

Antibiogram & Multidrug Resistance among Bacteria Isolated from Pigs with Respiratory Illness in Western Uttar Pradesh

Sachin Chaudhary¹, Shailja Katoch^{2*}, Naresh Chandra¹, Vikas Jaiswal¹, Aarti Bhatele¹, Rajeev Singh²

ABSTRACT

The present study was undertaken to identify the bacteria causing respiratory illness in pigs of western Uttar Pradesh, their antibiogram and multi-drug resistance. Fifty nasal samples were collected from pigs exhibiting respiratory clinical signs using sterile swabs. The samples were processed for isolation and identification of bacteria by conventional bacteriological methods. Forty-six bacteria were isolated, out of which 76.08% (35/46) were Gram negative and 23.91% (11/46) were Gram positive. Eight bacteria, viz., *Escherichia coli* (15.21%), *Pasteurella multocida* (15.21%), *Proteus vulgaris* (13.04%), *Bordetella bronchiseptica* (13.04%), *Pseudomonas aeruginosa* (13.04%), *Streptococcus suis* (10.86%), *Staphylococcus aureus* (10.86%) and *Klebsiella pneumonia* (8.69%) were identified. The *in-vitro* antibiotic sensitivity test of the bacterial isolates revealed, enrofloxacin and amikacin (78.26% each) as the most effective antibiotics followed by tetracycline, gentamicin, colistin (76.09% each) and streptomycin (67.39%). Among the bacterial isolates, highest resistance was found against amoxycylav (58.70%) followed by ampicillin (54.35%), chloramphenicol (47.83%) and cefixime (45.65%). In the present study, 31 (67.39%) isolates out of 46 showed multi-drug resistance (MDR). 34 (73.9%) bacterial isolates had multiple antibiotic resistance index (MARI) greater than 0.2. The study revealed that *E. coli*, *P. multocida*, *P. vulgaris*, *B. bronchiseptica*, *P. aeruginosa*, *S. suis*, *S. aureus* and *K. pneumonia* are the common bacteria that lead to respiratory diseases in pigs of western UP. The increased incidence of MDR isolates and MARI of > 0.2 emphasizes the significance of employing antimicrobials judiciously at the farms.

Key words: Antibiogram, Bacterial isolates, MARI, MDR, Pig, Respiratory Illness.

Ind J Vet Sci and Biotech (2026): 10.48165/ijvsbt.22.4.05

INTRODUCTION

The primary cause of morbidity and mortality in the global swine business is porcine respiratory infections (Sorensen *et al.*, 2006). There are a large number of bacterial and viral pathogens on the list of infectious agents that cause respiratory illness in pigs. Infectious agents and unfavourable environmental factors frequently combine to induce respiratory disease in pigs, which is a complex issue. Despite the efforts to manage and prevent respiratory infections, the present intensive pig breeding & husbandry practices increase the frequency and economic significance of respiratory disorders. The economic losses due to respiratory diseases are incurred both by direct and indirect losses. The direct losses are caused by death and forced slaughter, whereas the indirect losses are brought on by decreased daily gain, increased feed intake for average daily gain, extended fattening times, and increased treatment expenses. It has been determined that the following factors contribute to the economic losses caused by the incidence of respiratory disorders in the swine industry: lung condemnation (3%), condemnation of the sick animals (37%) and lower weight increase (60%) (Sorensen *et al.*, 2006).

Infectious pathogens that are both primary and opportunistic frequently work together to cause respiratory illness in pigs. Apart from the primary viral pathogens, the primary bacterial pathogens causing respiratory diseases

¹Department of Veterinary Pathology, College of Veterinary and Animal Science, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, Uttar Pradesh-250110 India

²Department of Veterinary Microbiology, College of Veterinary and Animal Science, SVP University of Agriculture and Technology, Meerut, Uttar Pradesh-250110 India

Corresponding Author: Dr. Shailja Katoch, Department of Veterinary Microbiology, College of Veterinary & Animal Science, SVP University of Agriculture and Technology Meerut-250110, Uttar Pradesh, India. e-mail: dr.shailjakatoch@gmail.com

How to cite this article: Chaudhary, S., Katoch, S., Chandra, N., Jaiswal, V., Bhatele, A., & Singh, R. (2026). Antibiogram & Multidrug Resistance among Bacteria Isolated from Pigs with Respiratory Illness in Western Uttar Pradesh. *Ind J Vet Sci and Biotech*, 22(4), 30-34.

