



A Study on Extended Spectrum β -Lactamase Producing (ESBL) and Fluoroquinolone-Resistant *Escherichia coli* in the Japanese Quails

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Authors' contributions

This work was carried out in collaboration between both authors. Both authors read and approved the final manuscript.

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ABSTRACT

Antimicrobial resistance (AMR) is a growing public health threat worldwide, and members of the Enterobacteriaceae family are among the clinically important bacteria rapidly developing resistance to available antibacterial agents. The development of extended-spectrum β -lactamase (ESBL) enzymes is the primary cause of resistance to third-generation cephalosporins among Enterobacteriaceae. Quails also represent a source of animal protein deficiency in developing

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countries including India. This study aimed to detect the presence of extended-spectrum β -lactamases (ESBLs) and fluoroquinolone-resistant *Escherichia coli* from fecal samples of quails in Puducherry. A total of 36 fecal samples of quails from six different retail outlets were collected. *E. coli* could be isolated from 27 fecal samples and confirmed as *E. coli* by polymerase chain reaction by targeting the *uspA* gene. The isolates were preliminarily screened for ESBL production by indicator antimicrobial disc and phenotypic ESBL production was confirmed by combination disc method. The isolates were subjected to genotypic detection of ESBL (*bla* CTX-M, *bla* TEM, and *bla* SHV) by PCR. Out of 27 isolates, 16 isolates were positive for the presence of ESBL-producing genes, in which, 9 harbored *bla* CTX-M, 2 harbored *bla* TEM, and 5 harboured *bla* SHV genes. Similarly, out of 27 isolates 13 isolates were found positive for fluoroquinolone resistance in which 13 (48.18%) isolates harbored the *qnrS* gene, and 11 (40.74%) isolates harbored the *qnrB* gene. Antimicrobial susceptibility test showed that the isolates exhibited a high level of resistance against Cefpodoxime (90%), Amoxicillin/clavulanic acid (70%), Ceftriaxone (60%), Cefotaxime (55%), Ceftazidime (45%), Ciprofloxacin (40%) and Aztreonam (30%).

Keywords: AMR; ESBL; Fluoroquinolone resistance; *E. coli*, *uspA*.

1. INTRODUCTION

“Over the past five decades, there has been a significant increase in poultry meat production, which now constitutes nearly one-third of global meat production” [1,2]. “The rearing of birds other than chickens as quails has been developed in recent years worldwide to supply human food requirements” [3]. Quail farming is increasing globally daily as it requires low-rearing investment and has fast financial returns. In addition, quails differ from other poultry species in that they use less feed, overgrow, reach sexual maturity early, have short generation intervals, have short incubation periods, have highly nutritious meat, and are less susceptible to viral diseases. [4-6]. Common bacteria in the poultry gut include *Escherichia coli*, which causes various diseases such as omphalitis, cellulitis, swollen head syndrome, coli granuloma, and colibacillosis [7]. The primary cause of the emergence, persistence, and dissemination of resistant bacteria is the overuse of antibiotics in intensive animal agriculture, particularly in raising pigs and poultry [8]. Swine, cattle, poultry, and turkey have all been found to harbor ESBL-producing bacteria [9]. “The emergence of plasmid-mediated quinolone resistance was first reported in strains of *Klebsiella pneumoniae* in the United States in 1998. In the following years, several distantly related plasmids-mediated *Qnr* determinants were described in Enterobacteriaceae (*qnrA*, *qnrB*, *qnrC*, *qnrD*, and *qnrS*). It is becoming more common to find ESBLs and additional plasmid-mediated antibiotic-resistance genes such as *qnr*” [10]. Humans may acquire multidrug-

resistant bacteria through zoonotic transmission from broiler farms and agricultural settings, or indirectly by food-borne diseases [11].

Puducherry, a state with intensive quail farming, lacks data regarding antibiotic use and antibiotic resistance in poultry farms. This study was therefore done to determine the antibiotic-resistant *E. coli*, study their antibiotic susceptibility pattern, and identify the resistance genes in quails in Puducherry.

