

## Molecular Detection and Antimicrobial Resistance Profiling of *Salmonella* spp. in Commercial Poultry Farms

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#### Abstract

*Salmonella* spp., particularly nontyphoidal serovars, remain a leading cause of zoonotic foodborne illness globally, with commercial poultry serving as a primary reservoir and contributing to an estimated 153 million human cases and over 155,000 deaths annually. This review synthesizes recent advances in molecular detection and antimicrobial resistance (AMR) profiling of *Salmonella* in poultry production systems. Conventional culture-based methods are increasingly supplemented or replaced by rapid, sensitive techniques including PCR (targeting *invA*, *trr*, *hlyA*), real-time qPCR, loop-mediated isothermal amplification (LAMP), digital PCR, and CRISPR-based serotyping (CRISPR-SeroSeq), enabling high-throughput identification and serovar discrimination even in complex matrices (cloacal swabs, litter, embryonated eggs). Prevalence varies widely (pooled estimates 12–14% in meta-analyses from Ethiopia, Bangladesh, and Nepal), with *S. Typhimurium*, *S.*

*Enteritidis*, and *S. Kentucky* frequently dominant. AMR profiling reveals alarming trends of multidrug resistance (MDR), including resistance to critically important classes (fluoroquinolones, third-generation cephalosporins, colistin), driven by extended-spectrum  $\beta$ -lactamases (ESBLs), plasmid-mediated quinolone resistance (PMQR), and integrons. Horizontal gene transfer and biofilm formation further complicate control. Integrated strategies—stringent biosecurity, vaccination,

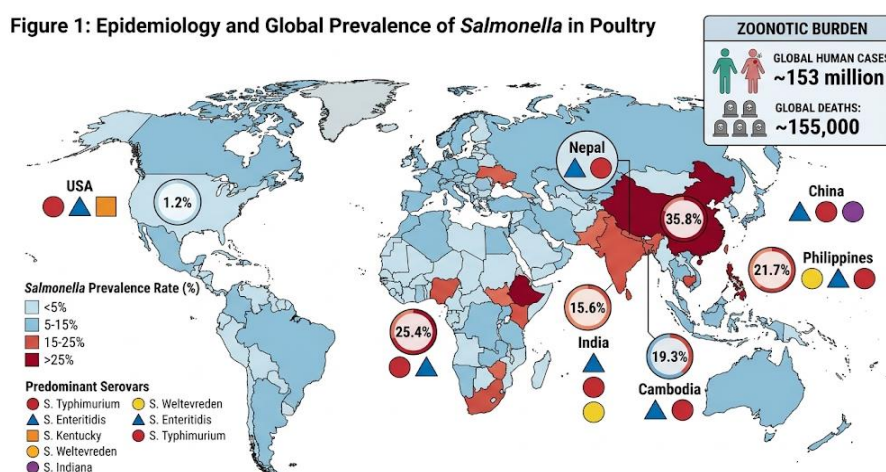
competitive exclusion, and prudent antimicrobial stewardship—are emphasized to mitigate transmission and preserve treatment efficacy in the face of rising AMR threats.

## 1. Introduction

The global poultry industry represents a cornerstone of agricultural economics and food security, yet it remains one of the most significant reservoirs for *Salmonella* species, a genus of Gram-negative, facultative anaerobic bacilli within the Enterobacteriaceae family (Basazinew et al., 2025). Nontyphoidal *Salmonella* (NTS) is a primary etiological agent of zoonotic gastroenteritis, responsible for an estimated 1.35 million illnesses and 420 deaths annually in the United States alone, with global estimates reaching 153 million cases and over 155,000 deaths (Frontiers in Microbiology, 2025). The persistence of *Salmonella* in commercial poultry complexes is facilitated by its ability to undergo both vertical transmission through the egg and horizontal transmission via environmental contamination, vectors, and direct contact (Siceloff, 2024). As international trade and intensive production systems expand, the challenges associated with managing *Salmonella* are compounded by the emergence of multidrug-resistant (MDR) strains, which significantly limit therapeutic options and increase the public health burden (Djemaoune et al., 2025).