Source of support: Nil

Conflict of interest: None

Submitted 06/05/2026 **Accepted** 26/05/2026 **Published** 10/07/2026

in pigs include *Mycoplasma hyopneumoniae*, *Actinobacillus pleuropneumoniae*, and *Bordetella bronchiseptica* (Brockmeier *et al.*, 2001). The bacteria that cause respiratory clinical signs are frequently commensal and opportunistic respiratory tract bacteria that play a significant role in the infection, aggravating the clinical signs and leading to more serious lesions (Opriessnig *et al.*, 2011). *Pasteurella multocida* is the most prevalent opportunistic pathogen, while *Haemophilus parasuis*, *Streptococcus suis*, *Actinobacillus*

suis, and *Arcanobacterium pyogenes* are also frequent opportunistic pathogens (Opriessnig *et al.*, 2011; De Jong *et al.*, 2014; Dayao *et al.*, 2016). The most common way for disease agents to enter a farm is through the purchase of infected pigs or semen for artificial insemination that comes from another swine farm.

Antimicrobials are frequently given to pigs to treat these respiratory illnesses. But the indiscriminate use of these antimicrobials can hasten the emergence and spread of bacterial infections with resistant strains. The spread of bacteria that are multidrug resistant (MDR) poses a risk to public health and could make it more difficult to treat diseases in both humans and animals (De Jong *et al.*, 2014). Thus, this study was aimed to identify and evaluate the antimicrobial susceptibility profile and multidrug resistance in the bacterial pathogens isolated from pigs exhibiting respiratory clinical signs in western Uttar Pradesh.

MATERIALS AND METHODS

Samples Collection

A total of 50 nasal samples from pigs reared at five farms of western Uttar Pradesh under an unorganized agricultural system and displaying respiratory clinical signs were collected. The clinical signs included coughing, nasal discharge, sneezing, difficulty in breathing, fever, loss of appetite and lethargic demeanor. Sterile cotton swabs were used for sampling the nasal cavities of animals. Swabs were inserted into the nasal cavity, gently rubbed against the mucosa for 20-30 sec in a circular motion, placed in normal saline and transported under refrigeration to the laboratory for further processing.

Bacterial Isolation and Identification

The nasal swabs were inoculated on 5 % Sheep blood agar and MacConkey Lactose Agar (MLA) plates. The plates were incubated under aerobic conditions for 24-48 h at 37°C. Following incubation each unique colony was studied macroscopically (cultural characteristics, haemolysis and pigment production) and microscopically (Gram staining). Conventional bacteriological techniques were used to identify the bacteria in accordance with standard manuals (Quinn *et al.*, 2011).

Antibiotic Sensitivity Test

On a Mueller Hinton Agar plate, the *in-vitro* antibiotic sensitivity test was performed using the Kirby-Bauer disc diffusion method (CLSI, 2021). The isolated colony of each isolate was transferred to 5 mL nutrient broth and incubated at 37°C for 12 h. After that, the broth was standardized to 0.5 McFarland standard using McFarland standards (Himedia). The lawn culture inoculation method was used to inoculate MHA plate with a swab dipped in broth. The selected 10 antimicrobial discs were applied almost at equidistance with sterile, fine-tipped forceps

over inoculated MHA plate and incubated at 37°C for 18 h. The effectiveness of antibiotics was assessed by calculating the size of the zones of inhibition surrounding the discs, with interpretation using the standard guidelines (CLSI, 2021). All the isolates were observed for multidrug resistance (MDR) and multiple antibiotic resistance (MAR). If an isolate in this study displayed resistance to at least one antimicrobial across three or more antibiotic classes, it was said to be multidrug-resistant (MDR) (Magiorakos *et al.*, 2012). The MAR index was derived using the formula: X/Y, where X is the number of antibiotics to which the test isolates demonstrated resistance and Y is the total number of antibiotics to which the test isolates have been examined for susceptibility (Bauer *et al.*, 1966).

