Svāsthya: Trends in General Medicine and Public Health
https://doi.org/10.70347/svsthya.v2i6.124

Original Article

Prevalence, Risk Factors, and Antimicrobial Susceptibility of *Pasteurella multocida* and *Mannheimia hemolytica*: Insights from Jigjiga, Ethiopia

Mustafa Ibrahim Ali[1]*, Bruk Abraha Fitwi[2], Shihun Shimelis[2], Yahia Yasin Hassan[3], Ahmed Abdi Mohomed[3], Hassan Abdi Arog[3]

[1] Faculty of Agriculture and Veterinary Medicine, East Africa University, Garowe, Puntland, Somalia; [2]College of Veterinary Medicine, Haramaya University, Dire Dawa, Haramaya, Ethiopia; [3] College of Veterinary Medicine, Jigjiga University, Jigjiga, Ethiopia

ABSTRACT

Background: Pasteurellosis pneumonia caused by *Mannheimia hemolytica* and *Pasteurella multocida* causes significant economic losses in sheep production and has zoonotic potential. However, epidemiological and antimicrobial resistance data from the Somali region are still limited. **Objective**: To estimate the prevalence of *M. hemolytica* and *P. multocida*, identify associated risk factors, and evaluate the antimicrobial resistance profile of sheep at the Jigjiga slaughterhouse in Ethiopia. **Methods:** A cross-sectional study was conducted from March to August 2023 in which 384 sheep lung samples at the Jigjiga slaughterhouse. Bacteriological isolation, biochemical identification, and antimicrobial susceptibility testing were performed via the disk diffusion method. Data were analyzed via STATA 16.0 with descriptive statistics, chi-square tests, and multivariate logistic regression analysis. **Results:** The overall prevalence of *Pasteurella spp.* isolates was 26.8% (95% CI: 22.46-31.55), with *M. hemolytica* and *P. multocida* accounting for 19.79% and 7.03%, respectively. Young sheep had a 2.15-fold greater risk (OR=2.15; 95% CI: 1.33–3.48; P=0.002) than adults did. Poor body condition increased the risk by 2.44 times (OR=2.44; 95% CI: 1.18–5.04; P=0.016) compared with moderate body condition. High sensitivity to gentamicin (100% *M. hemolytica*, 85.71% *P. multocida*) and kanamycin (97.36% *M. hemolytica*, 92.85% *P. multocida*) was detected. High resistance to oxytetracycline (92.10% *M. hemolytica*, 100% *P. multocida*), tetracycline (81.52% vs. 92.85%), penicillin-G (86.84% vs. 85.71%), and ampicillin (73.52% vs. 78.57%) was detected. The prevalence of multidrug resistance reached 81.57% in *M. hemolytica isolates* and 92.85% in *P. multocida* isolates. **Conclusion:** The prevalence of Pasteurellosis in sheep in Jigjiga is quite high, with *M. hemolytica* being the most dominant species. Antimicrobial surveillance programs, integrated control strategies, and molecular characterization of isolates are needed.

KEYWORDS
Respiratory disease, antimicrobial resistance, Pasteurellosis, epidemiology, risk factors, Ethiopia

ARTICLE INFO
Received Mar 19, 2025
Revised Jan 30, 2026
Accepted Jan 30, 2026
Online Jan 31, 2026

EDITOR
I Made Dwi Mertha Adnyana, M.Ked.Trop.

CORRESPONDENCE
Mustafa Ibrahim Ali, Faculty of Agriculture and Veterinary Medicine, East Africa University; mustafaibrahim@eaun.edu.so

CITE THIS ARTICLE

Ali MI., Fitwi., BA., Shimelis S., Hassan YY., Mohomed AA., and Arog HA (2025). Prevalence, risk factors, and antimicrobial susceptibility of *Pasteurella multocida* and *Mannheimia hemolytica*: Insights from Jigjiga, Ethiopia. *Svāsthya: Trends in General Medicine and Public Health*, 2(6): e124. https://doi.org/10.70347/svsthya.v2i6.124.

INTRODUCTION

Respiratory diseases are a major constraint on sheep productivity worldwide [1,2]. Pneumonia in small ruminants is a multifactorial disease complex involving interactions between pathogens (bacteria, viruses, and Mycoplasma), host factors (immune status, age, and body condition), and environmental conditions (stress, ventilation, and pen density). In Ethiopia, pneumonia causes morbidity of up to 35% and mortality of 5–10% in sheep populations [3,4].

Mannheimia hemolytica and *Pasteurella multocida* are opportunistic commensal pathogens of the upper respiratory tract that become invasive when the host's defenses are compromised [5,6]. Both species are gram-negative, nonmotile, facultatively anaerobic bacteria of the *Pasteurellaceae* family that are responsible for the majority of cases of Pasteurellosis pneumonia in sheep. *M. hemolytica* serotypes A1 and A2 are frequently isolated from patients with acute pneumonia, whereas *P. multocida* types A and D are associated with secondary infections and chronic pneumonia [3,7]. Pathogenesis involves the colonization and production of leukotoxins, lipopolysaccharides, and other virulence factors that cause massive lung damage [8,9].

Pasteurellosis diagnosis relies on bacteriological isolation, biochemical characteristics, and molecular confirmation. Disease management relies on prophylactic and therapeutic antimicrobial agents [10,11]. However, antimicrobial resistance (AMR) in *Pasteurellaceae* has increased globally owing to the inappropriate use of antibiotics in veterinary practice [12]. Recent studies have shown that resistance to tetracyclines reaches 80–100% in *P. multocida* isolates from various countries, while resistance to macrolides and fluoroquinolones is also increasing [13,14]. Resistance mechanisms are mediated by plasmids, integrative conjugative elements, and chromosomal mutations that facilitate horizontal transfer between bacterial species [15,16].