2. MATERIALS AND METHODS

2.1 Collection and Processing of Samples

A total of six retail outlets were chosen for sample collection and from each retail outlet six cloacal swabs were collected using a sterile swab aseptically from healthy quails randomly in and around Puducherry. The collected 36 cloacal swabs were transported to the Department of Veterinary Microbiology Laboratory, Rajiv Gandhi Institute of Veterinary Education and Research (RIVER), Puducherry for further processing.

2.2 Isolation and Identification of *E. coli*

Each collected cloacal swab was inoculated into a Luria broth and subjected to incubation overnight at 37°C. A loopful of the culture was streaked onto MacConkey agar and incubated. The pink colonies that were lactose fermenting were subjected to Gram staining. Bergey's Manual of Systematic Bacteriology (1984) was used to identify Gram-negative bacteria as

Table 1. Primers details used for PCR in this study and their amplicon size

Target	Primer sequence (5'-3')	Size (bp)	Annealing Temperature	References
<i>uspA</i>	CTGGAAGAGGCTAGCCTGGACGAG AAAATCGGCACCGGTGGAGCGATC	844	60°C	Chen et al. [12]
<i>bla</i> TEM	ATGAGTATTCAACATTTCCG CTGACAGTTACCAATGCTTA	867	56°C	Rasheed et al. [15]
<i>bla</i> SHV	AGGATTGACTGCCTTTTTG ATTTGCTGATTTTCGCTCG	393	56°C	Colom et al., [16]
<i>bla</i> CTX-M	GAAGGTCATCAAGAAGGTGCG GCATTGCCACGCTTTTCATAG	560	59°C	Sharma et al., [17]
<i>qnrS</i>	GCAAGTTCATTGAACAGGGT TCTAAACCGTCGAGTTCGGCG	428	52°C	Cattoir et al., [18]
<i>qnrB</i>	GGMATHGAAATTCGCCACTG TTTGCGYGYCGCCAGTCGAA	264	50°C	

E. coli up to the species level based on their biochemical tests and cultural characteristics.

PCR was employed for genotypic confirmation of the *E. coli* isolates, utilizing primers targeting the *uspA* gene [12]. PCR amplification was conducted using an automated thermal cycler (Eppendorf Mastercycler, Germany), following the PCR reaction conditions outlined in the protocol [12]. The PCR products were analyzed by agarose gel electrophoresis with the expected product size is 884 bp for the *uspA* gene. Following PCR confirmation of *E. coli* isolates, the resulting PCR products underwent analysis through agarose gel electrophoresis. Subsequently, all confirmed *E. coli* isolates were subjected to further detection of ESBL through both phenotypic and genotypic methods, along with genotypic detection of fluoroquinolone resistance.

2.3 Phenotypic Detection of ESBL Production

The preliminary phenotypic screening of ESBL production was carried out by using five indicator antimicrobial discs: ceftriaxone (30 µg), cefotaxime (30 µg), ceftazidime (30 µg), cefpodoxime (10 µg) and aztreonam (30 µg) discs. Among these five indicator discs isolates show resistance to at least one antibiotic was considered as positive for ESBL production. Further ESBL production was confirmed by following the combination disc method using cefotaxime and cefotaxime/ clavulanic acid, in the plate of Mueller-Hinton agar at a distance of 25 mm apart as per the recommendation of CLSI guidelines (2019). Plates were incubated for 16-18 hours at 37°C. The isolates were confirmed as ESBL producers if the inhibition zone

diameter around the combination disc was ≥ 5 mm when compared to the disc containing respective cephalosporin alone [13].

2.4 Genotypic Detection Antimicrobial Resistance Genes

Following identification as *E. coli*, all isolates underwent PCR analysis using primers targeting *bla* TEM, *bla* SHV, and *bla* CTX-M genes for ESBL confirmation and also confirmation of fluoroquinolone-resistant genes such as *qnrS*, and *qnrB* by PCR. Template DNA preparation from *E. coli* strains followed the method described by Zhang et al. [14].

