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Original Article

Molecular detection and pathological evaluation of *Mesomycoplasma ovipneumoniae* and its co-infecting agents in pneumonic goats of Akola district, India

Kadam, N.¹; Kamdi, B.^{2*}; Ingole, R.²; Awandkar, S.³; Hajare, S.⁴; Wade, M.⁵ and Deshpande, K.⁶

¹MVSc Student, Department of Veterinary Pathology, Post Graduate Institute of Veterinary and Animal Sciences, Maharashtra Animal and Fishery Sciences University, Krushinagar, Akola, Maharashtra, India; ²Department of Veterinary Pathology, Post Graduate Institute of Veterinary and Animal Sciences, Maharashtra Animal and Fishery Sciences University, Krushinagar, Akola, Maharashtra, India; ³Department of Veterinary Microbiology, Post Graduate Institute of Veterinary and Animal Sciences, Maharashtra Animal and Fishery Sciences University, Krushinagar, Akola, Maharashtra, India; ⁴Department of Veterinary Pharmacology and Toxicology, Post Graduate Institute of Veterinary and Animal Sciences, Maharashtra Animal and Fishery Sciences University, Krushinagar, Akola, Maharashtra, India; ⁵Department of Poultry Science, Post Graduate Institute of Veterinary and Animal Sciences, Maharashtra Animal and Fishery Sciences University, Krushinagar, Akola, Maharashtra, India; ⁶Department of Animal Nutrition, Post Graduate Institute of Veterinary and Animal Sciences, Maharashtra Animal and Fishery Sciences University, Krushinagar, Akola, Maharashtra, India

*Correspondence: B. Kamdi, Department of Veterinary Pathology, Post Graduate Institute of Veterinary and Animal Sciences, Maharashtra Animal and Fishery Sciences University, Krushinagar, Akola, Maharashtra, India. E-mail: bhupeshkamdi@gmail.com

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Abstract

Background: *M. ovipneumoniae* is one of the pathogens responsible for chronic non-progressive pneumonia in sheep and goats. The pathogen disrupts mucociliary clearance and exacerbates disease severity through secondary infections. **Aims:** The present study aimed to investigate the occurrence of *M. ovipneumoniae* from pneumonic goats and to identify related pathomorphology. **Methods:** A total of 680 goat carcasses from Akola, Maharashtra, India, were examined. From these, 80 lung samples exhibiting pneumonia were collected, processed for *M. ovipneumoniae* confirmation and characterized for pulmonary lesions. **Results:** PCR analysis using genus specific primers identified *Mycoplasma* spp. in 35 cases (43.75%), while species specific primers targeting a fragment of the 16S rRNA gene confirmed *M. ovipneumoniae* in 24 cases (30%). Additionally, *Mannheimia haemolytica* and *Pasteurella multocida* were detected in 8 (33.33%, 8/24) and 3 (12.5%, 3/24) cases by employing PCR with 2 (8.33%, 2/24) cases exhibiting concurrent infection of all three pathogens, respectively. Five PCR amplicons of *M. ovipneumoniae* were subjected to phylogenetic analysis, confirming their clustering with other *M. ovipneumoniae* strains from India, USA and Turkey, while remaining distinct from other *Mycoplasma* spp. Histopathological analysis of *M. ovipneumoniae* positive lungs revealed bronchopneumonia (73.3%), broncho-interstitial pneumonia (13.3%) and interstitial pneumonia (26.66%). Characteristic lesions included fibrinous pleuritis, bronchiolar epithelial hyperplasia, necrotic alveolitis with type II pneumocyte hyperplasia, thickened interalveolar septa, syncytial cell formation and infiltration of inflammatory cells. Co-infections resulted in more severe lesions. **Conclusion:** The study confirmed the occurrence of *M. ovipneumoniae* in pneumonic goats from the region underscoring the need for large scale studies to understand its epidemiology.

Key words: Brochopneumonia, Histopathology, *M. haemolytica*, *P. multocida*, PCR

Introduction

Small ruminant rearing constitutes an integral component of the Indian economy, providing essential livelihood support to marginal and landless farmers. However, respiratory diseases, particularly pneumonia, represent a major health concern, accounting for approximately 5.6% of all small ruminant diseases (Nicholas, 2002). The development of pneumonia in

animals is influenced by a combination of infectious, environmental, managerial and host related factors (Kamdi *et al.*, 2020). Adverse weather conditions and suboptimal management practices exacerbate stress in animals, thereby increasing their susceptibility to infections (Chen *et al.*, 2024; Jayasekara *et al.*, 2025). Small ruminants are especially prone to respiratory infections of viral, bacterial and fungal origin, with the risk further amplified by poor management,