RESULTS AND DISCUSSION

Bacterial Identification Findings

From the 50 nasal samples of the pigs exhibiting respiratory clinical signs, a total of 46 bacteria were isolated. Among the 46 isolates, 35 (76.08%) were Gram negative and 11 (23.91%) were Gram positive. The bacterial isolates identified included *Pasteurella multocida* (15.21%), *Escherichia coli* (15.21%), *Proteus vulgaris* (13.04%), *Bordetella bronchiseptica* (13.04%), *Pseudomonas aeruginosa* (13.04%), *Streptococcus suis* (10.86%), *Staphylococcus aureus* (10.86%) and *Klebsiella pneumoniae* (8.69%). These findings were in agreement with Dosen *et al.* (2007), who reported *Pasteurella* spp. (26.57%) & *E. coli* (26.57%) as the most frequently isolated bacteria from swine with respiratory tract infection, followed by *Streptococcus* spp. (16.7%), *Staphylococcus* spp. (5.59%) and *Klebsiella pneumoniae* (4.90%).

Among the main bacteria responsible for respiratory clinical signs in pigs, *P. multocida* is an opportunistic pathogen that lives as a commensal in the upper respiratory tract of animals (Quinn *et al.*, 2011). Atrophic rhinitis and pneumonia are conditions caused by *P. multocida* capsular types A and D, which are typically seen in pigs. Both serotypes have been linked to both disorders, with serotype A being most frequently found from lungs and serotype D from instances of atrophic rhinitis (Kim *et al.*, 2019). A common pathogen of pigs, *Bordetella bronchiseptica* causes pneumonia, tracheitis, bronchitis, and other respiratory illnesses. It is a primary pig pathogen that, by itself, may only cause minor illness, but its interactions with other bacteria, particularly the toxigenic *P. multocida*, have been widely characterised (Brockmeier *et al.*, 2001). It has also been demonstrated that *B. bronchiseptica* makes pigs more vulnerable to *S. suis* infection. Most healthy pigs typically have *S. suis* in their tonsils and nasopharynx (Baele *et al.*, 2001; O'Sullivan *et al.*, 2011), that is why these organisms are referred to as "pathobionts" (Votsch *et al.*, 2018). The conditions under which certain serotypes/strains of *S. suis* become pathogenic and cross the mucosal barrier into the blood causing a systemic infection are not fully understood (Segura *et al.*, 2016).

The commensal pathogen *Staphylococcus aureus* is frequently present on the skin and respiratory tracts of living hosts and causes serious illness in both humans and a wide range of animal species, including pigs (Lakhundi and Zhang, 2018). *S. aureus* nasal colonisation has been found in pigs all over the world, and it has the potential to be a serious human disease (Silpa *et al.*, 2018). One key risk factor for *S. aureus* nasal colonisation in humans is thought to be pig husbandry (Armand-Lefevre *et al.*, 2005). *Klebsiella* spp. are mostly associated with sepsis, infections of urinary and respiratory tracts, mastitis and meningitis etc (Brise and Duijkeren, 2005). If left untreated, *K. pneumoniae* related pulmonary infections frequently have a rapid clinical progression worsened by lung abscesses and result in significant mortality and morbidity (Cortes *et al.*, 2002). *Klebsiella pneumoniae* subsp. *pneumoniae* is recognized as a cause of sporadic disease in individual pigs often concurrent with other diseases. The pathogen is also an opportunistic pathogen that causes mastitis in cows and swine. As a commensal of the healthy pig digestive system, *Klebsiella pneumoniae* is found in the soil and water supplies.

Antibiotic Sensitivity Results

The bacterial organisms acquire antibiotic resistant factors or processes over time, changing their antibiogram patterns and developing resistance against frequently used chemotherapeutic agents. In this study, 10 antibiotics from various antibiotic classes were tested against all 46 isolates using the Kirby-Baur disc diffusion method. The antimicrobial susceptibility profile of the 46 bacterial isolates is shown in Fig. 1. Overall, 95.65% (44) of isolates were resistant to one or more antimicrobial agents, whereas only 4.35% (2)

of isolates were sensitive to all the antibiotics. Antibiotic sensitivity testing revealed that 78.26% bacterial isolates were sensitive to enrofloxacin and amikacin followed by 76.09% to tetracycline, gentamicin & colistin and 67.39% to streptomycin. Among the bacterial isolates highest resistance was found against amoxicillin/clavulanic acid (58.70%) followed by ampicillin (54.35%), chloramphenicol (47.83%) and cefixime (45.65%). Based on the antibiotic sensitivity test enrofloxacin, amikacin, tetracycline, gentamicin and colistin were recommended as a drug of choice for the treatment of respiratory diseases in swine of western Uttar Pradesh as more than 75% of the bacterial isolates recovered from pigs showing respiratory diseases were sensitive to these antibiotics.