## 2. Epidemiological Trends and Global Prevalence Dynamics

The prevalence of *Salmonella* in commercial poultry is highly variable, reflecting differences in geographic climate, biosecurity rigor, and the maturity of national surveillance programs (Siceloff, 2025). Systematic reviews and meta-analyses covering the period through 2025 highlight an overall pooled prevalence in some regions of approximately 12.46%, although specific localized studies report rates ranging from 2.20% in broad cross-matrix surveys to nearly 100% in certain retail environments (Tsogtbayar et al., 2025). *Salmonella* prevalence in poultry varies widely across regions, influenced by production systems, biosecurity, and sampling matrices. A global overview of prevalence and dominant serovars is summarized in Figure 1.



### 2.1 Regional Variation and Metadata Analysis

In Ethiopia, meta-regression models indicate that the highest pooled prevalence is found in the Western region (23.18%), with broilers exhibiting significantly higher infection rates (28.23%) compared to other production types (Chu et al., 2024). Age is a critical determinant, as poultry under 6 months of age show a higher susceptibility (14.45%) due to incomplete immune development. Research in Bangladesh has identified a 14.4% prevalence at the farm level, with layers showing higher rates than broilers, often attributed to longer production cycles that increase exposure time to environmental reservoirs (Siddiky et al., 2025). Recent surveillance of dead-in-shell embryonated eggs in Nepal further revealed a prevalence of 11.42%, identifying *S. Kentucky* and *S. Typhimurium* as significant isolates (Khanal et al., 2025).

**Table 1. Regional Variation and Pooled Prevalence of *Salmonella* in**

### Commercial Poultry

Geographic Region	Pooled Prevalence (%)	Predominant Serovars	Primary Sample Type
Ethiopia (National)	12.46%	S. Typhimurium, S. Enteritidis	Feces, Litter, Cloacal (Abdi et al., 2025)
Bangladesh	14.4%	S. Typhimurium, S. Enteritidis	Feces, Cloacal (Siddiky et al., 2025)
India (Patna/Haryana)	23.7%	S. Gallinarum, S. Typhimurium	Meat, Broiler Flocks (Microbiology Journal, 2025)
Cambodia	6.30%	S. Weltevreden, S. Typhimurium	Farm Swabs (Cambodian Journal, 2025)
Philippines	37.5%	S. Infantis, S. Brancaster	Retail Cut Samples (Frontiers in Microbiology, 2025)
China (Shandong)	18.2%	S. Infantis, S. Derby	Retail Chicken (Chu et al., 2024)
USA (Organic)	37.08%	S. Kentucky, S. Infantis	Carcass Rinse (Marchello et al., 2020)
USA (non-organic)	61.67%	S. Kentucky, S. Infantis	Carcass Rinse (Marchello et al., 2020)

### 3. Molecular Detection Methodologies: Evolution and Optimization

The necessity for rapid and accurate detection has driven a shift from traditional culture-based "gold standard" methods to molecular diagnostics. Traditional protocols, such as ISO 6579-1:2017, involve sequential enrichment and can take 3 to 5 days for a definitive result (Awang et al., 2021).

#### 3.1 Polymerase Chain Reaction and Genetic Markers

The most frequently targeted genetic marker for Salmonella identification is the *invA* gene, which encodes a component of the Type III Secretion System essential for host cell invasion (Mohammed, 2024). Multiplex PCR allows for the simultaneous detection of multiple serovars or resistance genes, such as the *spy* gene for *S. Typhimurium* and the *sdfI* gene for *S. Enteritidis* (Worley, 2025).

#### 3.2 AI-Powered Diagnostics and Vision Transformers

Novel diagnostic platforms are increasingly integrating Artificial Intelligence (AI) to enhance detection speed. A Modified Hierarchical Vision Transformer (HViT) model has been developed to detect Salmonella and other poultry diseases from fecal images, achieving a validation accuracy of 90.90% (IET Image Processing, 2025).