overcrowding, huddling and group rearing (Kumar *et al.*, 2014; Alwayel *et al.*, 2024). Among infectious diseases in goats, *Mycoplasma* infections cause major economic losses (Nicholas, 2002). The major *Mycoplasma* species linked to pneumonia in small ruminants are *Mesomycoplasma ovipneumoniae*, *Mycoplasma arginini*, *Mycoplasma mycoides* subspecies *capri*, *Mycoplasma capricolum* subspecies *capripneumoniae* (Mccp) and *M. capricolum* subspecies *capricolum* (Mcc) (Akwuobu *et al.*, 2016). Among these, *M. ovipneumoniae* is frequently involved in respiratory infections and an important agent causing non-progressive pneumonia (Ongor *et al.*, 2011; Jay *et al.*, 2020). The disease caused by *M. ovipneumoniae* has been given various names, such as atypical sheep pneumonia, mycoplasmal pneumonia, chronic bronchopneumonia, chronic non-progressive pneumonia and proliferative exudative pneumonia (Alley *et al.*, 1999; Sheehan *et al.*, 2007; Gonçalves *et al.*, 2010; Cassidy, 2026). *M. ovipneumoniae* primarily spreads through aerosolized droplets or close contact, with environmental factors, co-infections, host immune response and strain virulence all influencing disease severity, leading to variable morbidity and mortality (Nicholas *et al.*, 2008). Clinical signs include coughing, labored breathing, nasal discharge, weight loss and lung inflammation (Besser *et al.*, 2017). Animals infected with *M. ovipneumoniae* may display mild or inconspicuous symptoms, appearing healthy with a good appetite until secondary infections exacerbate the condition (Constable *et al.*, 2017). *M. ovipneumoniae* stimulates autoantibody production against ciliary antigens and inhibits lymphocyte function, which predisposes the host to secondary infections (Osman *et al.*, 2021). Additional risk factors that increase the risk include: overcrowding, poor ventilation in intensively reared lambs (Hervas *et al.*, 1996), stress caused by animal transportation (Alley *et al.*, 1999), varying ecological and climatic conditions and seasonal changes (Gonçalves *et al.*, 2010; Rifatbegovic *et al.*, 2011). In addition to affecting domesticated sheep and goats, *M. ovipneumoniae* can infect wild ruminants, including endangered species such as bighorn sheep (*Ovis canadensis*) (Besser *et al.*, 2013), musk oxen (*Ovibosmoschatus*) (Handeland *et al.*, 2014), porcupine caribou (*Rangifer tarandus granti*) (Rovani *et al.*, 2019) and white-tailed deer (*Odocoileus virginianus*) (Wolff *et al.*, 2019). This widespread susceptibility highlights its significance as a pathogen of concern in both domestic and wildlife animals.

Recent reports from various countries with established monitoring systems have indicated a rise in cases of *M. ovipneumoniae*, including Sweden, USA, France UK and India (Lindstrom *et al.*, 2018; Manlove *et al.*, 2019; Jay *et al.*, 2020; Deeney *et al.*, 2021). The most common pathological manifestation associated with *M. ovipneumoniae* is bronchopneumonia, marked by inflammation in the bronchioles and lung tissue, with hyperplasia of the cells lining the bronchial tubes (Constable *et al.*, 2017). Histopathological analysis of lungs infected with *M. ovipneumoniae* frequently shows

broncho-interstitial pneumonia and purulent or fibrinopurulent bronchopneumonia, characterized by significant alveolar, bronchial and bronchiolar damage due to the infiltration of polymorphonuclear cells (Waheed *et al.*, 2022). Diagnosing *M. ovipneumoniae* based on clinical signs and post-mortem lesions alone cannot provide a definitive diagnosis, as these symptoms may overlap with those of other significant infections (Santhiya *et al.*, 2021). Looking at a large geographical area of the country, region-wise information on epidemiology diseases will help to implement control measures. Currently, there is no data available on the occurrence of *M. ovipneumoniae* infection in the Akola district of Maharashtra State, India, despite the region housing 0.151076 million of goats (20th livestock census, India (2019)) (<https://dahd.maharashtra.gov.in/en/publication/20-th-livestock-census/>). Therefore, the present study was conducted to document the occurrence of *M. ovipneumoniae* by PCR, characterize pathomorphological alterations in *M. ovipneumoniae* affected goats so that it can help in planning effective disease treatment and control measures.

Materials and Methods

Ethics statement

The study was approved by Institutional Ethics Committee for Veterinary Clinical Research (IEC-VCR) (vide certificate NO. HS/TVCC/PGIVAS/226/2025 sr. 19). All samples used in the present study were collected from local butcherries and during diagnostic necropsy evaluation from Department of Veterinary Pathology, Post Graduate Institute of Veterinary and Animal Sciences, Akola. No animals were sacrificed specifically for research purposes. A total of 680 caprines were screened, out of which 80 samples were collected between April 2024 and December 2024 from goats of varying age, sex and breed in and around Akola.

Sampling

In the present study, samples were collected from selected local butcherries from Akola district, Maharashtra, India. Visits were arranged twice a week during April 2024 to December 2024 and 10-15 goat carcasses were examined carefully during each visit. As well as goat carcasses received for necropsy at the Department of Veterinary Pathology, PGIVAS, Akola, were also included in the study. Out of a total of 680 examined carcasses over a nine months period, 80 showing pneumonic lesions such as dark red to brown areas of consolidation, firm consistency, fibrin deposition, pleural adhesions and abscesses were selected for further pathological and molecular investigations to detect *Mesomycoplasma ovipneumoniae* and selected associated pathogens. Lung specimens at the margins of the lesions from selected 80 goats were collected for molecular confirmation of pathogens and histopathology in -20°C (deep freeze) and in 10% neutral buffered formalin respectively.