In Ethiopia, several studies have documented ovine Pasteurellosis in the highlands (Debre Birhan, Wollo, Fogera, and Amhara); however, data from the lowlands, particularly the Somali Region, are limited. Belina et al. [17] reported strain characterization in Wollo, but there have been no recent publications on the prevalence, risk factors, and antimicrobial resistance profiles in Jigjiga. This information gap hinders the development of evidence-based control strategies and rational antimicrobial use.

This study aimed to estimate the prevalence of *M. hemolytica* and *P. multocida* in sheep at the Jigjiga slaughterhouse, identify the associated risk factors, and evaluate the antimicrobial susceptibility profile of the isolates. These findings provide baseline data for the development of animal health policies, AMR surveillance programs, and antimicrobial use recommendations in the Somali Region of Ethiopia.

MATERIALS AND METHODS

Study design and location

A cross-sectional observational study was conducted from March to August 2023 at the Jigjiga slaughterhouse, the capital of the Somali Region, Ethiopia (9°20′N, 42°47′E, elevation 1,609 m; **Figure 1**). The Fafan zone has a semiarid climate with an average temperature of 20–35°C and bimodal rainfall of 660 mm/year. The dominant production system is agropastoral, with livestock populations of 558,229 cattle, 807,519 sheep, 712,699 goats, and 126,911 camels. The slaughterhouse slaughters an average of 30 sheep/day, sourced from the districts of Dhagahbur, Kebribayah, Babile, and Gursum.

Population and selection criteria

The target population was sheep slaughtered at the Jigjiga slaughterhouse during the study period. The inclusion criteria were as follows: sheep appeared healthy during *antemortem* inspection, no history of antimicrobial treatment 14 days prior to slaughter (based on owner interviews), and lungs without macroscopic lesions of abscesses or severe consolidation. The exclusion criteria were as follows: sheep with severe cachexia (body condition score <1), lungs with advanced pathological lesions indicating chronic infection, and samples contaminated during collection

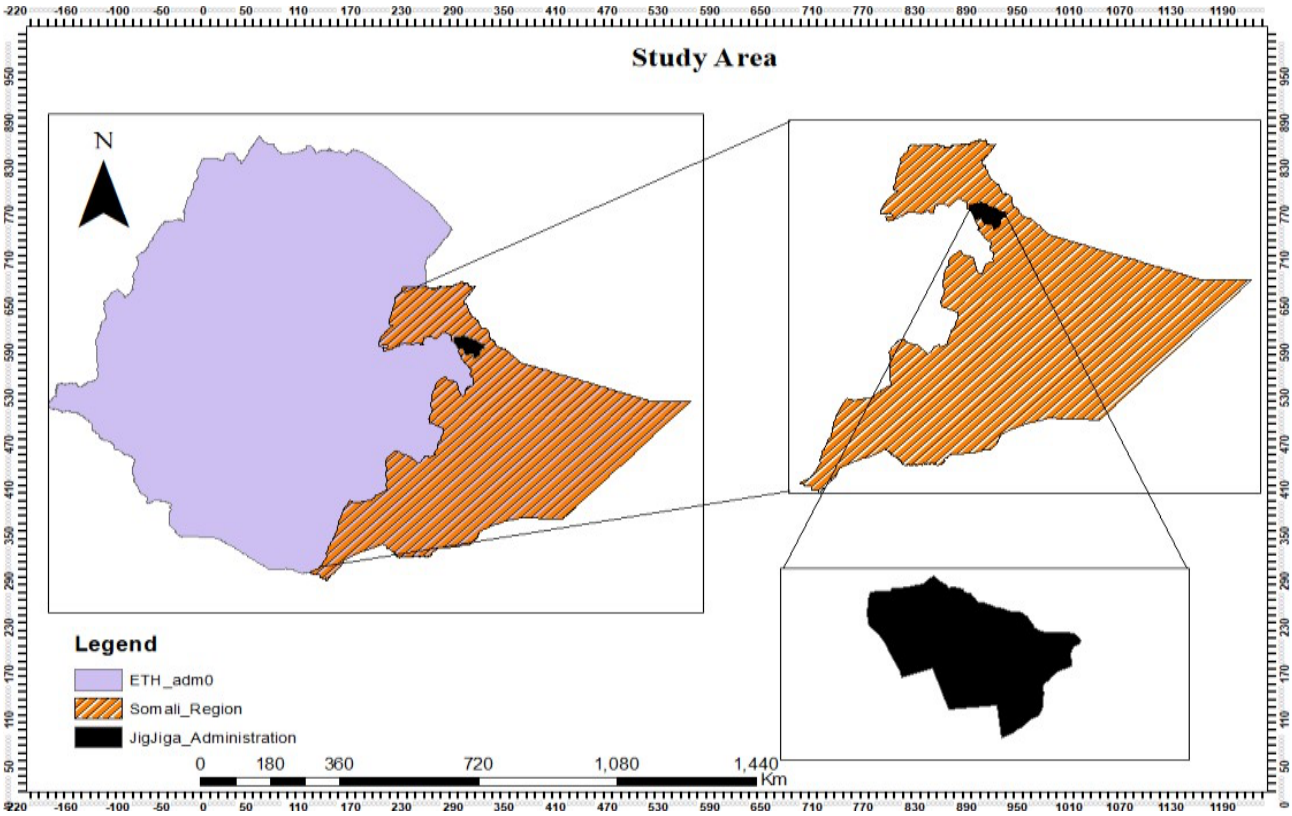

Figure 1. Research location in Jigjiga, Ethiopia

Sample size determination

The sample size was calculated via the prevalence formula for proportional data, assuming an expected prevalence of 50% (without prior data from this region), a confidence level of 95%, and an absolute precision of 5%, that is, $n = (Z^2 \times P \times (1-P))/d^2 = (1.96^2 \times 0.5 \times 0.5)/(0.05)^2 = 384$ samples

Sampling technique

Systematic random sampling was applied with a sampling interval of four. The slaughterhouses were visited twice a week (Tuesdays and Fridays) for 24 weeks. Every 4th sheep slaughtered was selected systematically until the target of eight sheep per day was reached. The sampling interval was calculated as follows: (50 days × 30 sheep/day) ÷ 384 = 3.9 ≈ 4.

