

Epidemiological characterization of bacterial pathogens and antimicrobial resistance profiles in porcine respiratory disease complex in Jiangxi Province, China

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Abstract

Background

Porcine respiratory disease complex (PRDC) causes substantial economic losses in swine production worldwide, and bacterial pathogens are key contributors to disease occurrence and severity. As a major swine-producing province in China, Jiangxi still lacks systematic regional epidemiological data of bacterial pathogens from clinical PRDC cases, which restricts the development of localized and evidence-based disease control strategies.

Results

From January 2022 to February 2026, 372 pneumonic lung samples were collected from diseased pigs across 11 cities of Jiangxi Province. Bacterial isolates were recovered from 173 of 372 samples, with an overall isolation rate of 46.5%. A total of 218 bacterial strains were identified, among which *Escherichia coli* (28.9%, 63/218) and *Streptococcus suis* (25.2%, 55/218) were the dominant pathogens, followed by *Pasteurella multocida* (11.0%). Distinct age-dependent infection patterns were observed: *Glaesserella parasuis* mainly infected younger piglets, while *P. multocida* and *Enterococcus faecalis* preferentially affected older pigs. For antimicrobial resistance profiles, *E. coli* showed high resistance to amoxicillin (92.1%), tetracyclines (92.1%), macrolides (96.3%) and sulfonamides (95.2%), with carbapenem resistance rates of 17.5% (imipenem) and 12.7% (meropenem). *S. suis* remained susceptible to β -lactams (resistance rate < 9%) but was highly resistant to macrolides and tetracyclines. *P. multocida* exhibited low resistance to most tested drugs. Multidrug resistance was most severe in *E. coli*, with 42.9% of isolates resistant to up to 9 classes of antimicrobials.

Conclusions

This study clarifies a distinct regional bacterial pathogen spectrum of PRDC in Jiangxi, dominated by *E. coli* and *S. suis*. The findings highlight the urgency of implementing age-specific prevention measures, promoting prudent antimicrobial use, and strengthening long-term resistance surveillance to reduce potential public health risks. This work also provides critical baseline data to support evidence-based PRDC prevention and control in Jiangxi.

Introduction

The porcine respiratory disease complex (PRDC) **represents** one of the most **cpressing** health challenges in the global swine industry. It is characterized by polymicrobial infections involving both viral and bacterial pathogens, which cause growth retardation, reduced feed efficiency, and substantial economic losses in pork production systems worldwide [1, 2]. Bacterial pathogens play a critical role in PRDC pathogenesis, serving as primary etiological agents or drivers of secondary infections that

exacerbate disease severity [3]. The bacterial species frequently detected from clinical PRDC cases include *Streptococcus suis*, *Glaesserella parasuis*, *Actinobacillus pleuropneumoniae*, *Pasteurella multocida*, and others [3]. The epidemiology, pathogenicity, and **clinical manifestations** of these pathogens differ across swine production systems, and this heterogeneity is largely shaped by variations in management practices, vaccination coverage, and polymicrobial interactions [4].

Given that China is the world's largest pork producer and consumer, the economic burden attributable to PRDC is considerable [5]. Although national surveys have confirmed the predominance of bacterial pathogens among clinical PRDC cases, growing evidence reveals marked geographical divergence not only in pathogen prevalence and dominant serotypes, but also in antimicrobial resistance (AMR) profiles [6]. The widespread, largely empirical use of antimicrobials in swine production has driven the emergence and spread of multidrug-resistant (MDR) bacterial strains, which not only reduce clinical therapeutic efficacy but also **both zoonotic and broader public health risks** via the food chain [7].

Jiangxi is a major swine-producing province in central China. Our previous studies have characterized the prevalence and AMR **profiles** of *S. suis* isolated from nasal swabs of clinically healthy commercial three-way crossbred pigs [8] and **indigenous** pig breeds [9]. Nevertheless, these studies focused solely on single-pathogen carriage in healthy populations. Large-scale multi-pathogen epidemiological investigations of PRDC based on isolates from clinically diseased pigs and pathological tissues remain scarce in this province, leaving the profiles of clinically pathogenic strains poorly characterized.

In the present study, we performed an epidemiological investigation of PRDC-associated bacterial pathogens based on respiratory tissue samples from clinically diseased pigs across Jiangxi. We characterized the prevalence and antimicrobial susceptibility profiles of all isolates obtained. These findings provide essential baseline data on clinical PRDC pathogens in the region and enhance our understanding of the regional epidemiology of PRDC.

Materials and methods

Clinical sample collection

From January 2022 to February 2026, a total of 372 porcine lung tissue samples were collected across 11 cities in Jiangxi. All samples were obtained from diseased or dead pigs presenting typical clinical signs of pneumonia, including coughing and respiratory distress. The pigs ranged in age from 1 to 330 days, **representing** suckling piglets, finishing pigs and breeding stock. The sampled population consisted of commercial **three-way crossbred** white pigs and indigenous pig breeds of Jiangxi. All samples were stored at 4°C in a portable car refrigerator (Alpicool, Foshan, China) and transported to the laboratory for subsequent analysis. Detailed information **regarding** sampling time, location, and host age of each strain is **provided** in Table S1.

Bacterial isolation

Lung tissue surfaces were disinfected with 75% ethanol. Approximately 0.5 g of tissue was aseptically excised and homogenized in 1 mL of sterile normal saline. Subsequently, 100 µL of the homogenate was plated onto tryptic soy agar (Hopebio, Qingdao, China) supplemented with 5% (v/v) newborn bovine serum (NBS; Sijiqing, Hangzhou, China) and 0.01% (m/v) nicotinamide adenine dinucleotide (NAD; Hopebio). Plates were incubated at 37°C for 18 h. Concurrently, the homogenate was streaked onto MacConkey agar (Hopebio) for preliminary bacterial identification.