Primers

The PCR confirmation of pathogens was done using both genus specific and species specific primers. For *Mycoplasma* genus, GPO3F (5'-TGG GGA GCA AAC AGG ATT AGA TAC C-3') and MGSO (5'-TGC ACC ATC TGT CAC TCT GTT AAC CTC-3') primers targeting the 16S rRNA gene were used (Dhaygude *et al.*, 2023). Whereas, *M. ovipneumoniae* was confirmed by using MOVPF (5'-GTT GGT GGC AAA AGT CAC TAG-3') and MOVPR (5'-CTT GAC ACT GTT TCG CTG-3') primers targeting the 16S rRNA gene (Weiser *et al.*, 2012). *Pasteurella multocida* was detected using KMT1F (5'-ATC CGC TAT TTA CCC AGT GG-3') and KMT1R (5'-GCT GTA AAC GAA CTC GCC AC-3') primers targeting the *KMT* gene (Townsend *et al.*, 1998; Rawat *et al.*, 2019). For *Mannheimia haemolytica*, PHSSA gene-specific primers Forward (5'-TTC ACA TCT TCA TCC TC-3') and Reverse (5'-TTT TCA TCC TCT TCG TC-3') were used (Sarpe *et al.*, 2024).

DNA extraction and PCR assay

Pneumonic lung tissue samples were used for genomic DNA extraction using the QIAwave DNA Blood and Tissue Kit (Qiagen, India) following the manufacturer's instructions with slight modifications and stored at -20°C until further use. PCR amplification was carried out in a 25 µL reaction mixture using 2X Green Taq Master Mix (TaKaRa Bio, India) for the detection of *M. ovipneumoniae* and other selected respiratory pathogens. The reaction mix consisted of 12.5 µL of master mix, 1 µL each of forward and reverse primers (10 pmol), 5 µL of DNA template and 5.5 µL of nuclease free water. The components were mixed thoroughly, briefly centrifuged and subjected to PCR amplification using a thermal cycler (TaKaRa, India). Thermal cycling conditions were optimized based on the melting temperatures of the primers specific to each target pathogen, using known positive controls. For *Mycoplasma* spp. (16S rRNA, 280 bp) and *M. ovipneumoniae* (16S rRNA, 418 bp), the PCR protocol involved an initial denaturation at 94°C for 2 min, followed by 35 cycles of denaturation at 94°C for 15 s, annealing at 53°C for 15 s and extension at 72°C for 15 s, with a final extension at 72°C for 5 min (Weiser *et al.*, 2012; Dhaygude *et al.*, 2023). *P. multocida* (*KMT* gene, 460 bp) was amplified with an initial denaturation at 95°C for 5 min, 35 cycles of denaturation at 95°C for 15 s, annealing at 55°C for 15 s, extension at 72°C for 1 min, and a final extension at 72°C for 10 min (Rawat *et al.*, 2019). For *Mannheimia haemolytica* (*PHSSA* gene, 325 bp), the cycling conditions included an initial denaturation at 94°C for 3 min, 35 cycles of denaturation at 94°C for 1 min, annealing at 43°C for 45 s, extension at 72°C for 15 s, and a final extension at 72°C for 3 min (Sarpe *et al.*, 2024).

DNA sequencing and phylogenetic analysis

Representative PCR amplicons were sequenced at EUROFIN Scientifics, Bangalore, India. The obtained nucleotide sequences were analyzed using BioEdit and

aligned separately using the ClustalW method in MEGA 11 software. Multiple sequence alignment and phylogenetic analysis were performed in MEGA 11 software. The phylogenetic tree was constructed using the p-distance substitution model.

Histopathological examination

Lung tissues positive for *M. ovipneumoniae* were fixed in 10% neutral buffered formalin (NBF) for 48 h, trimmed and transferred to fresh NBF. After overnight washing under running water, tissues were dehydrated in ascending grades of ethanol (70%-95%) and absolute alcohol, followed by clearing in xylene. Paraffin embedding was carried out in two stages, each lasting 2 h. Thin sections (4-6 µm) were cut using a microtome, mounted on glass slides and stained with Hematoxylin and Eosin (H&E) (Luna, 1972).

Results

Prevalence of pneumonia and identification of *M. ovipneumoniae* and associated *M. haemolytica* and *P. multocida*

In the present study, among 680 goat carcasses, 80 goats were diagnosed with pneumonia, yielding a prevalence of 11.76% (80/680) in Akola district Maharashtra state India. PCR targeting the 16S rRNA gene successfully detected *Mycoplasma* spp. in 35 out of 80 lung samples from pneumonic animals, showing the occurrence rate of 43.75%, with a 280 bp amplicon observed on agarose gel electrophoresis (Fig. 1a). Further, species specific PCR identified *M. ovipneumoniae* (MO) in 24 samples (30%, 24/80) with a distinct band of 418 bp on agarose gel electrophoresis (Fig. 1b). Concurrent infections of *M. haemolytica* (MH) was identified in 8 samples (33.33%, 8/24) based on amplification of a 325 bp *PHSSA* gene fragment (Fig. 1c) and *P. multocida* (PM) was confirmed in 3 sample (12.5%, 3/24) with a 460 bp product specific to the *KMT* gene (Fig. 1d) in *M. ovipneumoniae* affected cases. Notably, two samples (8.3%, 2/24) revealed mixed infections of *M. haemolytica* and *P. multocida* along with *M. ovipneumoniae*.