Data and specimen collection

Demographic data were recorded on a standardized form: origin (district), sex, age (based on dentition according to Girma et al., 2008: young <2 years with 0–6 permanent teeth; adult ≥2 years with ≥8 permanent teeth), and body condition score (1-5 according to Thompson et al., 1994, categorized as poor [1-2], moderate [3], good [4-5]). Immediately after slaughter and evisceration, lung tissue was aseptically collected from the edge of the diaphragmatic lobe via sterile surgical knives and forceps. Specimens measuring 2×2 cm were placed in labeled sterile plastic bags, stored in *a cool box* with *ice packs* (4–8°C), and transported within 2 h to the Jigjiga Regional Veterinary Diagnostic and Research Laboratory.

Laboratory procedures

Bacterial isolation

The surfaces of the lung samples were decontaminated with 70% alcohol and burned. The tissue was cut aseptically, weighed at 1 g, and homogenized in 3 ml of tryptose-soy broth (TSB, Oxoid, UK). The suspension was incubated at 37°C for 18–24 hours under aerobic conditions. One *loop* (10 µl) of the culture was inoculated onto 5% sheep blood agar (Oxoid, UK) and incubated at 37°C for 24 h.

Morphological identification

The colonies that grew were evaluated for the following characteristics: size, color, and hemolysis. *M. hemolytica* forms gray, moist, hemolytic (β-hemolysis) colonies with a diameter of 1–2 mm. *P. multocida* produces gray, round, nonhemolytic, sometimes mucoid colonies with a diameter of 1–3 mm. Colonies were purified on nutrient agar and subjected to Gram staining. The gram-negative coccobacillus isolates were further processed.

Biochemical tests

Catalase (production of O_2 bubbles with 3% H_2O_2), oxidase (purple color with tetramethyl-p-phenylenediamine), indole (red ring with Kovac's reagent), and growth on MacConkey agar, *triple sugar iron* (TSI: acid slope/acid base, H_2S negative) were used. *M. hemolytica*: catalase$^+$, oxidase$^+$, indole$^-$, MacConkey$^+$ (pink colonies). *P. multocida*: catalase$^+$, oxidase$^+$, indole$^+$, MacConkey$^-$, characteristic sweet odor.

Antimicrobial sensitivity testing

The Kirby–Bauer disk diffusion test was performed on Mueller-Hinton agar supplemented with 5% sheep blood, according to the CLSI VET01-A4 (2013) standards. The bacterial suspension was adjusted to a standard concentration of 0.5 McFarland (1.5×10^8 CFU/ml). The following antibiotic discs (Oxoid, UK) were applied: ampicillin (10 µg), gentamicin (10 µg), kanamycin (30 µg), oxytetracycline (30 µg), penicillin-G (10 IU), and tetracycline (30 µg). The plates were incubated at 37°C for 20–24 hours. The diameter of the inhibition zone was measured via a digital caliper and interpreted as sensitive (S), intermediate (I), or resistant (R) on the basis of CLSI M31-A3. Multidrug resistance (MDR) was defined as resistance to ≥3 different classes of antimicrobials.

Statistical analysis

The data were analyzed via STATA 16.0 (StataCorp USA). The prevalence was calculated as the proportion of positive samples with a 95% confidence interval via the Wilson method. Bivariate associations between categorical variables were tested via *the chi-square test* or *Fisher's exact test* (cells <5). Univariate logistic regression analysis was performed to calculate crude odds ratios (CORs). Variables with P<0.25 were included in the multivariate model. Multivariate logistic regression with backward elimination was used to calculate adjusted odds ratios (AORs). Interactions and confounding factors were evaluated. The goodness-of-fit was tested via the Hosmer–Lemesh test, and statistical significance was set at P<0.05 [18].

Ethical considerations

This study was approved by the Haramaya University Research Ethics Committee (Ref: CREC/011/2023). Operational permission was obtained from the Somali Regional Livestock Bureau of Ethiopia. Verbal consent was obtained from the sheep owners. All procedures followed the OIE animal welfare guidelines.

RESULTS

Prevalence of P. multocida and M. hemolytica

Among the 384 lung samples cultured, 103 (26.8%; 95% CI: 22.46-31.55) were positive for *Pasteurellaceae* species. Species identification revealed that 76 isolates (73.79% positive) were *M. hemolytica,* with a prevalence of 19.79% (95% CI: 15.93–24.24), and 27 isolates (26.21% positive) were *P. multocida,* with a prevalence of 7.03% (95% CI: 4.78–10.07). No coinfections were observed in the samples. The distributions of the prevalence rates based on the demographic variables are shown in Table 1. In terms of geographical origin, the highest prevalence was found in sheep from Gursum (32.0%), followed by those from Babile (27.63%), Kebribayah (26.22%), and Dhagahbur (23.42%) villages. For *M. hemolytica*, the highest prevalence was in Kebribayah (30.26% of total *M. hemolytica* isolates), whereas *P. multocida* was highest in Kebribayah and Gursum (33.33% of total *P. multocida* isolates).

In terms of sex, females had a greater prevalence (30.53%) than males did (24.9%), although the difference was not statistically significant. The proportion *of M. hemolytica* was greater in

males (64.47% of total isolates) than in females (35.53%), whereas *P. multocida* was relatively balanced (51.85% males vs. 48.15% females). The prevalence based on age was significantly different. Young sheep had a prevalence of 36.15% (47/130), which was significantly greater than that in adults (22.04%; 56/254). In terms of species distribution, 43.43% of the *M. hemolytica* isolates and 55.5% of the *P. multocida* isolates were from the young group. The prevalence based on body condition was poor at 35.18% (19/54), good at 28.93% (57/197), and moderate at 20.30% (27/133). Although poor conditions had the highest prevalence, the difference was not statistically significant (P=0.072).