Bacterial identification

After incubation, single bacterial colonies were inoculated into tryptone soya broth (Hopebio) supplemented with 5% NBS and 0.01% NAD or lysogeny broth (Hopebio) for pure culture. Genomic DNA was subsequently extracted using a Bacterial DNA Kit (Omega Bio-Tek, Norcross, GA, USA) in accordance with the manufacturer's instructions. The bacterial 16S rRNA gene was amplified via PCR using the universal primers 27F and 1492R. PCR cycling conditions were as follows: initial denaturation at 95 °C for 5 min; 30 cycles of 95 °C for 30 s, 57 °C for 30 s, and 72 °C for 1 min. The PCR products were sent to Sangon Biotech (Shanghai) Co., Ltd. for Sanger sequencing. Species identification was performed using NCBI Nucleotide BLAST **with** default parameters. All confirmed bacterial isolates were **stored at –80 °C in 25% (v/v) glycerol** for subsequent experiments.

Antibiotic drugs

A total of 20 antimicrobial agents for veterinary and clinical applications were selected for susceptibility testing. These agents covered multiple antimicrobial classes, including penicillins (amoxicillin [AMX], ampicillin [AMP]), cephalosporins (ceftiofur [FUR]), tetracyclines (doxycycline [DX], chlortetracycline [CT]), phenicols (florfenicol [FFC]), macrolides (erythromycin [E], tilmicosin [TIL]), polypeptides (colistin sulfate [CS]), sulfonamides (sulfamethoxazole-trimethoprim [SXT]), quinolones (enrofloxacin [ENR], ciprofloxacin [CIP]), pleuromutilins (tiamulin [T]), aminoglycosides (neomycin [N], spectinomycin [SPT], gentamicin [GM], kanamycin [K], apramycin [AP]), and carbapenems (imipenem [IMI], meropenem [MRP]). The CT disks were purchased from HiMedia Laboratories (Mumbai, India), while all other antimicrobial disks were obtained from Liofilchem S.r.l. (Roseto degli Abruzzi, Italy). Disk potencies for each agent are provided in Table S2.

Antimicrobial susceptibility assay

Antimicrobial susceptibility testing was performed using the Kirby–Bauer disk diffusion method on Mueller–Hinton (MH) agar (Hopebio). For fastidious bacterial strains, the medium was supplemented with 5% NBS, with or without 0.01% NAD. All procedures were performed in accordance with the Clinical and Laboratory Standards Institute (CLSI) guidelines [10]. Briefly, bacterial colonies harvested from fresh agar plates were resuspended in sterile normal saline, with turbidity adjusted to the 0.5 McFarland standard. The bacterial suspension was evenly spread onto MH agar plates using a sterile cotton swab. Antibiotic disks were placed onto the inoculated plates using a disk dispenser, followed by incubation at 37 °C for 18 h. *E. coli* ATCC 25922 was used as the quality control strain. Diameters of inhibition zones

were measured and interpreted according to CLSI interpretive breakpoints (Table S2), and isolates were categorized as susceptible, intermediate, or resistant.

Statistical analysis

Drawing of histograms and statistical analysis were performed on GraphPad prism 8.0 software (San Diego,USA).

Results

Prevalence of bacterial pathogens

An epidemiological investigation was conducted between January 2022 and February 2026 to characterize bacterial pathogens associated with clinical swine pneumonia across 11 cities in Jiangxi. A total of 372 lung tissue samples were collected from diseased and dead pigs on commercial swine farms, with the sampled animals spanning all major growth stages and including both commercial crossbred and Jiangxi indigenous pig breeds. Following bacterial isolation and identification, 218 bacterial isolates (Table S1) were recovered from 173 culture-positive lung samples, corresponding to an overall isolation rate of 46.5% (173/372). Single-pathogen infections were detected in 74.0% (128/173) of the positive samples, whereas mixed infections involving two or three bacterial species accounted for the remaining 26.0% (45/173).

The species distribution of the 218 isolates is summarized in Table 1. *Escherichia coli* was the most frequently isolated pathogen, accounting for 28.9% (63/218) of all isolates, followed by *S. suis* at 25.2% (55/218) (Figure 1). Together, these two species accounted for 54.1% of all isolates, representing the dominant etiological agents of bacterial pneumonia in swine in this region. *P. multocida* ranked third in prevalence, accounting for 11.0% (24/218). Other frequently isolated species included *Enterococcus faecalis* (5.1%, 11/218), *A. pleuropneumoniae* (4.1%, 9/218), *Salmonella* sp. (4.1%, 9/218), and *G. parasuis* (3.7%, 8/218) (Figure 1). In addition to these predominant pathogens, less prevalent bacterial species, including *Trueperella pyogenes*, *Streptococcus parasuis*, and *Proteus mirabilis* were also isolated (Table S1).

Age distribution of infected pigs

The age distribution of pigs infected with each major bacterial pathogen is shown in Figure 2, with red bars indicating the median age and interquartile range (IQR). Among the pathogens analyzed, *E. coli*, *S. suis*, and *Salmonella* sp. shared a median infection age of 40 days, with IQRs of 27–90 d, 19–90 d, and 18–70 d, respectively. Both *E. coli* and *S. suis* exhibited a broad infection age range, with sporadic isolates obtained from breeding pigs aged over 200 days, reflecting their widespread colonization across the swine production cycle. *G. parasuis* showed a narrow susceptible age window and the youngest median infection age (30 d, IQR: 18–48 d) among all tested pathogens, which is consistent with its

predominant occurrence in early nursery pigs. *A. pleuropneumoniae* had a median infection age of 60 d, with an IQR of 35–102 d, indicating broad occurrence across the growing to finishing stages.