Sequence analysis

Representative PCR amplicons (n=5) of 16S rRNA gene fragment of *M. ovipneumoniae*, were sequenced in both directions with the help of forward and reverse primers and the sequences were analyzed to ascertain the PCR diagnosis. The obtained nucleotide sequences were checked and trimmed using BioEdit software to generate consensus sequence. These sequences were then subjected to BLAST analysis, confirming their maximum similarity to *M. ovipneumoniae* strains available in the NCBI database. Further phylogenetic tree comprising 21 nucleotide sequences of the present study amplicons and corresponding nucleotide sequences of *M. ovipneumoniae* (05), *M. arginini* (02), *M. agalactiae*

(02), *M. capricolum* subsp. *Capripneumoniae* (02), *M. mycoides* subsp. *Capri* (02), *M. mycoidesmycoides* LC type (02), *M. capricolum* subsp. *Capricolum* retrieved from the NCBI. The phylogenetic analysis confirmed that the PCR amplicons from the present study clustered with *M. ovipneumoniae* sequences from NCBI including sequences from India, USA and Turkey, while

maintaining distinct separation from other *Mycoplasma* species. These findings provided molecular evidence of *M. ovipneumoniae* in the analyzed samples (Fig. 2). All five amplicons were submitted to the NCBI database with accession numbers PV413006, PV413005, PV413004, PV413003, and PV413002.

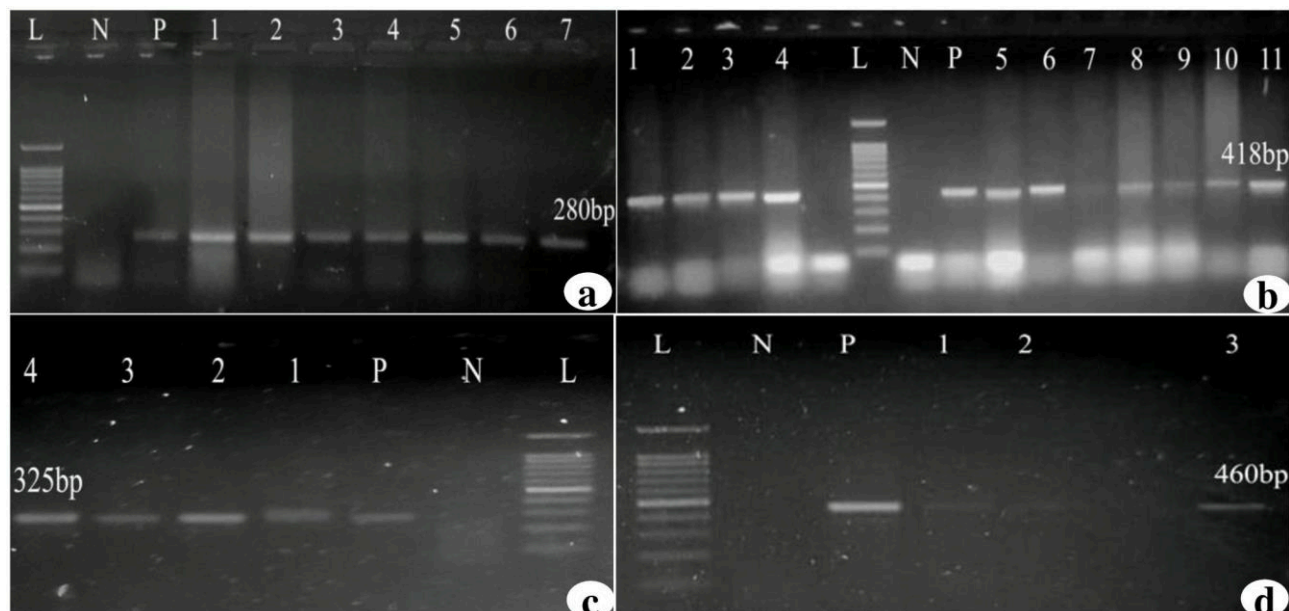


Fig. 1: Ethidium bromide-stained agarose gel electrophoresis showing lanes of P: Positive control, N: Negative control, L: 100 bp DNA ladder and positive samples (1, 2, ... n) for (a) *Mycoplasma* spp. (280 bp, *16S rRNA* gene), (b) *M. ovipneumoniae* (418 bp, *16S rRNA* gene), (c) *M. haemolytica* (325 bp, *PHSSA* gene), and (d) *P. multocida* (460 bp, *KMT* gene)