Table 1. Prevalence of *M. hemolytica* and *P. multocida* on the basis of demographic characteristics

Variable	Category	n (Examined)	n (Positive, %)	Prevalence (95% CI)	*M. hemolytica* n (%)	*P. multocida* n (%)
Origin	Dhagahbur	111	26 (23.42)	18.88-28.70	21 (27.63)	5 (18.51)
	Kebribayah	122	32 (26.22)	19.02-34.59	23 (30.26)	9 (33.33)
	Babile	76	21 (27.63)	18.27–38.92	17 (22.37)	4 (14.81)
	Gursum	75	24 (32.00)	21.91-43.75	15 (19.74)	9 (33.33)
Gender	Male	253	63 (24.90)	19.79-30.68	49 (64.47)	14 (51.85)
	Female	131	40 (30.53)	23.01-39.08	27 (35.53)	13 (48.15)
Age	Young	130	47 (36.15)	28.08-44.98	33 (43.42)	14 (51.85)
	Adult	254	56 (22.05)	17.11–27.79	43 (56.58)	13 (48.15)
Physical Condition	Good	197	57 (28.93)	22.77-35.80	41 (53.95)	16 (59.26)
	Moderate	133	27 (20.30)	14.01–28.09	21 (27.63)	6 (22.22)
	Poor	54	19 (35.19)	23.06-49.06	14 (18.42)	5 (18.52)
Total		**384**	**103 (26.82)**	**22.46-31.55**	**76 (19.79)**	**27 (7.03)**

Risk factor analysis

Bivariate analysis via the chi-square test revealed that age was significantly associated with the prevalence of Pasteurellosis (χ^2=8.72; P=0.003), whereas origin (P=0.631), sex (P=0.238), and body condition (P=0.072) were not significantly associated (Table 2).

Table 2. Bivariate analysis of factors associated with the occurrence of Pasteurellosis

Variable	Category	n Examined	n Positive	Prevalence (%)	χ^2	P value
Origin	Dhagahbur	111	26	23.42	1.72	0.631
	Kebribayah	122	32	26.22		
	Babile	76	21	27.63		
	Gursum	75	24	32.00		
Gender	Male	253	63	24.90	1.40	0.238
	Female	131	40	30.53		
Age	Young	130	47	36.15	8.72	0.003*
	Adult	254	56	22.05		
Physical Condition	Good	197	57	28.93	5.25	0.072
	Moderate	133	27	20.30		
	Poor	54	19	35.19		

Remarks: * indicates a significant difference (p<0.05)

The results of the univariate and multivariate logistic regression analyses are presented in Table 3. According to the univariate analysis, young age (OR=2.00; 95% CI: 1.26-3.18; P=0.003) and poor physical condition (OR=2.13; 95% CI: 1.09-4.18; P=0.027) were significantly associated. In the final multivariable model, after adjusting for all covariates, young age remained a significant independent predictor (AOR=2.15; 95% CI: 1.33-3.48; P=0.002), indicating that young sheep were 2.15 times more likely to be infected than adults were. Poor body condition also remained significant (AOR=2.44; 95% CI: 1.18–5.04; P=0.016), with a 2.44-fold greater chance of infection than moderate body condition. Geographic origin and sex did not show significant independent associations after adjustment. The multivariable model showed good *goodness-of-fit* (Hosmer–Lemeshow χ^2=6.32; P=0.611), with an area under the ROC curve of 0.68 (95% CI: 0.62-0.74), indicating moderate discriminatory ability.

Table 3. Univariate and multivariate logistic regression of Pasteurellosis risk factors

Variable	Category	Positive/ Total	COR (95% CI)	P value	AOR (95% CI)	P value
Origin	Dhagahbur	26/111	1.00 (Ref)	-	1.00 (Ref)	-
	Kebribayah	32/122	1.16 (0.65-2.05)	0.609	1.17 (0.63–2.16)	0.616
	Babile	21/76	1.24 (0.65–2.37)	0.503	1.32 (0.66–2.63)	0.423
	Gursum	24/75	1.54 (0.81–2.91)	0.182	1.70 (0.86–3.34)	0.123
Gender	Male	63/253	1.00 (Ref)	-	1.00 (Ref)	-
	Female	40/131	1.32 (0.83-2.11)	0.239	1.25 (0.77–2.03)	0.352
Age	Adult	56/254	1.00 (Ref)	-	1.00 (Ref)	-
	Young	47/130	2.00 (1.26-3.18)	0.003*	2.15 (1.33–3.48)	0.002*
Body Condition	Moderate	27/133	1.00 (Ref)	-	1.00 (Ref)	-
	Good	57/197	1.59 (0.94-2.66)	0.079	1.72 (1.00–2.94)	0.050
	Poor	19/54	2.13 (1.09–4.18)	0.027	2.44 (1.18–5.04)	0.016

Remarks: * indicates a significant difference (p<0.05), COR: crude odds ratio; AOR: adjusted odds ratio; CI: confidence interval.

Antimicrobial sensitivity profile

Among the 103 positive isolates, 52 (38 *M. hemolytica isolates* and 14 *P. multocida isolates*) were tested against six antimicrobial agents via the disk diffusion method. The results are shown in Table 4. For *M. hemolytica*, the highest sensitivity was observed for gentamicin (100%, 38/38) and kanamycin (97.36%, 37/38). In contrast, high resistance to oxytetracycline (92.10%, 35/38), penicillin-G (86.84%, 33/38), tetracycline (81.58%, 31/38), and ampicillin (73.68%, 28/38) was detected. The proportion of intermediate resistance was low for all antimicrobials tested (<14%). For *P. multocida*, high sensitivity was observed for kanamycin (92.86%, 13/14) and gentamicin (85.71%, 12/14), and universal resistance was observed against oxytetracycline (100%, 14/14). High resistance rates were also detected for tetracycline (92.86%, 13/14), penicillin-G (85.71%, 12/14), and ampicillin (78.57%, 11/14).