In contrast to pathogens that primarily infect younger pigs, *P. multocida* and *E. faecalis* were predominantly detected in older age groups. *P. multocida* had a median infection age of 80 d (IQR: 48–108 d). Most positive isolates were obtained from pigs in late nursery and growing stages, consistent with its higher prevalence in mid-to-late production phases. *E. faecalis* exhibited the highest median infection age of all pathogens, at 90 d (IQR: 40–110 d), indicating a **higher propensity to infect** older pigs, **which likely reflects** its opportunistic nature.

Antimicrobial resistance analysis

Antimicrobial susceptibility testing was performed on all isolates, with a panel of 18 commonly used veterinary antibiotics and 2 last-resort antimicrobial agents active against Gram-negative bacilli. Susceptibility profiles of Gram-negative and Gram-positive bacteria are summarized in Figure 3. Gram-positive isolates exhibited high susceptibility to β -lactam agents, with susceptibility rates of 96.7% for AMX and 86.7% for AMP, whereas Gram-negative isolates showed lower susceptibility to both penicillins, at 32.8% each. A similar pattern was observed for FUR, with a susceptibility rate of 67.8% among Gram-positive isolates versus 50.0% among Gram-negative isolates. Fluoroquinolones displayed moderate activity against both groups, whereas tetracyclines and macrolides had low overall efficacy. CS exhibited potent activity against Gram-negative bacteria (93.8%) but negligible activity against Gram-positive strains (2.2%). Aminoglycosides exhibited greater activity against Gram-negative bacteria, with the susceptibility rate to GM reaching 60.9% in this group. The two last-resort carbapenems, IMP and MRP, retained high activity against both groups.

We further characterized species-specific AMR profiles, with resistance, intermediate, and susceptibility rates of *E. coli*, *S. suis*, and *P. multocida* summarized in Figure 4. *E. coli* isolates exhibited a widespread MDR phenotype (Figure 4A). High rates of resistance were observed against TIL (100.0%), E (96.3%), SXT (95.2%), AMX (92.1%), CT (92.1%), and AMP (90.5%). Resistance rates to aminoglycosides ranged from 28.6% for N to 58.7% for SPT. Notably, CS maintained potent activity against *E. coli*, with a resistance rate below 2%. IMI and MRP also retained high efficacy, with resistance rates of 17.5% and 12.7%, respectively.

S. suis isolates exhibited a distinct antimicrobial susceptibility profile (Figure 4B). β -lactam antibiotics (AMX, AMP, FUR) displayed antibacterial activity, with all resistance rates below 9%, indicating their role as first-line therapeutic options against *S. suis* infections. Conversely, isolates exhibited near-complete resistance to TIL (100.0%), CT (98.2%), and CS (98.2%). All *S. suis* isolates remained fully susceptible to IMI and MRP.

P. multocida isolates exhibited low resistance rates to most tested agents (Figure 4C), with resistance rates for AMX, AMP, FUR, DX, E, CS, ENR, CIP, N, and GM all below 10%. Moderate resistance rates were

observed for FFC (54.2%), TIL (58.3%), SXT (41.7%), and AP (37.5%). No carbapenem-resistant *P. multocida* isolates were identified, with all isolates remaining susceptible to IMI and MRP.

Multidrug resistance

MDR, defined as acquired resistance to three or more distinct classes of antimicrobial agents [11], was further evaluated for all isolates (Table S1). The distribution of isolates exhibiting resistance to 1–11 antimicrobial classes among *E. coli*, *S. suis*, and *P. multocida* is presented in Figure 5, revealing interspecies differences observed in their MDR profiles.

E. coli isolates presented the most severe MDR burden, with the distribution skewed toward higher numbers of antimicrobial classes. Isolates resistant to 9 antimicrobial classes were the most prevalent, accounting for 42.9% of all *E. coli* isolates. High proportions were also observed among isolates resistant to 8 and 10 classes (22.2% and 12.7%, respectively), indicating that broad-spectrum MDR predominates in this species.

The resistance profiles of *S. suis* strains were mostly concentrated in the range of 4 to 9 antimicrobial classes, with the highest proportion observed for isolates resistant to 5 classes (21.8%). Compared with *E. coli*, the proportion of *S. suis* isolates resistant to 9 or more antimicrobial classes decreased substantially, and only a few strains showed resistance to 11 antimicrobial classes.

Most *P. multocida* isolates showed resistance to 2 to 6 antimicrobial classes, with a peak at 3 classes (29.2%). The proportion of isolates resistant to 8 or more classes was low, and no isolates resistance to 11 classes were detected, reflecting a low overall MDR level in this species.

Discussion

A systematic epidemiological investigation of PRDC-associated bacterial pathogens was performed in this study, based on clinical lung samples collected over a five-year period in Jiangxi. Our results demonstrate that *E. coli* (28.9%) and *S. suis* (25.2%) are the predominant isolates, together accounting for 54.1% of all recovered strains. Beyond defining the local pathogen landscape, our data further reveal age-dependent susceptibility patterns and interspecies differences in AMR profiles, including the clinically concerning detection of carbapenem resistance among *E. coli* isolates.