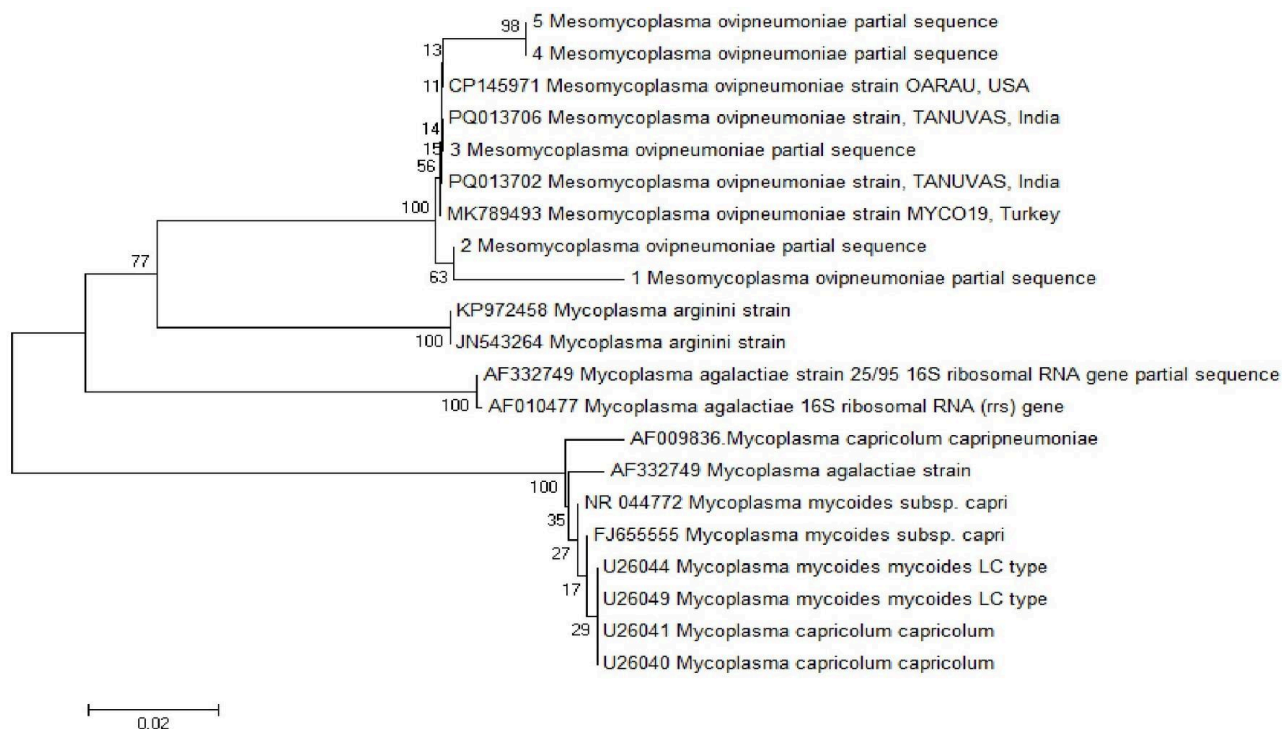


Fig. 2: Dendrogram showing phylogenetic analysis of partial fragments of *16S rRNA* of *M. ovipneumoniae* using Maximum Likelihood method with Neighboring-Joining bootstraps value (1000 replicates)

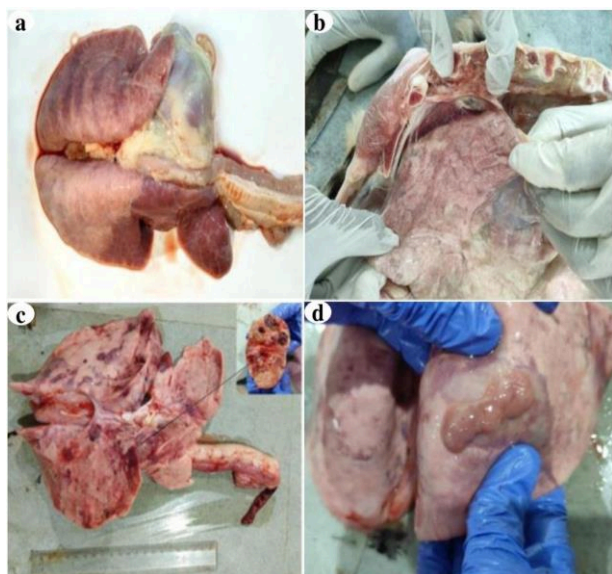


Fig. 3: Anatopathological findings in *M. ovipneumoniae* affected cases. (a) Lung showing marked consolidation of right cranial, middle and cranial diaphragmatic lobe, (b) Fibrinous adhesion between parietal and visceral pleura and thoracic wall, (c) Lung showing severe emphysema and multifocal areas of consolidation (Inset-dilated thickened bronchi obliterated with blood clots), and (d) Lung showing abscess on diaphragmatic lobe of right lung

Morphopathological findings

Necropsy on *M. ovipneumoniae* infected cases commonly exhibited chronic bronchopneumonia, characterized by pleural adhesions to the thoracic wall, thickened bronchial walls and multiple patches of dark brown consolidation primarily in the cranioventral regions (Figs. 3a and b). In some cases, consolidation extended throughout the lung parenchyma. Four cases revealed inflated lungs due to emphysema and congestion along with presence of multifocal dark reddish areas of consolidation throughout the parenchyma, wherein cut sections showed dilated thick walled bronchi obliterated with blood clots (Fig. 3c). In one case, focally extensive large abscess was noted on diaphragmatic lobe and on cut section, oozed a creamy purulent exudate (Fig. 3d).