2.5 Antibiotic Susceptibility Testing

Antimicrobial susceptibility test was done on Mueller-Hinton agar (HiMedia, Mumbai) plate as per the recommendation of Clinical Laboratory Standard Institute (2019) using the following commercially (HiMedia, Mumbai) available antimicrobial discs (HiMedia) used in this study were Amoxicillin/clavulanic acid (30 µg), Cefpodoxime (30 µg), Cefotaxime (30 µg), Aztreonam (30 µg), Ceftazidime (30 µg), Enrofloxacin (30 µg), and Ceftriaxone (30 µg).

2.6 Statistical analysis

Statistical analysis was performed by using SPSS software version 27. Chi-square analysis was conducted to compare the ESBL and fluoroquinolone-resistant genes in *E. coli* isolated from the cloacal swabs.

3. RESULTS AND DISCUSSION

In this study, among 36 cloacal swabs examined, a total of 27/36 (75%) *E. coli* isolates were obtained, using cultural and biochemical

characterization followed by genotypic confirmation of PCR using *uspA* gene specific for *E. coli* (844 bp) (Fig.1). The higher occurrence rate of *E. coli* is about 65%, and a lower rate of *E. coli* 3.5 % reported from quail cloacal samples [3,19].

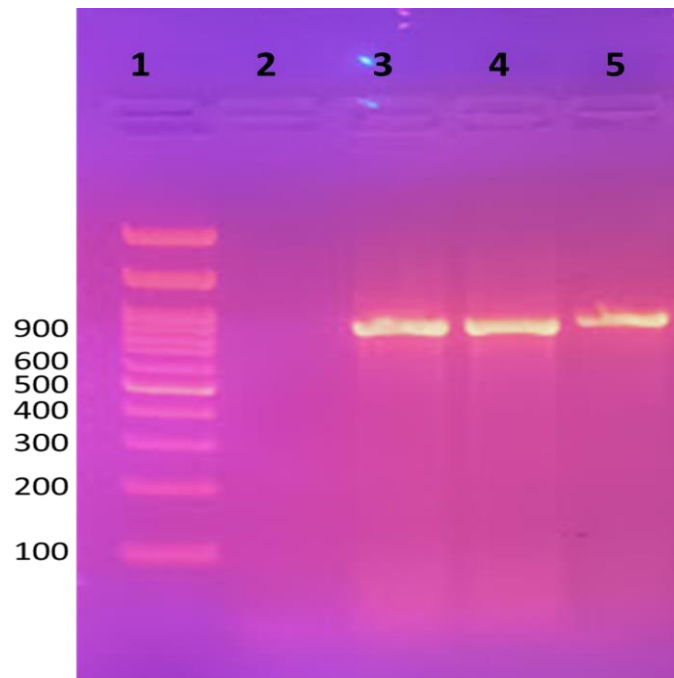


Fig. 1. Agarose gel electrophoresis showing the results of polymerase chain reaction amplified product of 844 bp for the *uspA* gene in *E. coli* isolates. Lane 1: 100 bp ladder; Lane 2: Negative control; Lane 3: Positive control; Lane 4,5: Field isolates for *uspA* gene in *E. coli*