Previous studies indicate that the pathogen spectrum of PRDC varies across countries and geographical regions, whereas *E. coli* is generally not considered a core respiratory pathogen. Across Europe, *S. suis*, *A. pleuropneumoniae*, *P. multocida*, and *Bordetella bronchiseptica* are the predominant bacterial agents associated with PRDC [12]. A nationwide Spanish study ranked *G. parasuis*, *S. suis*, and *Mesomycoplasma hyorhinis* as the top three bacterial isolates from PRDC cases [13]. Similarly, diagnostic data from South Korea identified *G. parasuis*, *P. multocida*, and *A. pleuropneumoniae* as the predominant bacterial causes of porcine pneumonia, with *S. suis* and *E. coli* recovered at low rates from pneumonic lung tissues [14]. Within China, multiple national and regional surveys have consistently

identified *S. suis* as the dominant bacterial pathogen in PRDC cases, with the highest detection prevalence among all bacterial agents. For instance, a large-scale multicenter study covering 25 provinces reported that *S. suis*, *G. parasuis*, and *P. multocida* were the leading bacterial species [6]. Likewise, investigations in Xinjiang [3] and Guangxi [15] identified *S. suis*, *G. parasuis*, and *A. pleuropneumoniae* as primary pathogenic agents.

The pathogen profile observed in our study differs from those reported in the previous surveys. Several factors may account for this discrepancy. Methodologically, most previous studies employed either targeted PCR assays limited to established PRDC pathogens [3, 15] or metagenomic sequencing approaches [6]. Although these molecular methods are highly sensitive, they detect nucleic acid signals and cannot distinguish viable pathogenic bacteria from transient colonizers or non-viable microbial material. In contrast, our culture-based strategy recovers live bacteria directly from diseased lung tissues. This approach preferentially captures readily culturable species such as *E. coli* and provides more direct evidence for pathogens driving active pulmonary infection. Regional characteristics in Jiangxi, including the humid subtropical climate and high stocking density typical of small and medium sized farrow-to-finish farms, may also facilitate airborne spread and pulmonary colonization of *E. coli* [16]. Importantly, recent studies have increasingly recognized *E. coli* as a significant disease agent in porcine pneumonia, which can lead to significant losses in the swine industry and supports the validity of our findings [17, 18].

Consistent with previous reports, our age-stratified analysis revealed distinct infection patterns among major PRDC pathogens. *G. parasuis* showed the youngest median age and narrowest susceptible window, reflecting waning maternal immunity and immune immaturity in early nursery pigs [19]. In contrast, *P. multocida* and *E. faecalis* were predominantly recovered from growing and finishing pigs, consistent with their opportunistic nature, as they colonize the upper respiratory tract asymptomatically and cause disease only when host defenses are impaired by co-infections, stress, or poor air quality [20, 21]. Notably, *E. coli* and *S. suis* exhibited broad age distributions from suckling piglets to breeding stock, indicating endemic circulation throughout the production cycle and their capacity to act as primary or secondary pathogens depending on host conditions. These age-specific patterns suggest that nursery-focused interventions alone are insufficient and that comprehensive biosecurity across all production stages is needed.

Among the dominant pathogens, the AMR profile of *E. coli* is of major clinical concern. *E. coli* isolates exhibited high resistance to multiple commonly used veterinary drug classes, including amoxicillin, tetracyclines, macrolides, and sulfonamides. Moreover, the detection of carbapenem resistance against IMI and MRP among *E. coli* isolates warrants particular attention. Carbapenems are classified as critically important antimicrobials in human medicine, and the presence of carbapenem-resistant *E. coli* in swine lung tissues suggests a potential reservoir of resistance genes that could be transferred to human pathogens through direct contact or via the food chain [22]. Although colistin sulfate exhibited potent in vitro activity against *E. coli* isolates in this study, its clinical utility for porcine respiratory infections remains limited, as colistin is poorly absorbed after oral administration and is only indicated

for enteric infections [23]. Taken together, the widespread resistance and severe MDR phenotype of *E. coli* isolates from Jiangxi substantially limit the available therapeutic options for local respiratory *E. coli* infections and increase the risk of treatment failure.

In contrast to *E. coli*, *S. suis* isolates in this study remained highly susceptible to β -lactam antibiotics such as amoxicillin, while exhibiting high-level resistance to macrolides and tetracyclines. This resistance pattern is consistent with our previous surveys of healthy pig populations in Jiangxi (conducted during 2017–2019 and 2024–2025) [8, 9], indicating that the regional resistance profile of *S. suis* has remained relatively stable over time and that macrolides and tetracyclines have limited therapeutic efficacy. Moreover, *P. multocida* exhibited the most favorable susceptibility profile among the three dominant pathogens, with low resistance rates across most tested antimicrobial agents and no carbapenem-resistant isolates detected. This relatively low multidrug resistance burden is consistent with findings from other regions of China and globally, and likely reflects the fact that *P. multocida* is less frequently exposed to routine antimicrobial prophylaxis than *E. coli* and *S. suis* [24].

Several limitations of this study should be acknowledged. First, our investigation was limited to culturable bacterial pathogens and did not encompass viral pathogens or mycoplasmas, which are widely recognized as primary initiating agents of PRDC, as they disrupt respiratory mucosal barriers and exacerbate secondary bacterial infections [25]. This omission limits our ability to fully delineate the polymicrobial interaction dynamics underlying the observed clinical cases. Second, our antimicrobial resistance analysis was restricted to phenotypic susceptibility testing; the underlying molecular mechanisms of resistance, plasmid backgrounds, and clonal relatedness of multidrug- and carbapenem-resistant isolates have yet to be fully elucidated via whole-genome sequencing. Third, all samples were collected from pigs with apparent pneumonia, a sampling strategy that may introduce selection bias and means the findings cannot fully represent the colonization status of pathogens in the general swine population. Additionally, the culture-based approach may underestimate the prevalence of fastidious pathogens such as *G. parasuis* and *A. pleuropneumoniae*, which have stringent growth requirements.