Similarly, MobileNetV2-based systems have demonstrated 98.02% accuracy in distinguishing Salmonella infections in resource-constrained settings, providing a scalable, farmer-friendly tool for early diagnosis (Poultry Science, 2025).

### 3.3 MALDI-TOF MS and Proteomic Profiling

Matrix-Assisted Laser Desorption/Ionization - Time of Flight Mass Spectrometry (MALDI-TOF MS) has emerged as a transformative tool for the rapid detection of AMR. By analyzing metabolic or proteomic changes induced by antibiotic exposure, this phenotypic method enables the direct inference of resistance in just 2 to 4 hours (Beyer, 2025). Recent workflows using MALDI-TOF MS have achieved high accuracy in detecting resistance across multiple classes, including the direct identification of hydrolyzed beta-lactam products (Chung et al., 2023).

### 3.4 Isothermal Amplification and Point-of-Care Tools

Loop-mediated Isothermal Amplification (LAMP) has emerged as a powerful alternative to PCR for field applications, operating at a constant temperature of 60 to 65 degrees C (Zhang et al., 2014). Recent advancements have optimized HNB-based LAMP assays to detect the *aadA1* gene responsible for streptomycin resistance in as little as 35 minutes with high sensitivity (Veterinary Sciences, 2025).

### 3.5 Digital PCR and Absolute Quantification

Digital PCR (dPCR) represents the third generation of PCR, enabling absolute quantification of target DNA without external standard curves (Cleveland et al., 2024). This technology is extremely tolerant to PCR inhibitors common in poultry rinses, such as peracetic acid and chlorine, and can provide a standardized estimate of Salmonella load in 8 to 9 hours (Mao et al., 2019).

## 4. Genomic Characterization and High-Resolution Surveillance

Whole-Genome Sequencing (WGS) has transformed Salmonella surveillance by consolidating serotyping, virulence profiling, and AMR genotyping into a single workflow (Clark, 2021).

### 4.1 CRISPR-SeroSeq and Deep Serotyping

CRISPR-SeroSeq analyzes the spacers within CRISPR arrays to detect multiple serovars within a single sample, overcoming the bias of culture-based methods that often isolate only the dominant strain (Thompson et al., 2018). This method has identified multiseroovar populations in 18% of environmental samples from broiler breeder farms, revealing complex dynamics where certain serovars, like *S. Kentucky*, may exclude others (Quinn et al., 2023).

## 5. Antimicrobial Resistance (AMR): Mechanisms and Profiling

Widespread antimicrobial use in poultry has led to high rates of multidrug resistance. In Algeria, 100% of *S. Gallinarum* isolates from laying hens exhibited resistance to quinolones, aminoglycosides, and sulfonamides (Djemaïoune et al., 2025).

**Table 2. Key Resistance Genes and Molecular Mechanisms Associated with Salmonella AMR**

Antimicrobial Class	Key Resistance Genes	Molecular Mechanism	Notable Prevalence/Findings
Beta-lactams	<i>bla</i> TE M, <i>bla</i> SHV, <i>bla</i> CTX-M-65	Enzymatic Hydrolysis	92.68% carry <i>bla</i> CTX-M (Nigeria Study, 2021)
Tetracyclines	<i>tet</i> A, <i>tet</i> B	Efflux Pump	89.2% of TET-R isolates harbor <i>tet</i> B (Abdi et al., 2025)

<b>Sulfonamides</b>	sul1, sul2	Target Bypass (DHPS)	94.4% resistance in Bangladesh (Siddiky et al., 2025)
<b>Fluoroquinolones</b>	qnrS, qnrB, gyrA mutations	Target Protection	21.13% qnr prevalence in China (Chu et al., 2024)
<b>Aminoglycosides</b>	aadA1, aadA2, strA/B	Enzymatic Inactivation	Associated with <i>S. Infantis</i> pESI (Nhung et al., 2024)

### 5.1 The Role of the pESI Megaplasmid in *S. Infantis*

The emergence of MDR *S. Infantis* is inextricably linked to the acquisition of the pESI megaplasmid (approximately 300 kb), which carries ESBL, tetracycline, and sulfonamide resistance genes. pESI-positive strains demonstrate increased biofilm formation and environmental fitness, facilitating their spread through the broiler production chain (Kim et al., 2024).