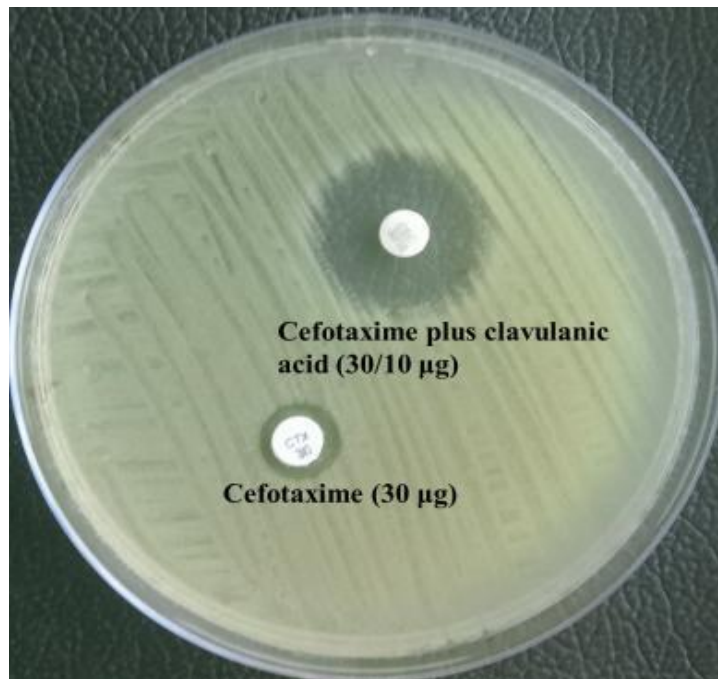


Fig. 2. Phenotypic confirmation of ESBL production of *E. coli* isolates

In this study, 20 (74.07%) isolates were found preliminarily positive for ESBL production by indicator antimicrobial agents. Out of 20, phenotypically 17 (62.9%) isolates were confirmed as ESBL producers by combination disc method (Fig. 2).

In Kerala, 6/22 (27.27%) isolates were phenotypically positive for ESBL production in quails were reported [20]. The genotypic method

confirms the presence of genes associated with ESBL production in *E. coli* isolates. In this study, out of 27 isolates, 16 (59.25%) isolates were found positive for ESBL-producing genes in which 9 (33.33%) isolates harbored *bla* CTX-M (Fig. 3), 2 (7.4%) isolates harbored *bla* TEM (Fig. 4) and 5 (18.51%) isolates harbored *bla* SHV gene (Fig. 5). Two isolates (7.4%) harbored both *bla* TEM and *bla* SHV.

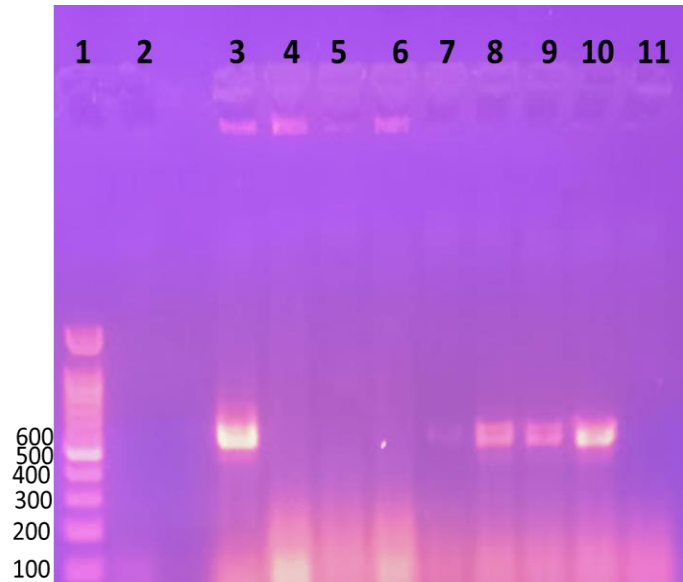


Fig. 3. Agarose gel electrophoresis showing the results of polymerase chain reaction amplified product of 540 bp for the CTX-M gene in *E. coli* isolates. Lane 1: 100 bp ladder; Lane 4 to 11: Field isolates for CTX-M gene in *E. coli*; Lane 2: Negative control; Lane 3: Positive control

