresponding distributions assumed in BLCM to estimate Se and Sp of ELISA, FS, and PCR in four different ruminant species.

Parameter	Prior information (% and 2.5 <sup>th</sup> or 97.5 <sup>th</sup> percentile) and corresponding $\beta$ distribution							
	Camels		Sheep		Goats		Cattle	
<b>Prevalence</b>	NA	$\beta(1, 1)$	NA	$\beta(1, 1)$	NA	$\beta(1, 1)$	NA	$\beta(1, 1)$
<b>Se-ELISA</b>	NA	$\beta(1, 1)$	32 (68)	$\beta(3.2, 5.7)$	69 (46)	$\beta(13.7, 6.7)$	27.3 (38.3)	$\beta(21.6, 55.9)$
<b>Sp-ELISA</b>	95 (80)	$\beta(56.6, 7.1)$	97 (94)	$\beta(100, 4.0)$	95 (90)	$\beta(100, 6.2)$	97.4 (96.6)	$\beta(100, 3.6)$
<b>Se-FS</b>	NA	$\beta(1, 1)$	NA	$\beta(1, 1)$	NA	$\beta(1, 1)$	43.7 (48.7)	$\beta(100, 128.5)$
<b>Sp-FS</b>	NA	$\beta(1, 1)$	NA	$\beta(1, 1)$	NA	$\beta(1, 1)$	98 (95.4)	$\beta(100, 3.0)$
<b>Se-PCR</b>	NA	$\beta(1, 1)$	36 (58)	$\beta(8.1, 13.6)$	19 (35)	$\beta(7.5, 29.1)$	50.3 (36.4)	$\beta(24.3, 24.0)$
<b>Sp-PCR</b>	95 (80)	$\beta(56.6, 7.1)$	98 (94)	$\beta(100, 3.0)$	98 (93)	$\beta(98.2, 2.9)$	93.5 (87.5)	$\beta(100, 7.8)$

## RESULTS

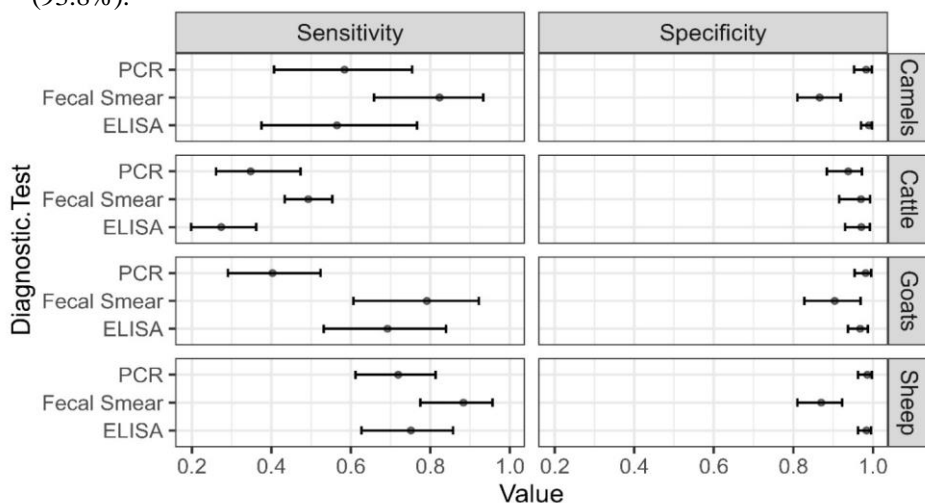
- The number of tested animals per herd/flock ranged from 10 to 41 camels, 6 to 55 sheep, 11 to 38 goats, and 6 to 11 cattle.
- Overall, FS yielded more positive results than ELISA or PCR across all species.
- At least one positive test result was observed in each herd/flock.
- Cross-tabulated results by species are shown in **Table 2**.



**Table 2.** Cross tabulated test results by species used in the BLCM to estimate Se and Sp of ELISA (Test 1), FS (Test 2), and PCR (Test 3)

Species	+/+/+	+/+/-	+/-/+	+/-/-	-/+/+	-/+/-	-/-/+	-/-/-	Total
Camels	17	5	0	0	9	31	0	178	240
Sheep	52	5	0	0	10	23	0	130	220
Goats	19	6	0	0	4	13	0	81	123
Cattle	12	2	0	0	4	17	0	31	66

- The highest MAP prevalence was observed in cattle (78.5%), followed by sheep (32.5%), goats (29.0%), and camels (15.0%).
- Across all species, FS showed the highest median Se among tests (**Figure 1**).
- Median Se estimates for all tests were generally lower in cattle (<50%) compared to other species.
- In sheep, Se values for all tests exceeded 70%, while in camels, Se ranged from 56.7% for ELISA to 82.3% for FS (**Figure 1**).
- Among goats, PCR had a lower Se (median = 40.3) compared to ELISA (median = 69.3) and FS (median = 79.1).
- Median Sp across tests was above 86%, with FS yielding the lowest Sp in camels (86.6%), sheep (87.0%), and goats (90.4%). In cattle, PCR had the lowest Sp (93.8%).



**Figure 1.** Median (point) and 95% Bayesian credible intervals (bars) of Se and Sp of ELISA, FS, and PCR to detect MAP infections in four different ruminant species

## CONCLUSIONS

- Considering individual and population test metrics, cost, and laboratory turnaround time, ELISA appears to be a suitable option for identifying MAP-infected animals in this region and prevalence context.
- Our results underscore the importance of understanding population context and pre-test disease probability when interpreting test accuracy estimates.