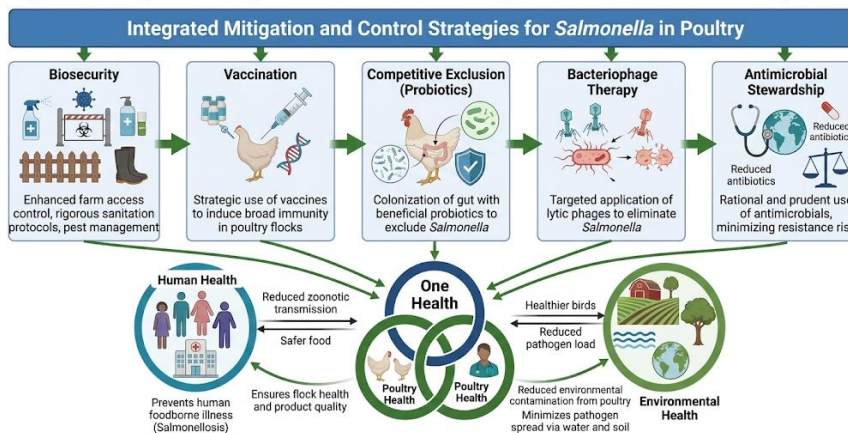
## 6. Contributing Factors to Salmonella Persistence and AMR Spread

The presence of *Salmonella* and the dissemination of resistance are driven by a multifactorial system encompassing management practices and environmental reservoirs. Large flock sizes (more than 8,000 to 10,000 birds) are statistically associated with increased *Salmonella* prevalence (Lamichhane et al., 2024). Poor biosecurity protocols, such as sourcing chicks from multiple multiplication centers, facilitate the entry of various serovars (Berry & Wells, 2018).

## 7. Integrated Mitigation and Control Strategies

Combating *Salmonella* requires balancing biosecurity with innovative alternatives to antibiotics. Recent research has focused on encapsulated leads for AMR mitigation, which have proven safe for commensal gut lactobacilli while effectively reducing pathogen load (Sindhushree et al., 2025). Effective control of *Salmonella* requires a multifaceted One Health strategy integrating biosecurity, vaccination, probiotics, bacteriophage therapy, and prudent antimicrobial use. A summary of these mitigation measures is shown in Figure 2.

Figure 2: Integrated Mitigation and Control Strategies for *Salmonella* in Poultry



### 7.1 Probiotics and Bacteriophage Therapy

Probiotics like *Lactobacillus* and *Bifidobacterium* promote gut health through competitive exclusion, adhering to the mucosa and producing short-chain fatty acids. Therapeutic bacteriophages offer a cost-effective tool for selectively lysing *Salmonella* without disrupting the beneficial microbiota (Mills, 2025).

## 8. Conclusion

The persistence of *Salmonella* in commercial poultry systems, coupled with the rapid emergence and dissemination of multidrug-resistant strains, poses a persistent and escalating threat to public health and food safety worldwide. Molecular diagnostics particularly real-time PCR, LAMP, digital PCR, and CRISPR-based serotyping have revolutionized surveillance by providing rapid, sensitive, and serovar-specific detection that outperforms traditional culture methods, enabling earlier intervention and traceability across the production chain. Concurrently, AMR profiling underscores the urgent need for global harmonized monitoring, as resistance to last-resort antimicrobials (e.g., colistin, carbapenems) compromises both human and veterinary therapeutics. Effective mitigation demands a One Health approach integrating enhanced biosecurity, *Salmonella*-free breeder programs, targeted vaccination, competitive exclusion probiotics, and strict antimicrobial stewardship policies. Continued investment in molecular epidemiology, whole-genome sequencing for resistance gene tracking, and international collaboration will be essential to curb transmission, reduce zoonotic burden, and safeguard poultry-derived food supplies in an era of intensifying production and AMR pressure.

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