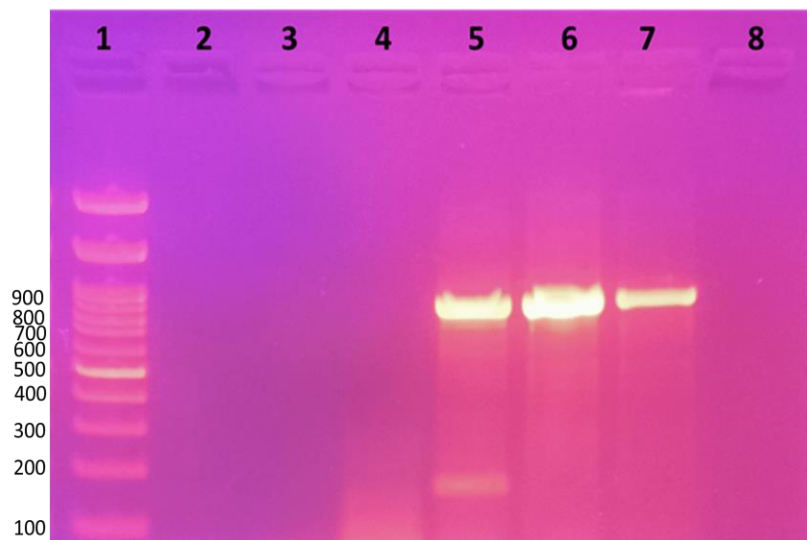


Fig. 4. Agarose gel electrophoresis showing the results of polymerase chain reaction amplified product of 867 bp for the TEM gene in *E. coli* isolates. Lane 1: 100 bp ladder; Lane 2&3,4,5,6: Field isolates for TEM gene in *E. coli*; Lane 7: Positive control; Lane 8: Negative control

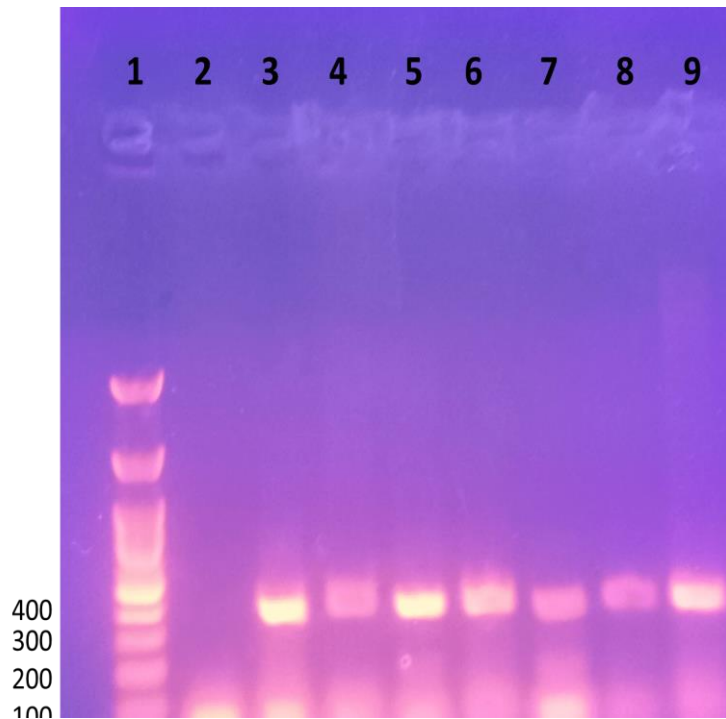


Fig. 5. Agarose gel electrophoresis showing the results of polymerase chain reaction amplified product of 393 bp for the SHV gene in *E. coli* isolates. Lane 1: 100 bp ladder; Lane 4,5,6,7,8,9: Field isolates for SHV gene in *E. coli*; Lane 3: Positive control; Lane 2: Negative control