Table 4. Antimicrobial sensitivity profiles *of M. hemolytica* and *P. multocida*

Antimicrobial (Concentration)	*M. hemolytica* (n=38)			*P. multocida* (n=14)		
	S n (%)	I n (%)	R n (%)	S n (%)	I n (%)	R n (%)
Ampicillin (10 µg)	7 (18.42)	3 (7.89)	28 (73.68)	1 (7.14)	2 (14.29)	11 (78.57)
Gentamicin (10 µg)	38 (100)	0 (0.00)	0 (0.00)	12 (85.71)	2 (14.29)	0 (0.00)
Kanamycin (30 µg)	37 (97.36)	1 (2.63)	0 (0.00)	13 (92.86)	1 (7.14)	0 (0.00)
Oxytetracycline (30 µg)	0 (0.00)	3 (7.89)	35 (92.11)	0 (0.00)	0 (0.00)	14 (100)
Penicillin-G (10 IU)	1 (2.63)	4 (10.53)	33 (86.84)	1 (7.14)	1 (7.14)	12 (85.71)
Tetracycline (30 µg)	2 (5.26)	5 (13.16)	31 (81.58)	0 (0.00)	1 (7.14)	13 (92.86)

Remarks: S: sensitive; I: intermediate; R: resistant.

Multidrug resistance patterns

Analysis of multidrug resistance (MDR) patterns revealed that 31 of 38 *M. hemolytica* isolates (81.58%) and 13 of 14 *P. multocida* isolates (92.86%) were resistant to three or more classes of antimicrobials. For *M. hemolytica*, the dominant MDR pattern was simultaneous resistance to four drugs (tetracycline-oxytetracycline-penicillin G-ampicillin), which was detected in 55.26% of the isolates (21/38). Resistance to three drugs was detected in 26.32% of the isolates in the following groups: oxytetracycline-penicillin G-ampicillin (13.16%), tetracycline-oxytetracycline-penicillin G (10.53%), and tetracycline-oxytetracycline-ampicillin (2.63%). For *P. multocida*, the proportion of MDR bacteria was greater (92.86%). The four-drug pattern (tetracycline-oxytetracycline-penicillin G-ampicillin) was found in 64.29% of the isolates (9/14). Three-drug resistance was detected in 28.57% of the isolates, with the following patterns: tetracycline-oxytetracycline-penicillin G (14.29%), tetracycline-oxytetracycline-ampicillin (7.14%), and oxytetracycline-penicillin G-ampicillin (7.14%). The drug resistance patterns (Table 5).

Table 5. Multidrug resistance patterns

Number of Resistant Drugs	Resistance Pattern	Number of Isolates (%)
M. hemolytica **(n=38)**		
	OTC-PEN-AMP	5 (13,16)
3 drugs	TET-OTC-PEN	4 (10.53)
	TET-OTC-AMP	1 (2.63)
4 drugs	TET-OTC-PEN-AMP	21 (55.26)
Total MDR		**31 (81.58)**
Non-MDR		**7 (18.42)**
P. multocida **(n=14)**		
	TET-OTC-PEN	2 (14.29)
3 drugs	TET-OTC-AMP	1 (7.14)
	OTC-PEN-AMP	1 (7.14)
4 drugs	TET-OTC-PEN-AMP	9 (64.29)
Total MDR		**13 (92.86)**
Non-MDR		**1 (7.14)**

Remarks: TET: Tetracycline; OTC: Oxytetracycline; PEN: Penicillin-G; AMP: Ampicillin

DISCUSSIONS

This study provides the first comprehensive epidemiological data on ovine Pasteurellosis and the antimicrobial resistance profiles *of M. hemolytica* and *P. multocida* in the Somali Region of Ethiopia. The overall prevalence of 26.8% is consistent with several reports from the Ethiopian highlands [17,19–21], but lower than that reported by Abdulkadir et al. [4]. This variation reflects differences in agroecology, management practices, and climatic factors [22]. The Somali region, a semiarid lowland region, has lower humidity than highlands do, which can reduce the transmission of respiratory pathogens [2,5,23,24].

The greater proportion of *M. hemolytica* (73.79%) than *P. multocida* (26.21%) is consistent with global findings and previous Ethiopian reports [4,7,19]. The dominance of *M. hemolytica* can be explained by its superior virulence capacity, which is mediated by leukotoxin (LktA), lipopolysaccharides, capsules, and adhesion factors that facilitate the colonization and invasion of the lungs [25,26]. A recent study by Garzon et al. [24] via whole-genome sequencing revealed that *M. hemolytica* has a more complete arsenal of virulence genes than does *P. multocida*, including iron acquisition systems, biofilm formation genes, and secretion systems. Although the proportion *of P. multocida* is relatively low, its role in coinfection and secondary pneumonia should not be overlooked.

Multivariate analysis revealed that young age (AOR=2.15) was a significant, independent risk factor. These findings are consistent with the global literature showing that lambs are more susceptible to infection because of immature immune systems, inadequate passive immunity transfer, and weaning stress [7,20,27]. The adaptive immune response of young sheep to

Pasteurellaceae capsule antigens requires 4–6 weeks to reach protective levels. Additionally, colonization of the upper respiratory tract by *M. hemolytica* increases during stressful periods, such as during transport, which is common in young sheep. Poor body condition (AOR=2.44) was also a significant independent predictor. Malnutrition causes immunosuppression through multiple pathways, including decreased lymphocyte proliferation, complement deficiency, impaired phagocyte function, and decreased antibody production [28]. Deficiencies in micronutrients, such as selenium, vitamin E, and zinc, which are common in sheep with poor body conditions, exacerbate susceptibility to respiratory infections. These findings are consistent with those of Abate et al. [7], who reported a higher prevalence in sheep with low body condition scores.

The absence of a significant association with geographic origin (P=0.123) and sex (P=0.352) after multivariable adjustment indicated that these factors were not independent determinants in the context of this study. The variation in prevalence between districts (23.42–32.00%) likely reflects differences in management practices, vaccination status, and prevalence of viral coinfections rather than intrinsic geographical factors. The absence of significant sex-based differences is consistent with several studies, although some reports suggest that females are more susceptible to stress due to reproductive and lactation stress [22].