Conclusion

Our epidemiological survey provides comprehensive baseline data on the bacterial pathogen spectrum and AMR profiles associated with clinical PRDC in Jiangxi Province. The study reveals a distinct regional etiological pattern dominated by *E. coli* and *S. suis*, characterized by clear age-dependent infection tropisms and marked interspecies differences in AMR and MDR. The detection of carbapenem-resistant *E. coli* in clinical respiratory samples highlights a public health risk. These findings advance our epidemiological understanding of clinical PRDC in this region and provide supporting data for the formulation of region-specific pathogen control strategies, rational antimicrobial stewardship guidelines, and public health risk mitigation measures.

Abbreviations

PRDC porcine respiratory disease complex

AMR antimicrobial resistance

MDR multidrug-resistant

NBS newborn bovine serum

NAD nicotinamide adenine dinucleotide

AMX amoxicillin

AMP ampicillin

FUR ceftiofur

DX doxycycline

CT chlortetracycline

FFC florfenicol

E erythromycin

TIL tilmicosin

CS colistin sulfate

SXT sulfamethoxazole-trimethoprim

ENR enrofloxacin

CIP ciprofloxacin

T tiamulin

N neomycin

SPT spectinomycin

GM gentamicin

K kanamycin

AP apramycin

IMI imipenem

MRP meropenem

MH Mueller–Hinton

CLSI Clinical and Laboratory Standards Institute

IQR interquartile range

Declarations

Ethics approval and consent to participate

All sampling procedures involving live pigs were reviewed and approved by the Animal Ethics Committee of the Institute of Animal Husbandry and Veterinary Medicine, Jiangxi Academy of Agricultural Sciences (approval number: 2022-JXAAS-XM-01). All animal experiments were conducted in strict accordance with institutional animal ethical guidelines. All necessary measures were taken to minimize pain and distress during sample collection.

Consent for publication

Not applicable.

Availability of data and materials

Not applicable.

Competing interests

The authors declare no competing interests.

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Authors' contributions

T.M.: Data curation, Software, Visualization, Original draft, Funding acquisition; L.C.: Data curation, Investigation, Methodology, Resources; Z.Q.: Project administration, Resources; Y.Q.: Data curation, Methodology, Resources; G.T.: Formal analysis, Resources; W.M.: Project administration, Validation; J.H.: Methodology; J.H.: Conceptualization, Funding acquisition, Data curation, Investigation. All authors reviewed the manuscript.

Acknowledgments

Not applicable.

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Table

Table 1 Characteristics of bacterial strains in this study.

Genus	Species	No. of strains	Proportion of bacteria
<i>Escherichia</i>	<i>Escherichia coli</i>	63	28.90%
<i>Streptococcus</i>	<i>Streptococcus suis</i>	55	25.23%
	Other <i>Streptococcus</i> sp.	8	3.67%
<i>Pasteurella</i>	<i>Pasteurella multocida</i>	24	11.01%
	<i>Pasteurella aerogenes</i>	5	2.29%
<i>Enterococcus</i>	<i>Enterococcus faecalis</i>	11	5.05%
<i>Actinobacillus</i>	<i>Actinobacillus pleuropneumoniae</i>	9	4.13%
	<i>Actinobacillus suis</i>	3	1.38%
<i>Salmonella</i>	<i>Salmonella</i> sp.	9	4.13%
<i>Glaesserella</i>	<i>Glaesserella parasuis</i>	8	3.67%
	Other species	23	10.55%
	Total	218	