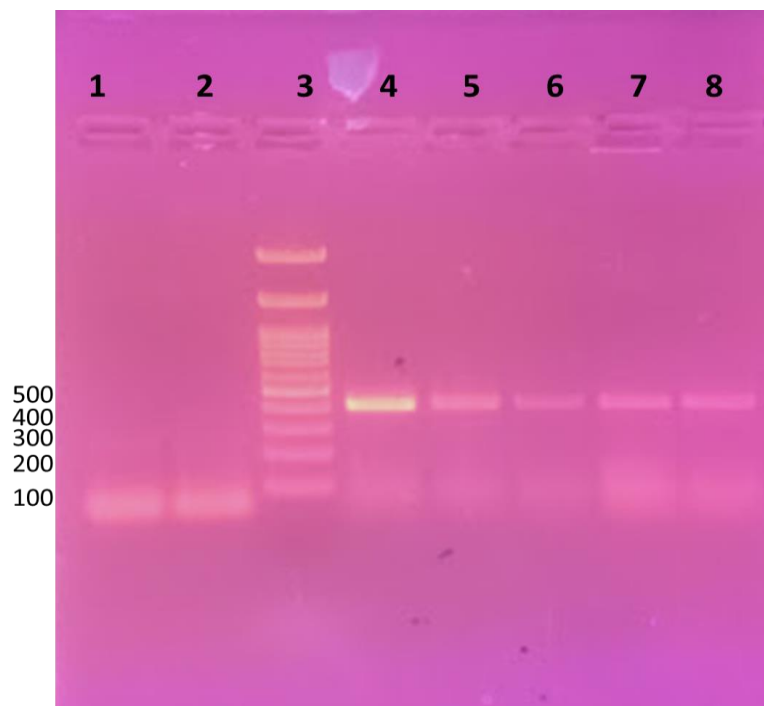


Fig 6. Agarose gel electrophoresis showing the results of polymerase chain reaction amplified product of 428 bp for the *qnrS* gene in *E. coli* isolates. Lane 3: 100 bp ladder; Lane 1,5,6,7,8,9,10: Field isolates for *qnrS* gene in *E. coli*; Lane 2: Negative control; Lane 4: Positive control

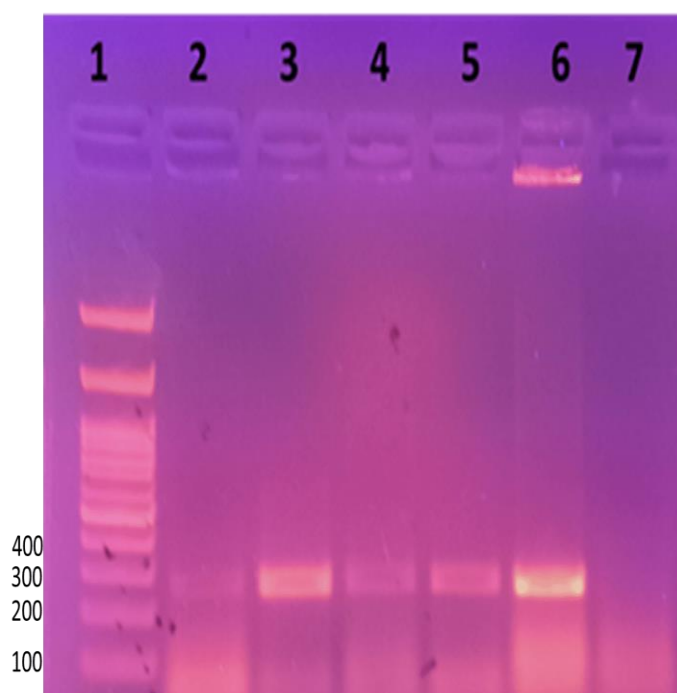


Fig. 7. Agarose gel electrophoresis showing the results of polymerase chain reaction amplified product of 264 bp for the *qnrB* gene in *E. coli* isolates. Lane 1: 100 bp ladder; Lane 2&3,4,5: Field isolates for *qnrB* gene in *E. coli*; Lane 6: Positive control; Lane 7: Negative control

The overall presence of the *bla* TEM gene about 42.85% was reported in *E. coli* isolates from Japanese quails [21]. 20 isolates (90.9%) harbored at least one ESBL gene, 10 isolates (45.45%) harbored *bla* CTX-M gene, and 15 isolates (68.18%) harbored *bla* TEM gene in quails reported in India [20]. In poultry, the occurrence of *bla* TEM, *bla* CTXM, and *bla* SHV were detected in 21.7%, 34.7%, and 43.4% of the isolates respectively and another study in poultry droppings showed 50% of the isolates pose the *bla* CTXM gene and *bla* TEM genes [22,23]. In India from fecal samples of diarrhoeic piglets, *E. coli* isolates harbored *bla* TEM (6.47%) and *bla* CTX-M (2.94%) genes [24]. A much higher prevalence of the *bla* TEM and *bla* SHV of 20% and 31.6% of the *E. coli* isolates were reported from fecal samples of dairy cattle from Chhattisgarh, India [25]. A study conducted in the Ivory Coast reported the presence of ESBL genes in *E. coli* isolates from collected fecal samples, shown *bla* CTX-M, *bla* SHV, and *bla* TEM at frequencies of 73,3%, 66,7%, and 100% [26]. In this study, out of 27 isolates 13 isolates were found positive for fluoroquinolone resistance in which 13 (48.18%) isolates harbored the *qnrS* gene (Fig. 6), and 11 (40.74%) isolates harbored the *qnrB* gene (Fig. 7).