The antimicrobial sensitivity profile revealed interesting findings. High sensitivity to gentamicin (100% *M. hemolytica*, 85.71% *P. multocida*) and kanamycin (97.36% vs. 92.86%) indicates that aminoglycosides remain effective. These findings are consistent with those of Marshall et al. [29], who reported high sensitivity to aminoglycosides in isolates from sheep in California. The effectiveness of gentamicin may be attributed to its more limited use in ruminant veterinary practice in Ethiopia than first-line antibiotics do, resulting in minimal selection pressure for resistance. The mechanism of action of aminoglycosides, which inhibit 30S ribosomal protein synthesis with high affinity, makes the development of spontaneous resistance difficult.

Conversely, the high resistance to tetracycline (81.58% *M. hemolytica*, 92.86% *P. multocida*) and oxytetracycline (92.11% vs. 100%) reflects excessive and inappropriate use in Ethiopian veterinary practice. Tufa et al. [19] reported that oxytetracycline is the most commonly prescribed and most misused antibiotic by Ethiopian farmers. Tetracycline resistance is mediated by the tet(H) and tet(R) genes, which encode efflux pumps, and the tet(M) gene, which causes ribosomal protection [30]. These genes are often located on integrative conjugative elements (ICEs) that facilitate horizontal transfer between *Pasteurellaceae* species and other gram-negative bacterial genera [31,32].

Penicillin-G resistance (86.84% *M. hemolytica*, 85.71% *P. multocida*) and ampicillin resistance (73.68% vs. 78.57%) are likely mediated by the production of β-lactamases encoded by the bla gene on plasmids. Rahman et al. [33] explained that the extensive use of penicillin in global human and veterinary medicine has triggered strong selection for resistance. A study by Dieb et al. [34] in Egypt reported high β-lactam resistance in *Pasteurellaceae* from various animals. The very high proportion of multidrug resistance (81.58% *M. hemolytica*, 92.86% *P. multocida*) was the most concerning finding of this study. The MDR prevalence in this study was higher than that reported by Vu-Khac et al. [35] 74.19% in *M. hemolytica* from Vietnam and close to that reported by Tang et al. [31] 93% in *P. multocida* from Chinese pigs). The dominant MDR pattern against four drugs (tetracycline-oxytetracycline-penicillin G-ampicillin) in 55.26% of *M. hemolytica* and 64.29% of *P. multocida* indicates the coselection of resistance genes located on the same mobile genetic elements. Genomic studies by Jian et al. [16] revealed that ICEs carrying multiple resistance gene clusters can be transferred horizontally through conjugation, even between different species of bacteria.

Clinical and public health implications

The findings of this study have practical implications for sheep health management and antimicrobial use policy in the Somali Region. Widespread resistance to tetracycline, oxytetracycline, penicillin G, and ampicillin necessitates the revision of treatment protocols. Gentamicin and kanamycin should be considered first-line options for confirmed cases of

Pasteurellosis, with pretherapy sensitivity testing to guide rational therapy. Identifying young sheep and animals in poor body condition as high-risk populations facilitates targeted intervention strategies: (1) preweaning nutritional supplementation to enhance passive immunity transfer; (2) minimizing transport stress and grouping of young sheep; (3) implementing risk-based vaccination programs for vulnerable age groups; and (4) regular body condition monitoring with proactive nutritional interventions. From a public health perspective, the high prevalence of MDR in potential zoonotic pathogens, such as *P. multocida,* is a cause for concern. Although transmission of Pasteurellaceae from sheep to humans is rare, cases of pneumonia and sepsis have been reported in slaughterhouse workers and farmers. Antimicrobial resistance in veterinary pathogens can contribute to reservoirs of resistance genes that can be transferred to human pathogens through horizontal gene transfer in the environmental microbiome (One Health perspective).

Limitations

This study has several limitations that need to be considered when interpreting the results. First, isolation was limited to *M. hemolytica* and *P. multocida* without including *Bibersteinia trehalosi*, an emerging Pasteurellosis pathogen in sheep. Second, bacterial identification relies on conventional bacteriological methods without molecular confirmation (PCR) or *whole-genome sequencing*, making it impossible to identify specific virulence genes, serotypes, and genotypic resistance mechanisms. Third, samples were obtained from apparently healthy sheep that were slaughtered, thus not fully representing the prevalence of pneumonia in sheep with clinical manifestations of pneumonia in the field. Fourth, only 50% of the isolates (52/103) were tested for antimicrobial sensitivity due to the limited availability of antibiotic discs, which may affect the precision of resistance prevalence estimates. Fifth, the *cross-sectional* design does not allow for causal inference and cannot capture temporal variations in prevalence. Sixth, several potential risk factors, such as vaccination status, history of antimicrobial use, viral or parasitic coinfections, and specific management parameters, were not collected or analyzed

CONCLUSIONS

This study revealed that ovine Pasteurellosis has a substantial prevalence (26.8%) in sheep in Jigjiga, Somali Region, Ethiopia, with *M. hemolytica* being the dominant species. Young sheep and animals in poor body condition are high-risk groups. The antimicrobial resistance profile revealed widespread resistance to commonly used antibiotics (tetracycline, penicillin, and ampicillin), with an alarming prevalence of multidrug resistance (>80%). Aminoglycosides remain effective and should be considered for evidence-based therapies. In the future, it is necessary to (1) implement a systematic antimicrobial resistance surveillance program for respiratory pathogens in sheep and other animals with zoonotic potential; (2) develop and disseminate guidelines for prudent antimicrobial use by veterinary practitioners; (3) impose regulatory restrictions on access to antimicrobials without a veterinary prescription; (4) implement education programs for farmers on biosecurity, nutritional management, and early disease detection; (5) evaluate and optimize vaccination programs using locally serotype-based vaccines; (6) conduct further research using molecular techniques (*whole-genome sequencing*, serotyping, and resistome analysis) for comprehensive characterization of local isolates; and (7) conduct longitudinal studies to understand the temporal dynamics and additional risk factors affecting transmission and resistance

CONFLICT OF INTEREST

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

AUTHOR CONTRIBUTIONS

Conceptualization: MIA, BAF; Methodology: MIA, BAF; Software: MIA, SS; Validation: MIA, BAF, SS; Formal analysis: MIA, BAF; Investigation: MIA, BAF, YYH; Resources: YYH, AAM; Data Curation: YYH, AAM, HAA; Writing - Original Draft: MIA, BAF, SS; Writing - Review & Editing: MIA, BAF, YYH, HAA; Visualization: SS, AAM; Supervision: MIA, BAF; Project administration: MIA; Funding acquisition: MIA.