Concurrently affected cases showed more severe lesions characterized by marked hyperemia of the nasal turbinates often accompanied by seromucoid to mucopurulent nasal secretions. The tracheal mucosa appeared diffusely congested, with accumulation of frothy exudate extending caudally to the level of the tracheal bifurcation. Furthermore, the mediastinal lymph nodes were diffusely enlarged and edematous. Six cases of co-infection with *M. ovipneumoniae* and *M. haemolytica* showed pale-yellow fibrinous coverings over areas of dark cranioventral consolidation and congestion of the diaphragmatic lobes. One case co-infected with *M. ovipneumoniae* and *P. multocida* revealed cranioventral consolidation accompanied by emphysematous changes. Additionally, two animals concurrently infected with *M. ovipneumoniae*, *M.*

haemolytica and *P. multocida*, had fibrinous bronchopneumonia along with well-demarcated cranioventral consolidation and congestion with emphysema in the remaining lung lobes.

Histopathological examination of pneumonic lungs in goats revealed a wide range of lesions across both single and concurrent infections involving *M. ovipneumoniae*, *M. haemolytica* and *P. multocida*. In *M. ovipneumoniae* infections, based on the presence of exudates within the bronchi, bronchioles and alveoli, the pneumonia cases were categorized as bronchopneumonia, broncho-interstitial pneumonia and interstitial pneumonia. Among the 15 cases, bronchopneumonia was the most prevalent (73.3%, 10/15), followed by interstitial pneumonia (20%, 3/15) and broncho-interstitial pneumonia (13.3%, 2/15). Bronchopneumonia cases were further categorized based on the nature of exudates into suppurative (acute) bronchopneumonia (13.33%, 2/15), fibrinous bronchopneumonia (13.33%, 2/15), subacute bronchopneumonia (6.66%, 1/15) and chronic bronchopneumonia (26.66%, 4/15) and, these forms showed characteristic infiltration of neutrophils, bronchiolar necrosis, fibrin deposition and fibrous tissue proliferation. Fibrinous pleuritis and severe BALT hyperplasia were noted in chronic cases. Bronchointerstitial pneumonia showed epithelial necrosis and luminal exudates, while interstitial pneumonia featured thickened septa, mononuclear infiltration and type II pneumocyte hyperplasia. Syncytial giant cells were observed in one case. Interstitial pneumonia cases exhibited fibrous thickening of septa, lymphocytic infiltration and type II pneumocyte proliferation (Figs. 4a-d).

Co-infected cases showed more severe and extensive lesions involving both upper and lower respiratory tracts. Nasal turbinates revealed goblet cell hyperplasia, congestion, hemorrhages and submucosal inflammatory cell infiltration, while the trachea displayed epithelial necrosis with mononuclear infiltration. Pulmonary lesions ranged from acute suppurative to fibrinous and subacute bronchopneumonia. These included severe epithelial necrosis with necrotic exudation in the bronchial lumen, obstruction of bronchiolar lumens due to epithelial desquamation and inflammatory exudate. Acute suppurative bronchopneumonia was characterized by a predominant infiltration of neutrophils within the bronchiolar and alveolar lumina with appearing as basophilic, spindle-shaped or oat shaped cells arranged in a streaming pattern around alveoli, an important characteristic of *M. haemolytica* infection. Fibrinous bronchopneumonia with fibrino-necrotic exudation, fibrinous pleuritis, central necrotic foci surrounded by fibrinous tissue, vascular thrombosis, proteinaceous alveolar exudates and type II pneumocyte proliferation were also recorded in 3 co-infected cases. Subacute forms demonstrated mononuclear infiltration, necrotic exudation and peribronchial lymphoid hyperplasia caused by concurrent infection of *M. ovipneumoniae* with *P. multocida*.