In a previous study by El-Garch *et al.* (2016), respiratory tract pathogens from swine across Europe were highly susceptible (100% to 98%) to amoxicillin/clavulanic acid, ceftiofur, enrofloxacin, florfenicol, tulathromycin, tiamulin and tilmicosin, while the 20.4% of *P. multocida* and 88.1% of *S. suis* isolates were tetracycline resistant. These findings are contrary to our findings as the isolates in the present study showed highest resistance to amoxicillin/clavulanic acid and cefixime and were sensitive to tetracycline while both the studies are in agreement for the susceptibility of isolates to enrofloxacin. In the present study, 7 (15.21%) isolates were resistant to only one antibiotic class antimicrobial, 10 (21.73%) were resistant to antimicrobials in two antibiotic classes and 31 (67.39%) isolates were resistant to at least one antimicrobial across three or more antibiotic classes and showed multi drug resistance. Only 31.25% (50/160) of the isolates from



Fig. 1: Heat map representation of the antimicrobial-resistant profile, MDR and MARI of bacterial isolates (n=46) recovered from nasal swabs of swine. {Heat map was generated using Python (v3.11; Python Software Foundation, 1991-2025) and the matplotlib visualization library (v3.11; Hunter *et al.*, 2007-2025), with distinct color codes applied for antibiotics (sensitive = yellow, resistant = black), MARI (≤ 0.2 = blue, > 0.2 = orange), and MDR (absent = green, present = red)}.

pigs exhibiting clinical respiratory signs were found to be multidrug resistant in a prior investigation by Serpa *et al.* (2020). The high number of isolates (67.39%) in the present study showing multi drug resistance can be associated with the massive use of antimicrobials in swine, which is especially important considering that some of the agents, viz., *S. suis* and *S. aureus*, are important zoonotic pathogens (Palmieri *et al.*, 2011; Silpa *et al.*, 2018) and are a potential risk to public health (Landers *et al.*, 2012; De Jong *et al.*, 2014). The high number of MDR and their widespread distribution in western Uttar Pradesh, highlights the importance of the careful use of antimicrobials in animal production.

An array of Multiple Antibiotic Resistance Index (MARI) trends were found among the bacterial isolates based on the estimated data of antibiotic susceptibility of different bacterial isolates. The MARI for all the isolates ranged from 0.0 to 0.8. The MAR index of 73.9% of the isolates was greater than 0.2; while 26.08% of them had index values less than or equal to 0.2. The proportions of isolates with the MAR index values from 0.0, 0.1, 0.2, 0.3, 0.4, 0.5, 0.6 and 0.8 were 4.34%, 4.34%, 17.39%, 23.91%, 30.43%, 2.17%, 15.21% and 2.17%, respectively. A MARI score of greater than 0.2 denotes the frequent usage of antibiotics to treat infections in settings with high contamination levels. Our findings suggest that the isolates with high MAR indices were probably exposed to more drugs, which would indicate a rise in infections in the field with numerous antibiotic-resistant bacteria. The MAR index approach is fairly quick, inexpensive, and straightforward to use for tracing the sources of bacteria and keeping track of how much antibiotics are being consumed in the field.

Antibiotic use that is irrational and reckless results in the development of resistant bacterial strains that obstruct the use of antibiotics to treat infections effectively and frequently cause an uncontrollable increase in the mortality toll. Therefore, the antibiotics for which all the isolates in this study were found susceptible could be used in emergency situations for treating animals suspected of respiratory diseases till the isolate specific cultural sensitivity test reports become available. However, antimicrobial susceptibility patterns can change with time (Holmer, 2019) and this is one of the main reasons to determine it across time in order to select the most suitable antimicrobial, taking into account efficacy criteria and the one-health approach (WHO, 2020).