FUNDING

This study did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

ACKNOWLEDGMENTS

The authors gratefully acknowledge all slaughterhouses across Jigjiga that participated in this study and provided access to their facilities for research purposes. Their willingness to collaborate was essential to the success of this investigation. Special thanks are extended to PT. Mega Science Indonesia for their meticulous proofreading services and valuable contributions to enhancing the quality and clarity of this manuscript.

DECLARATION OF ARTIFICIAL INTELLIGENCE USE

We hereby confirm that no artificial intelligence (AI) tools or methodologies were utilized at any stage of this study, including during data collection, analysis, visualization, or manuscript preparation. All work presented in this study was conducted manually by the authors without the assistance of AI-based tools or systems.

REFERENCES

[1] Lachowicz-Wolak A, Chmielina A, Przychodniak I, Karwańska M, Siedlecka M, Klimowicz-Bodys M, et al. Antimicrobial-resistance and virulence-associated genes of Pasteurella multocida and Mannheimia haemolytica isolated from polish dairy calves with symptoms of bovine respiratory disease. Microorganisms 2025;13:491. https://doi.org/10.3390/microorganisms13030491.

[2] Klima CL, Alexander TW, Hendrick S, McAllister TA. Characterization of Mannheimia haemolytica isolated from feedlot cattle that were healthy or treated for bovine respiratory disease. Can J Vet Res 2014;78:38–45.

[3] Abera D, Mossie T. A review on pneumonic pasteurellosis in small ruminants. J Appl Anim Res 2023;51:1–10. https://doi.org/10.1080/09712119.2022.2146123.

[4] Abdulkadir M, Nigussie T, Kebede IA. Isolation and identification of Pasteurella multocida and Mannheimia haemolytica from pneumonic small ruminants and their antibiotic susceptibility in Haramaya District, Eastern Ethiopia. Sci World J 2024;2024:1–10. https://doi.org/10.1155/2024/5605552.

[5] Storoni C, Preziuso S, Attili A-R, Li Y, Cuteri V. Bacterial bovine respiratory disease: A comprehensive review of etiology, pathogenesis and management strategies. Microbiol Res (Pavia) 2026;17:18. https://doi.org/10.3390/microbiolres17010018.

[6] Jesse FFA, Amira NA, Isa KM, Maqbool A, Ali NM, Chung ELT, et al. Association between Mannheimia haemolytica infection with reproductive physiology and performance in small ruminants: A review. Vet World 2019;12:978–83. https://doi.org/10.14202/vetworld.2019.978-983.

[7] Abate FM, Fentie Kassa T. Isolation and identification of Mannheimia haemolytica and Pasteurella multocida from symptomatic and asymptomatic sheep and their antibiotic susceptibility patterns in three selected districts of north Gondar zone, Gondar Ethiopia. Vet Med Sci 2023;9:1803–11. https://doi.org/10.1002/vms3.1166.

[8] Lucas R, Hadizamani Y, Gonzales J, Gorshkov B, Bodmer T, Berthiaume Y, et al. Impact of bacterial toxins in the lungs. Toxins (Basel) 2020;12:223. https://doi.org/10.3390/toxins12040223.
[9] Aulik NA, Hellenbrand KM, Klos H, Czuprynski CJ. Mannheimia haemolytica and Its leukotoxin cause neutrophil extracellular trap formation by bovine neutrophils. Infect Immun 2010;78:4454–66. https://doi.org/10.1128/IAI.00840-10.
[10] Rahman M, Akther S, Alam M, Hassan M, Sarkar M, Ali M, et al. Prevalence and identification of caprine pasteurellosis in pneumonic goats in Bangladesh. J Adv Vet Anim Res 2023;10:538–44. https://doi.org/10.5455/javar.2023.j707.
[11] Akane AE, Alemu G, Tesfaye K, Ali DA, Abayneh T, Kenubih A, et al. Isolation and molecular detection of pasteurellosis from pneumonic sheep in selected areas of Amhara Region, Ethiopia: An implication for designing effective ovine pasteurellosis vaccine. Veterinary Medicine: Research and Reports 2022; 13:75–83. https://doi.org/10.2147/vmrr.s365267.
[12] Khalida Shaikh DD, Magar ZAA, Gaikwad PS, Adnyana IMDM, Sudaryati NLG, Eljatin DS, et al. One health integration: Global perspectives on animal health and sustainable agriculture. 1st ed. United States: John Wiley & Sons, Inc.; 2026. https://doi.org/10.1002/9781394295982.
[13] Abou-Jaoudeh C, Andary J, Abou-Khalil R. Antibiotic residues in poultry products and bacterial resistance: A review in developing countries. J Infect Public Health 2024;17:102592. https://doi.org/10.1016/j.jiph.2024.102592.
[14] Pintér K, Domán M, Wehmann E, Gantelet H, Magyar T. Comparative analysis of phenotypic and genotypic antibiotic susceptibility of Pasteurella multocida isolated from various host species in France and Hungary. Antibiotics 2025;14:906. https://doi.org/10.3390/antibiotics14090906.
[15] Castañeda-Barba S, Top EM, Stalder T. Plasmids, a molecular cornerstone of antimicrobial resistance in the One Health era. Nat Rev Microbiol 2024;22:18–32. https://doi.org/10.1038/s41579-023-00926-x.
[16] Jian Z, Zeng L, Xu T, Sun S, Yan S, Yang L, et al. Antibiotic resistance genes in bacteria: Occurrence, spread, and control. J Basic Microbiol 2021;61:1049–70. https://doi.org/10.1002/jobm.202100201.
[17] Belina D, Hailu Y, Gobena T, Hald T, Njage PMK. Prevalence and epidemiological distribution of selected foodborne pathogens in human and different environmental samples in Ethiopia: a systematic review and meta-analysis. One Health Outlook 2021;3:19. https://doi.org/10.1186/s42522-021-00048-5.
[18] Paulus AY, Sulaeman, Mayasari AC, Ayu JD, Musniati N, Sari MP, et al. Biostatistika Epidemiologi. 1st ed. Bandung: CV. Media Sains Indonesia; 2023.
[19] Tufa TB, Gurmu F, Beyi AF, Hogeveen H, Beyene TJ, Ayana D, et al. Veterinary medicinal product usage among food animal producers and its health implications in Central Ethiopia. BMC Vet Res 2018;14:409. https://doi.org/10.1186/s12917-018-1737-0.
[20] Tewodros A, Annania T. Sheep and goats pasteurellosis: Isolation, identification, biochemical characterization and prevalence determination in Fogera Woreda, Ethiopia. J Cell Animal Biol 2016;10:22–9. https://doi.org/10.5897/JCAB2016.0449.
[21] Alemu S, Belachew Y, Tefera T. Isolation and molecular detection of Mannheimia haemolytica and Pasteurella multocida from clinically pneumonic pasteurellosis cases of bonga sheep breed and their antibiotic susceptibility tests in selected areas of Southwest Ethiopian peoples regional s. Vet Med Res Rep 2023; 14:233–44. https://doi.org/10.2147/VMRR.S435932.
[22] Tüfekci H, Sejian V. Stress Factors and Their effects on productivity in sheep. Animals 2023;13:2769. https://doi.org/10.3390/ani13172769.
[23] Pica N, Bouvier NM. Environmental factors affecting the transmission of respiratory viruses. Curr Opin Virol 2012;2:90–5. https://doi.org/10.1016/j.coviro.2011.12.003.
[24] Garzon A, Miramontes C, Weimer BC, Profeta R, Hoyos-Jaramillo A, Fritz HM, et al. Comparison of virulence and resistance genes in Mannheimia haemolytica and Pasteurella