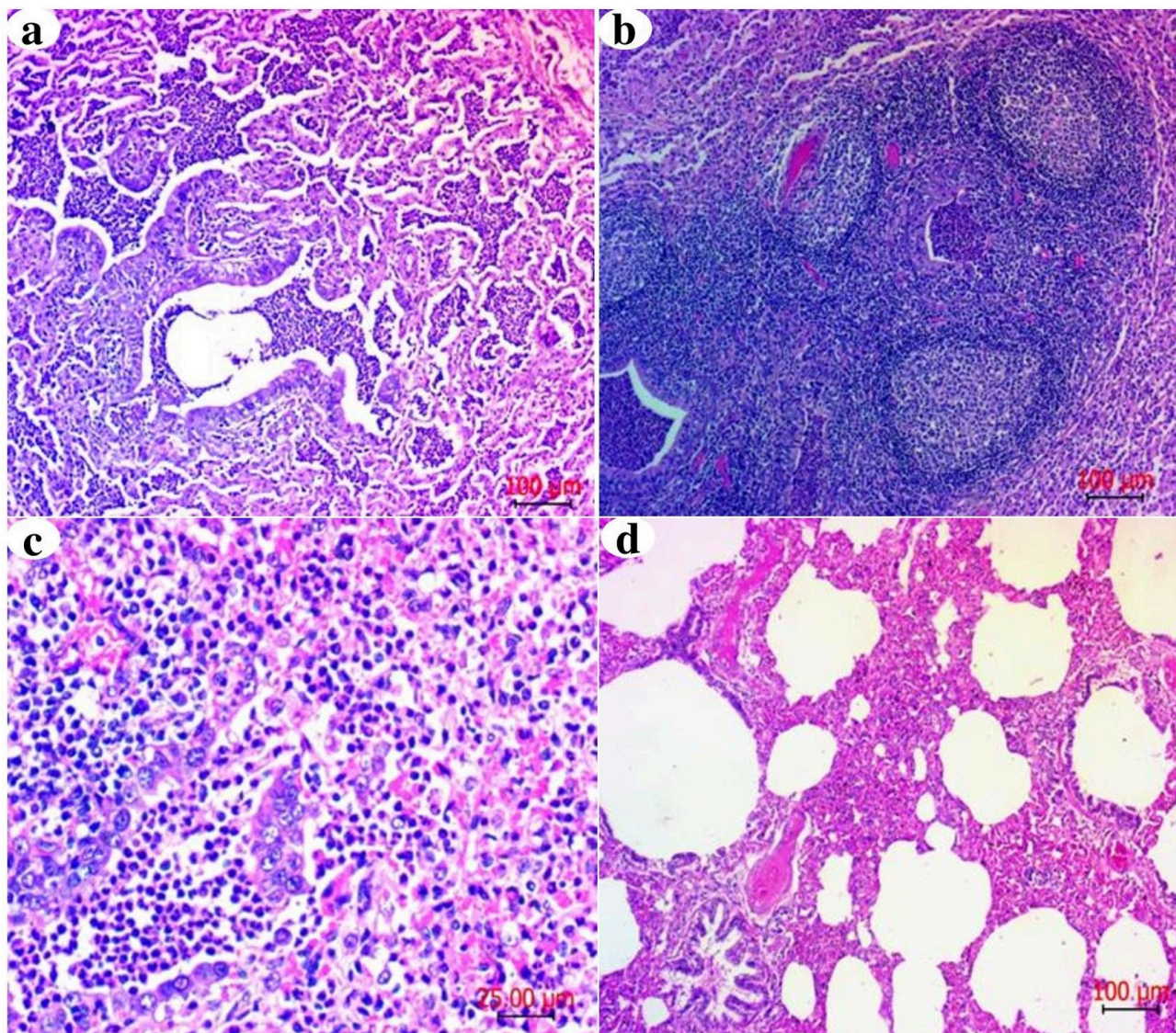


Fig. 4: Microphotographs stained with H&E from *M. ovipneumoniae* affected cases with (a) Marked infiltration of neutrophils within bronchiolar and alveolar lumen, (b) Marked hyperplasia of bronchial associated lymphoid tissue, (c) Syncytial cells along with infiltration of mononuclear cells in alveolar and bronchiolar lumen, and (d) Widened interalveolar septa, infiltration of mononuclear cells, type II pneumocyte hyperplasia and congestion (scale bars: 100 µm is applicable to a, b, d, and 25 µm to c)

Discussion

Respiratory diseases are among the most prevalent health issues affecting small ruminants globally, particularly in livestock-rearing countries (Lacasta *et al.*, 2008). *M. ovipneumoniae* is a well recognized pathogen responsible for respiratory infections in sheep and goats worldwide (Nicholas *et al.*, 2008). In the present study, the prevalence of pneumonia was found to be 11.76% (80/680) in goats from Akola district, Maharashtra. This is consistent with a similar prevalence reported by Baghezza (11%; 1440/13,084) in sheep at the Batna municipal slaughterhouse, Algeria. Higher prevalence rates have been reported at other locations: Udhayavel *et al.* (2025) noted 30% (60/200) in the southern part of India, and Mohammed *et al.* (2022) observed 26.9% (141/525) in Libya. Conversely, lower prevalence was reported by Daee *et al.* (2020) in Iran (2.77%; 50/1800)

and Asare *et al.* (2016) in Ghana (4.07%; 55/1350). These variations may be attributed to factors such as age, sex, immune status, seasonality, environmental conditions and herd management practices (Emikpe *et al.*, 2013).

PCR remains a reliable and rapid method for detecting *Mycoplasma* infections due to its superior sensitivity and specificity (Nicholas, 2002). In this study, a partial fragment of 16S *rRNA* gene was targeted, as previously described (Weiser *et al.*, 2012; Sarpe *et al.*, 2024). *Mycoplasma* spp. was detected in 43.75% (35/80) of pneumonic samples, closely aligning with the findings of Sarpe *et al.* (2024), who reported 40.62% positivity in sheep and goat lungs. Pavone *et al.* (2023) reported a slightly higher detection rate (52.5%) in goats from Italy, whereas Kilic *et al.* (2013), Rong *et al.* (2014), and Ghauri *et al.* (2024) reported lower rates of 16.16%, 26.1%, and 15.6% in Turkey, China, and Thailand,

respectively.

Species specific PCR identified *M. ovipneumoniae* in 30% (24/80) of cases. Comparable detection rates have been reported by Santhiya *et al.* (2021) in Kerala (25.16%) and Cheng *et al.* (2015) in China (28.89%). Concurrent infection with *M. haemolytica* and *P. multocida* highlights their potential synergism in exacerbating respiratory disease. Phylogenetic analysis of five representative *M. ovipneumoniae* PCR amplicons confirmed their identity and clearly differentiated them from other *Mycoplasma* spp.