Figures

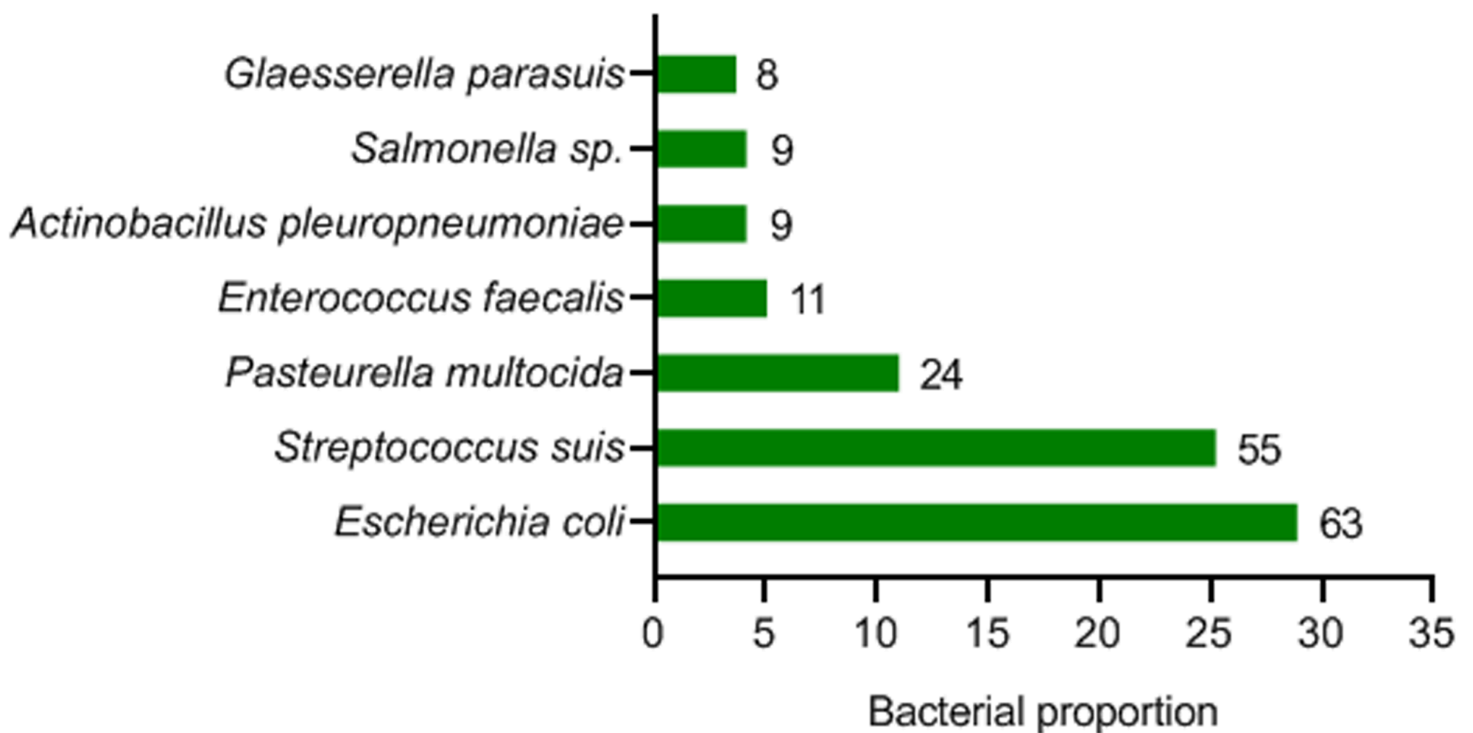


Figure 1

Proportion of pathogenic bacteria isolated from the lungs of diseased pigs. Numbers above the columns represent the corresponding counts of bacterial isolates.

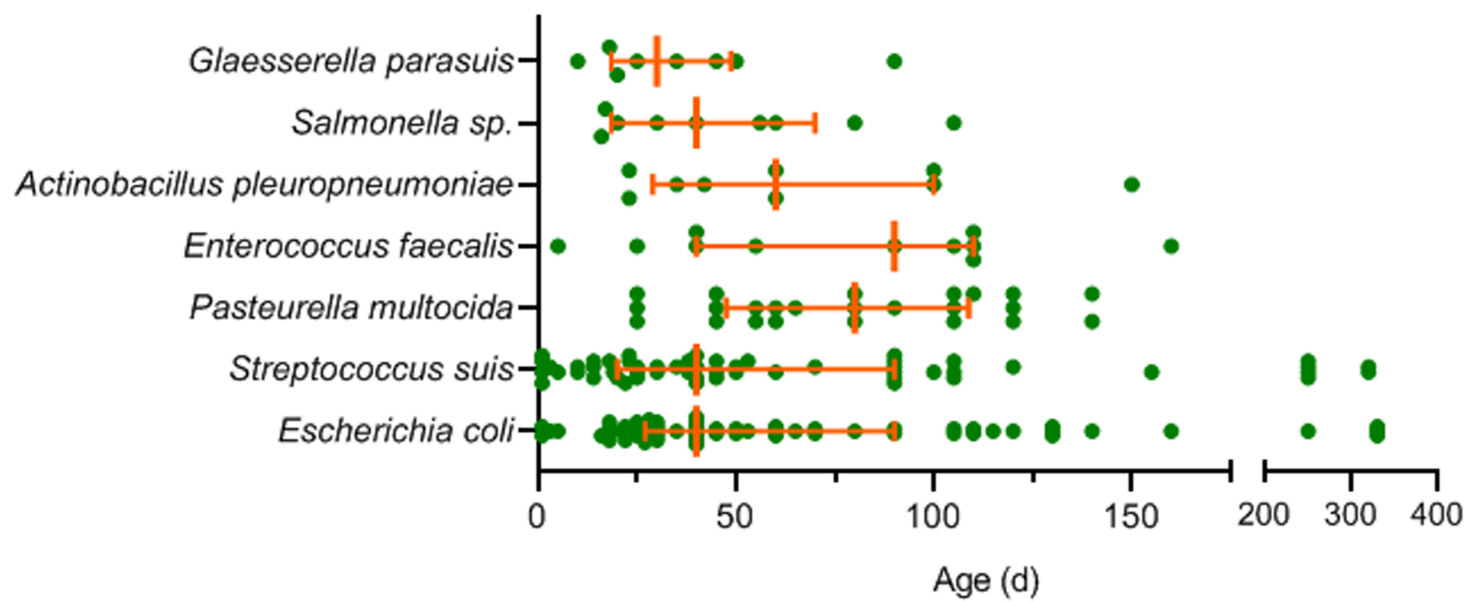


Figure 2

Age distribution of pigs infected with each pathogen. Red bars represent the median and interquartile range.