multocida from dairy cattle with and without bovine respiratory disease. Microbiol Spectr 2025;13:e1200-25. https://doi.org/10.1128/spectrum.01200-25.

[25] Liang C, Kareem K, Zhang L, Liang Y, Wu H, Li B, et al. Isolation, Pathogenicity and Genomic Analysis of Mannheimia haemolytica Strain XJCJMh1 in Bovine-Mycoplasma Co-Infection. Microorganisms 2025;13:2258. https://doi.org/10.3390/microorganisms13102258.

[26] Singh K, Ritchey JW, Confer AW. Mannheimia haemolytica. Vet Pathol 2011;48:338–48. https://doi.org/10.1177/0300985810377182.

[27] Girma S, Getachew L, Beyene A, Tegegne DT, Tesgera T, Debelo M, et al. Identification of serotypes of Mannheimia haemolytica and Pasteurella multocida from pneumonic cases of sheep and goats and their antimicrobial sensitivity profiles in Borana and Arsi zones, Ethiopia. Sci Rep 2023;13:9008. https://doi.org/10.1038/s41598-023-36026-2.

[28] Pike VL, Lythgoe KA, King KC. On the diverse and opposing effects of nutrition on pathogen virulence. Proceed Royal Soc B Biol Sci 2019;286:20191220. https://doi.org/10.1098/rspb.2019.1220.

[29] Jackson W, Tucker J, Fritz H, Bross C, Adams J, Silva M, et al. Antimicrobial susceptibility profiles among commensal Mannheimia haemolytica and Pasteurella multocida isolated from apparently healthy sheep processed in California: Results from a cross-sectional pilot study. Prev Vet Med 2024;233:106360. https://doi.org/10.1016/j.prevetmed.2024.106360.

[30] Alhamami T, Chowdhury P, Gomes N, Carr M, Veltman T, Khazandi M, et al. First emergence of resistance to macrolides and tetracycline identified in Mannheimia haemolytica and Pasteurella multocida isolates from beef feedlots in Australia. Microorganisms 2021;9:1322. https://doi.org/10.3390/microorganisms9061322.

[31] Tang X, Zhao Z, Hu J, Wu B, Cai X, He Q, et al. Isolation, Antimicrobial resistance, and virulence genes of Pasteurella multocida strains from swine in China. J Clin Microbiol 2009;47:951–8. https://doi.org/10.1128/JCM.02029-08.

[32] Li Z, Tang J, Wang X, Ma X, Yuan H, Gao C, et al. The environmental lifecycle of antibiotics and resistance genes: Transmission mechanisms, challenges, and control strategies. Microorganisms 2025;13:2113. https://doi.org/10.3390/microorganisms13092113.

[33] Rahman MdM, Alam Tumpa MstA, Zehravi M, Sarker MdT, Yamin Md, Islam MdR, et al. An overview of antimicrobial stewardship optimization: The use of antibiotics in humans and animals to prevent resistance. Antibiotics 2022;11:667. https://doi.org/10.3390/antibiotics11050667.

[34] Dieb Bahr A, Awad-allah Salib F, Adel Soliman Y, Mohamed Amin M. Multi-drug resistant Pasteurella multocida and Mannheimia haemolytica strains isolated from different hosts affected by pneumonic pasteurellosis in Egypt. Adv Anim Vet Sci 2020;9:364. https://doi.org/10.17582/journal.aavs/2021/9.3.356.364.

[35] Vu-Khac H, Trinh TTH, Nguyen TTG, Nguyen XT, Nguyen TT. Prevalence of virulence factor, antibiotic resistance, and serotype genes of Pasteurella multocida strains isolated from pigs in Vietnam. Vet World 2020;13:896–904. https://doi.org/10.14202/vetworld.2020.896-904.