Gross pathological lesions associated with *M. ovipneumoniae* in this study were consistent with previous findings by Daee *et al.* (2020) in Iran and Waheed *et al.* (2022) in Iraq. The right lung lobe was more frequently affected, similar to observations in West African Dwarf goats by Emikpe and Akpavie (2010), likely due to the anatomical positioning of the tracheobronchial tree favoring initial airflow toward the right lung. Multifocal consolidation and severe emphysema observed in some cases may result from elastin degradation by proteolytic enzymes released by necrotic macrophages and leukocytes (Dar *et al.*, 2014). Similar lesions, including cranial and middle lobe consolidation and lymphadenopathy, were also reported by Jacobson *et al.* (2025) in experimentally infected lambs.

Lesions in co-infected animals were in agreement with those described in previous studies (Ettorre *et al.*, 2007; Sheehan *et al.*, 2007; Lindstrom *et al.*, 2018; Taunde *et al.*, 2019). Lung consolidation involving adjacent lobes, especially between the right cranial and middle lobes, suggests spread via endobronchial or direct contact routes (Ozyildiz *et al.*, 2013). Sarpe *et al.* (2024) similarly documented co-infections in sheep and goats in Akola, with typical lesions such as cranioventral consolidation, frothy tracheal exudates and congested lungs. In the present study, lesions were predominantly confined to the cranioventral lung region, likely due to anatomical and physiological features of the respiratory tract, including abrupt bronchial branching, poor regional perfusion, impaired mucociliary clearance and gravitational exudate deposition.

Histopathologically, bronchopneumonia was most common, followed by interstitial and broncho-interstitial pneumonia, consistent with the findings of Al-Dujaily *et al.* (2023). Chronic bronchopneumonia, as observed in this study, is a hallmark of *M. ovipneumoniae* infection (Constable *et al.*, 2017). Similarly, histological alterations were reported by Kilic *et al.* (2013), Daee *et al.* (2020), and Al-Dujaily *et al.* (2023). The intense neutrophilic infiltration and alveolar necrosis may be attributed to pro-inflammatory cytokines such as IL-1 β , IL-6 and TNF- α (Waheed *et al.*, 2022). Chronic antigenic stimulation by *M. ovipneumoniae* likely drives the observed BALT hyperplasia (Li *et al.*, 2023). The presence of syncytial giant cells in one case may indicate a concurrent PPRV infection (Shanmugavadivu *et al.*, 2023). *M. ovipneumoniae* is known to impair host immunity by suppressing lymphocyte function, altering

macrophage activity and inducing autoantibodies against ciliary antigens (Maksimovic *et al.*, 2022), rendering the lungs susceptible to secondary infections (Chen *et al.*, 2024). While *M. ovipneumoniae* alone causes mild to moderate pneumonia, co-infections with *M. haemolytica* significantly exacerbate pathology. This is evident from the increased neutrophilic exudation and presence of “oat cells” (degenerating neutrophils) and macrophages a result of leukotoxin activity (Dag *et al.*, 2018). Pulmonary vascular thrombosis, as observed in this study, may result from rapid bacterial proliferation and endotoxin release, triggering widespread intravascular coagulation and subsequent ischemic necrosis (Lopez, 2001; Gharib *et al.*, 2021). Additional findings included bronchiolar hyperplasia, epithelial desquamation and fibrin deposition in alveoli hallmarks of barrier disruption and cytokine-mediated tissue injury (Lopez and Martinson, 2017).

Pathogenesis in *P. multocida* infections is primarily driven by endotoxins, lipopolysaccharides and outer membrane proteins (Amin, 2020). The capsular material of *M. haemolytica* also enhances epithelial adherence by interacting with pulmonary surfactant (Whiteley *et al.*, 1990). *M. ovipneumoniae* colonizes the ciliated respiratory epithelium, impairing mucociliary clearance and promoting chronic inflammation. Although *M. ovipneumoniae* typically causes subclinical or mild disease, its pathogenic potential is amplified in the presence of co-infections, leading to severe fibrinous pneumonia and necrosis (Pavone *et al.*, 2023). Predisposing factors such as overcrowding, inadequate housing conditions, transportation stress, abrupt environmental changes and nutritional deficiencies significantly contribute to the onset and severity of the disease (Jesse Abdullah *et al.*, 2014). These findings highlight the complex interplay between pathogen virulence, host immunity and management practices in shaping respiratory disease outcomes in small ruminants.

The present study reveals a presence of *Mesomycoplasma ovipneumoniae* infection in goats from Akola, Maharashtra, with co-infections involving *M. haemolytica* and *P. multocida*. Associated gross and microscopic lesions confirm its role in respiratory pathology. The findings highlight the complex etiology of pneumonia in goats and emphasize the need for improved diagnostics and surveillance so that control strategies can be implemented to mitigate economic losses and enhance animal health in the region.

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Conflict of interest

The authors have no conflict of interest to declare.

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Use of generative AI and AI-assisted technologies statements

The authors used AI-assisted Technologies to improve the language of the manuscript. Subsequently, the authors reviewed and revised the text to ensure accuracy. The authors assume full responsibility for the final version of the work.

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