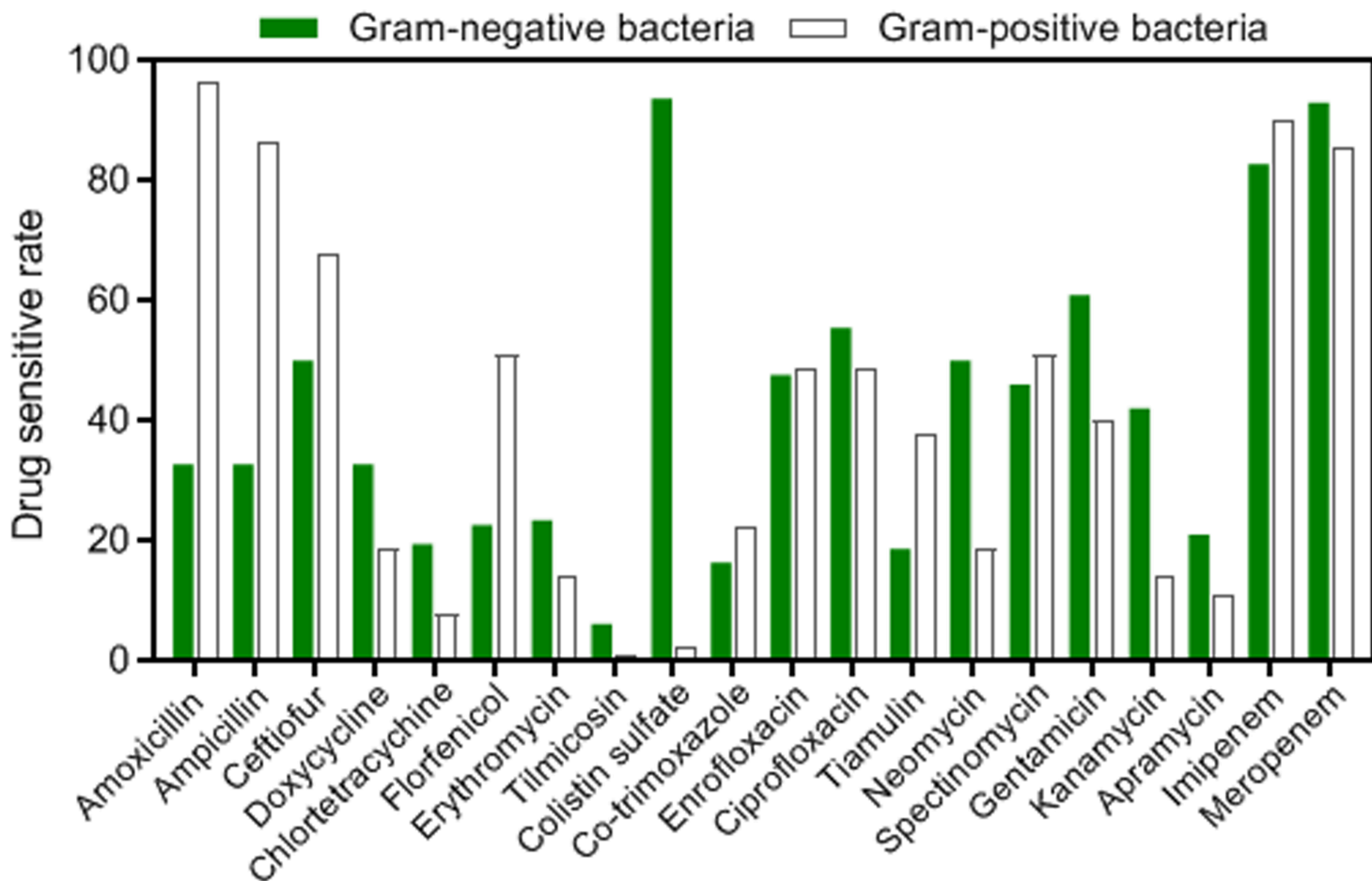


Figure 3

Comparison of antimicrobial susceptibility profiles between gram-positive and gram-negative bacteria.