Table 2. Antibiotic resistance genes in *E. coli* from quails

	Positive	Negative	<i>p</i> value
ESBL	16	11	<i>p</i> =
Fluoroquinolone resistance	13	14	0.586

Chi-square analysis showed no significant association ($P \geq 0.05$) between the occurrence of ESBL and fluoroquinolone-resistant genes in *E. coli* isolated from the cloacal swabs. To our knowledge, no study has reported the presence of fluoroquinolone resistance genes in Japanese quails in India. In poultry farms of Southern Karnataka, a study was conducted and found results that the *qnrB* gene 38% was commonly detected followed by the *qnrS* gene 27% and *qnrA* gene 21.5% in *Escherichia coli* in collected fecal samples [27]. From North India, the prevalence of *qnrS*, and *qnrB* were 37. 50% and 5.83% respectively in from the cloacal swabs of commercial chickens reported [28]. High-level resistance to fluoroquinolones was detected in five *E. coli* isolates from wildlife in the Province of Vojvodina [29]. This is the first study conducted on Japanese quails of Puducherry and detected the presence of ESBL-producing and

fluoroquinolone-resistant *E. coli* in fecal samples of quails in Puducherry. In this study, antimicrobial susceptibility test showed that the majority of the isolates exhibited a high level of resistance against Amoxicillin/clavulanic acid (100%), Cefpodoxime (100%), Cefotaxime (80%), Aztreonam (70%), Ceftazidime (70%), Enrofloxacin (70%) and Ceftriaxone (40%). In a report of Kerala in Japanese quails, 59.09% of *E. coli* were found as Imipenem- intermediate, five were Imipenem resistant (22.72%), seven (31.81%) were Meropenem-intermediate and three (13.63%) were Meropenem resistant on Antibiotic susceptibility testing [20]. The ESBL *E. coli* isolates from poultry origin revealed 100 percent resistance to Oxytetracycline, Cefotaxime, and Cefperazone followed by Ceftazidime (94.23%), Cefpodoxime (88.46%) and Ceftriaxone (82.69%), while resistance to Chloramphenicol (76.92%), Gentamicin and Enrofloxacin exhibited lower resistance and no resistance observed against Cefepime and Amoxicillin-clavulanic acid [21]. Resistance of antimicrobials obtained in this study in field conditions were also reported by the different researchers [23,30]. There are only a few reports of ESBL in the quails of India, and there is no report of fluoroquinolone-resistant *E. coli* Japanese quail farms in Puducherry. Thus, the present study's findings revealed the quails as a reservoir of antimicrobial-resistant bacteria and can be used as preliminary data for further research on the subject.

4. CONCLUSION

The present study's findings indicate that Japanese quails may serve as a reservoir for ESBL and fluoroquinolone resistance *E. coli*. Similarly, the presence of ESBL-producing and fluoroquinolone-resistant *E. coli* in quails was a major concern indicating infection at the farm level. The present study showed the increased occurrence of ESBL-producing *E. coli* in quails in the Puducherry region and their resistant antibiogram pattern among quails. Antimicrobial resistance is a complex and long-term biological challenge that requires coordinated, science-based actions to mitigate its impact on human civilization. Effective measures should balance the economic efficiency of the poultry industry with the promotion of public health. Integrating environmental, social, and governance initiatives in the poultry sector, aligned with one health principle, is encouraged to address this issue.

DISCLAIMER (ARTIFICIAL INTELLIGENCE)

Author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc) and text-to-image generators have been used during writing or editing of manuscripts.

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COMPETING INTERESTS

Authors have declared that no competing interests exist.

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