CONCLUSION

Overall, the findings of the present study indicated that the respiratory tract pathogens commonly found in swine of western Uttar Pradesh were *Escherichia coli*, *Pasteurella multocida*, *Proteus vulgaris*, *Bordetella bronchiseptica*, *Pseudomonas aeruginosa*, *Streptococcus suis*, *Staphylococcus aureus*, and *Klebsiella pneumoniae*. A great level of resistance among bacterial respiratory pathogens was observed against amoxicillin/clavulanic acid followed by ampicillin, chloramphenicol and cefixime. In addition, a large number

of the isolates also showed signs of MDR and a high MAR score. These findings highlight the necessity of evaluating antimicrobial susceptibility in pig respiratory illnesses in order to optimize antimicrobial treatment on a case-by-case basis and provide rigorous criteria to choose the most appropriate antimicrobials while taking the one-health approach.

ACKNOWLEDGEMENTS

The authors are thankful to the Vice Chancellor, Sardar Vallabhbhai Patel University of Agriculture and Technology, Meerut, UP, India, for providing the necessary facilities for the study.

REFERENCES

- Armand-Lefevre, L., Ruimy, R., & Andremon, A. (2005). Clonal comparison of *Staphylococcus aureus* isolates from healthy pig farmers, human controls, and pigs. *Emerging Infectious Diseases*, 11(5), 711-714.
- Baele, M., Chiers, K., Devriese, L.A., Smith, H., Wisselink, H., Vanechoutte, M., & Haesebrouck, F. (2001). The Gram-positive tonsillar and nasal flora of piglets before and after weaning. *Journal of Applied Microbiology*, 91, 997-1003.
- Bauer, A.W., Kirby, W.M.M., Sherris, J.C., & Turck, M. (1966). Antibiotic susceptibility testing by standardized single disk method. *American Journal of Clinical Pathology*, 45, 493-496.
- Brisse, S., & Duijkeren, V.E. (2005). Identification and antimicrobial susceptibility of 100 *Klebsiella* animal clinical isolates. *Veterinary Microbiology*, 105, 307-312.
- Brockmeier, S.L., Palmer, M.V., Bolin, S.R., & Rimler, R.B. (2001). Effects of intranasal inoculation with *Bordetella bronchiseptica*, porcine reproductive and respiratory syndrome virus, or a combination of both organisms on subsequent infection with *Pasteurella multocida* in pigs. *American Journal of Veterinary Research*, 62, 521-525.
- CLSI (2021). Performance Standards for Antimicrobial Susceptibility Testing, CLSI supplement M100. 30th edn., Wayne, PA, USA.
- Cortes, G., Alvarez, D., Saus, C., & Albert, S. (2002). Role of Lung epithelial cells in defense against *K. pneumoniae*. *Infection & Immunity*, 70(3), 1075-1080.
- Dayao, D., Gibson, J.S., Blackall, P.J., & Turni, C. (2016). Antimicrobial resistance genes in *Actinobacillus pleuropneumoniae*, *Haemophilus parasuis* and *Pasteurella multocida* isolated from Australian pigs. *Australian Veterinary Journal*, 94(7), 227-231.
- Dosen, R., Prodanov, J., Milanov, D., Stojanov, I., & Pusic, I. (2007). The bacterial infections of respiratory tract of swine. *Biotechnology in Animal Husbandry*, 23(5-6), 237-243.
- De Jong, A., Thomas, V., Simjee, S., Moyaert, H., El, G.F., Maher, K., Morrissey, I., Butty, P., Klein, U., Marion, H., Rigaut, D., & Valle, M. (2014). Antimicrobial susceptibility monitoring of respiratory tract pathogens isolated from diseased cattle and pigs across Europe: The VetPath study. *Veterinary Microbiology*, 172(1-2), 202-215.
- El-Garch, F., de, J.A., Simjee, S., Moyaert, H., Klein, U., Ludwig, C., Marion, H., Haag-Diergarten, S., Richard-Mazet, A., Thomas, V., & Siegwart, Ed. (2016). Monitoring of antimicrobial susceptibility of respiratory tract pathogens isolated from diseased cattle and pigs across Europe, 2009-2012: VetPath Results. *Veterinary Microbiology*, 194, 11-22.