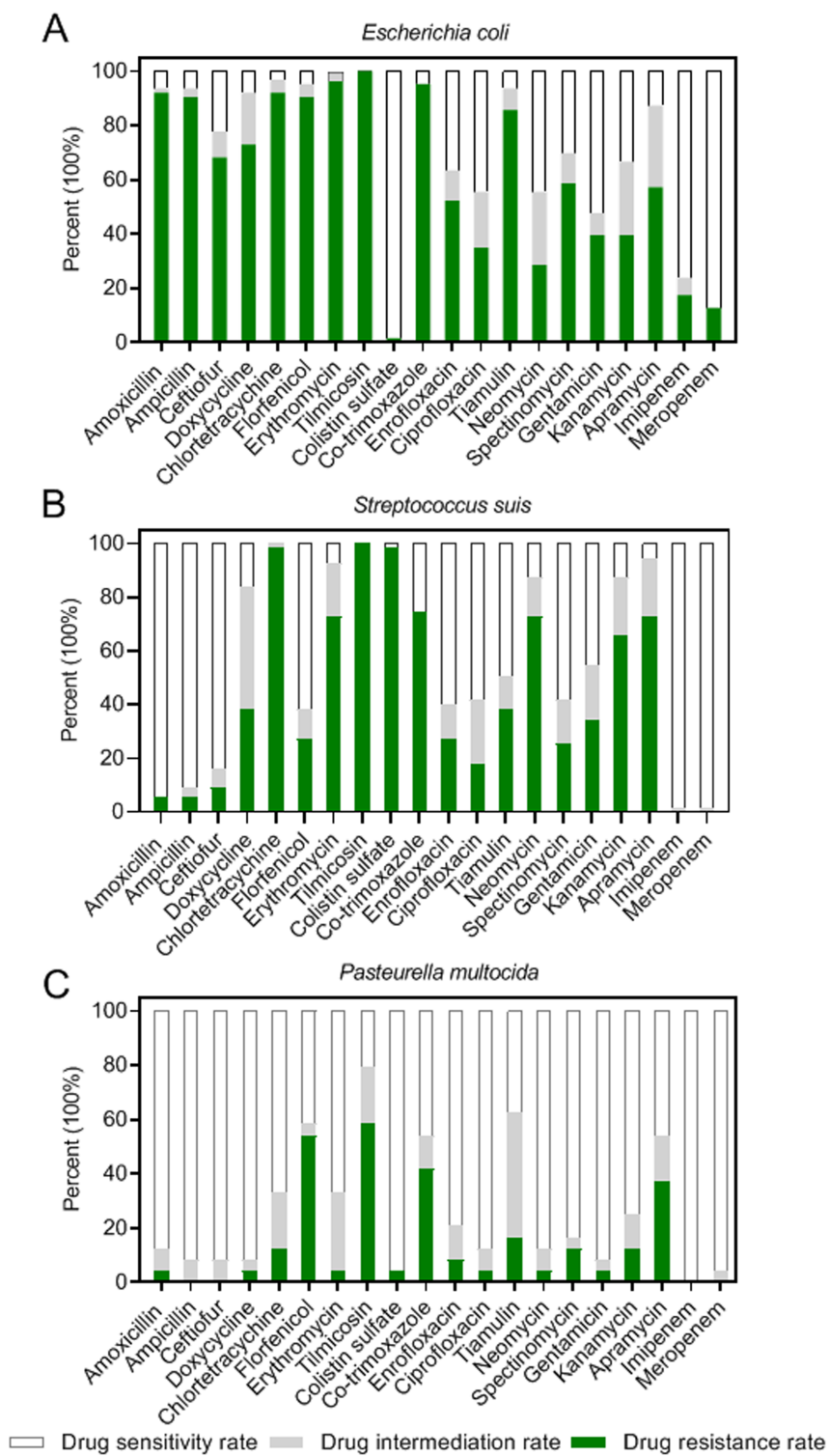


Figure 4

Antimicrobial resistance profiles of *Escherichia coli* (A), *Streptococcus suis* (B), and *Pasteurella multocida* (C).

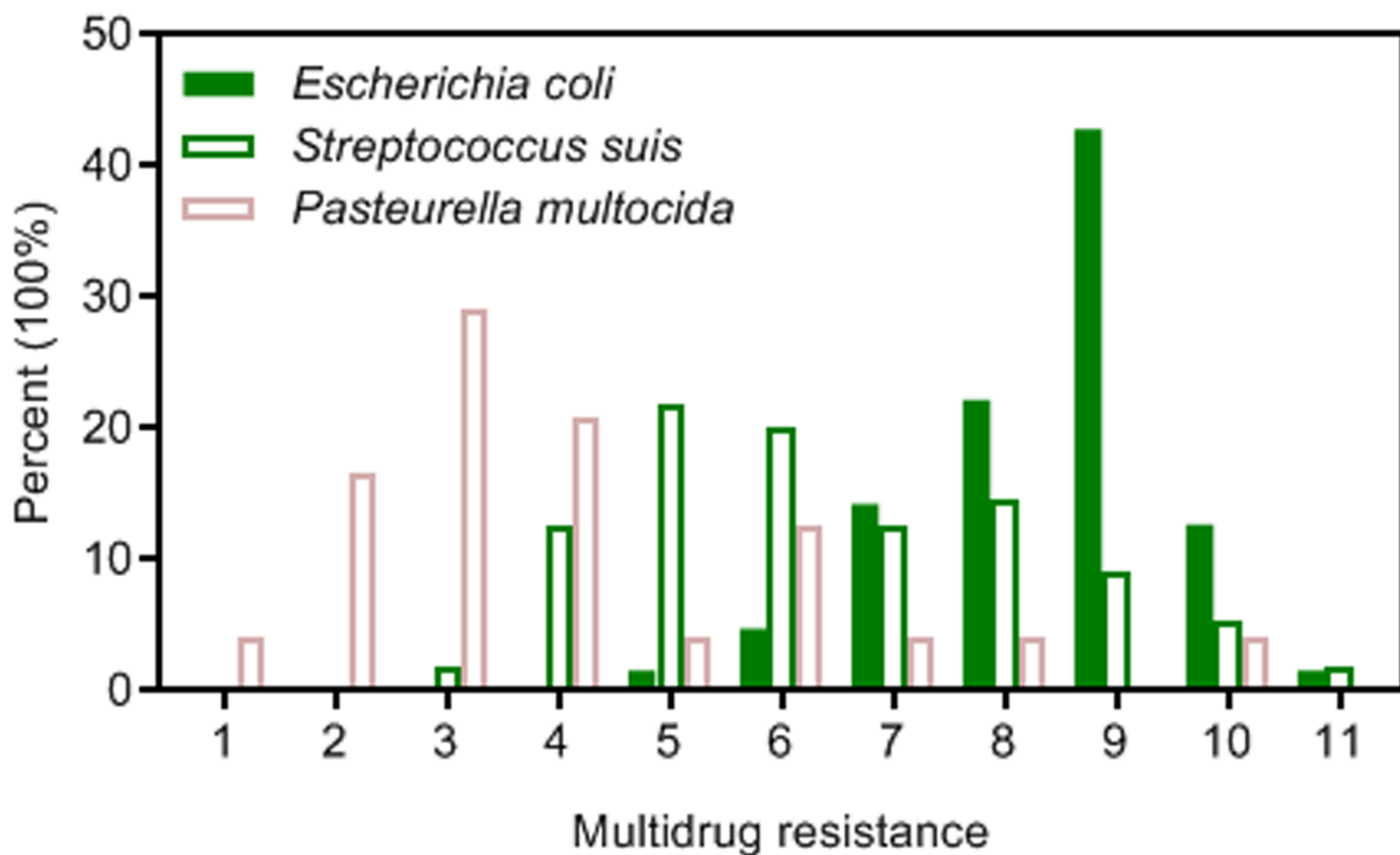


Figure 5

Analysis of multidrug resistance. The X-axis represents the number of isolates resistant to 1–11 categories of antimicrobial drugs.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [TableS1.xlsx](#)
- [TableS2.docx](#)