- Holmer, I., Salomonsen, C.M., Jorsal, S.E., Astrup, L.B., Jensen, V.F., Hog, B.B., & Pedersen, K. (2019). Antibiotic resistance in porcine pathogenic bacteria and relation to antibiotic usage. *BMC Veterinary Research*, 15, 449.
- Kim, J., Kim, J.W., Oh, S.I., So, B.J., Kim, W.I., & Kim, H.Y. (2019). Characterisation of *Pasteurella multocida* isolates from pigs with pneumonia in Korea. *BMC Veterinary Research*, 15(1), 119.
- Lakhundi, S., & Zhang, K. (2018). Methicillin-Resistant *Staphylococcus aureus*: Molecular Characterization, Evolution, and Epidemiology. *Clinical Microbiology Reviews*, 31(4), e00020-18.
- Landers, T.F., Cohen, B., Wittum, T.E., & Larson, E.L. (2012). A review of antibiotic use in food animals: perspective, policy, and potential. *Public Health Reports*, 127(1), 4-22.
- Magiorakos, A.P., Srinivasan, A., Carey, R.B., Carmeli, Y., Falagas, M.E., Giske, C.G., Harbarth, S., Hindler, J.F., Kahlmeter, G., Olsson-Liljequist, B., & Paterson, D.L. (2012). Multidrug-resistant, extensively drug-resistant and pan drug-resistant bacteria: An international expert proposal for interim standard definitions for acquired resistance. *Clinical Microbiology and Infection*, 18(3), 268-281.
- O'Sullivan, T., Friendship, R., Blackwell, T., Pearl, D., McEwen, B., Carman, S., Slavić, D., & Dewey, C. (2011). Microbiological identification and analysis of swine tonsils collected from carcasses at slaughter. *Canadian Journal of Veterinary Research*, 75, 106-111.
- Opriessnig, T., Gimenez-Lirola, L.G., & Halbur, P.G. (2011). Polymicrobial respiratory disease in pigs. *Animal Health Research Reviews*, 12(2), 133-148.
- Palmieri, C., Valardo, P.E., & Facinelli, B. (2011). *Streptococcus suis*, an emerging drug-resistant animal and human pathogen. *Frontiers in Microbiology*, 2, 235.
- Quinn, P.J., Markey, B.K., Leonard, F.C., Hartigan, P., Fanning, S., & Fitzpatrick, E.S. (2011). *Veterinary Microbiology and Microbial Disease*. 2ndedn., Willey Blackwell, UK.
- Segura, M., Calzas, C., Grenier, D., & Gottschalk, M. (2016). Initial steps of the pathogenesis of the infection caused by *Streptococcus suis*: fighting against nonspecific defenses. *FEBS Letters*, 590, 3772-3799.
- Serpa, M., Nascimento, J.A.F.B., Alves, M.F., Guedes, M.I.M.C., Reis, A.T., Heinemann, M.B., Lage, A.P., Lobato, Z.I.P., & Dorneles, E.M.S. (2020). Antimicrobial resistance in bacteria isolated from pigs with respiratory clinical signs in Brazil. *Brazilian Journal of Veterinary Research in Animal Science*, 57(1), e160956.
- Silpa, R.S., Justin, D.K., Vinodkumar, K., Mathew, B., & Vijayakumar, K. (2018). Isolation and molecular characterization of *Staphylococcus aureus* from pigs in Thrissur district, Kerala. *Journal of Pharmaceutical Innovation*, 7(9), 139-141.
- Sorensen, V., Jorsal, S.E., & Mousing, J. (2006). Diseases of the respiratory system. In: *Diseases of Swine*, 9thedn., Ed: B.E. Straw, J.J. Zimmerman, S. D'Allaire and D.J. Taylor, Blackwell Publishing, Iowa, pp. 149-177.
- Votsch, D., Willenborg, M., Weldearegay, Y.B., & Valentin-Weigand, P. (2018). *Streptococcus suis* – the “two faces” of a pathobiont in the porcine respiratory tract. *Frontiers in Microbiology*, 9, 480.
- WHO (2020). Global Action Plan on Antimicrobial Resistance. Available online: <https://www.who.int/antimicrobial-resistance/global-action-plan/en/>.

