Transactions on Materials, Biotechnology and Life Sciences
ISSN: 2960-1932, eISSN: 2960-2319 | Volume 8
MMTCS 2025

Progress in the study of drug resistance mechanism of Salmonella

Ruoyao Liu*

Guangdong University of Technology, Guangzhou, China

*Corresponding author: 1349186428@qq.com

Abstract. Foodborne Salmonella is a Gram-negative bacteria that is widely spread globally and is capable of causing typhoid fever, paratyphoid fever, and poisoning in the human body. Meanwhile, Salmonella is one of the four leading causes of diarrheal diseases worldwide. More and more reports indicate that the status of Salmonella resistance to antibiotics is not optimistic. Studies have shown that the resistance mechanisms of Salmonella is related to enzyme inactivation, efflux pumps, removable progenitors, and biofilm changes. In terms of rapid detection, the new generation of molecular techniques and detection methods, such as biosensors, have dramatically shortened the detection times and reduced the cost of Salmonella detection in food. In this paper, we will reveal the complex resistance mechanisms of Salmonella to antibiotics by integrating the latest advances in global research and the latest development direction of Salmonella detection technology.

Keywords: Salmonella, Antimicrobial Resistance, Multidrug Resistance, Mechanisms of Drug Resistance.

1. Introduction

Antibiotics are secondary metabolites produced by microorganisms (bacteria, fungi, etc.) or by higher plants and animals in the course of their life activities, which have bacteriostatic or bactericidal effects.

At present, the problem of antibiotic abuse is quite serious, which is reflected in medical treatment, animal husbandry and aquaculture. In 2023, the Defined Daily Doses (DDDs) is about 49.3 billion. An estimation of increase of DDDs is about 16.3% from 29.5 to 34.3 since 2016[1].

Between 2000 and 2015, total global antibiotic consumption increased by 65%, from 21.1 billion DDDs to 34.8 billion DDDs[2]. In recent research indicated that 66% of patients with non-bacterial infections were prescribed antibiotic drugs[3].

In the animal breeding industry, antibiotics are often added to feed in large quantities to promote growth, prevent and treat diseases. The development of drug-resistant bacteria as a result of long-term antibiotic use threatens the health of both humans and animals (spread of drug-resistant strains, decreased effectiveness of antibiotic treatments, etc.). For example, Dong found that livestock-exposed populations had a significantly higher proportion of livestock-associated Staphylococcus aureus (LA-SA) compared to non-livestock-exposed people. Also, there was a significant positive correlation between animals exposure and human

livestock-associated Methicillin-resistant Staphylococcus aureus (LA-MRSA) carriage[4].

The transmission of resistant strains is also not negligible, as it is possible to carry resistant strains through direct transmission (for example, humans through direct contact with food animals carrying resistant bacteria), indirect transmission (for example, food chain, exposure to contaminated environments), which can lead to further spread of drug-resistant strains. On the environmental side, medical wastewater, agricultural runoff, and sewage treatment plants all have the potential to contaminate water sources, which can spread drug-resistant strains to humans.

Therefore, it is important to elucidate the mechanisms of resistance and how to detect drug-resistant strains. Understanding the mechanisms of drug-resistant and its spread will provide ideas for controlling drug-resistant strains, while the rapid detection of drug-resistant strains can help in the management of related microorganisms.

2. Current Status OF Research ON Drug Resistance Mechanisms AND THE Significance

2.1. Current status of Salmonella resistance to antibiotics

Salmonella is one of the major foodborne pathogens that cause diarrhea and is characterized by flagellated, partially anaerobic, Gram-negative organisms with more than 2,600 serotypes including O, H, and Vi antigens. Currently, globally, more than 93 million reports of gastroenteritis caused by Salmonella infections were reported annually, including 155,000 deaths. Approximately 85% of these cases are associated with foodborne Salmonella [5]. This is because treatment with antibiotics is the most widely used and has the longest lasting. Over time, Salmonella have developed varying levels of resistance to antibiotics, with a high incidence of antibiotic resistance, and multi-drug resistance (MDR) being particularly severe. For example, Marchello found that 25.9% of the 34,996 strains of Salmonella isolated worldwide were resistant to chloramphenicol; 38.8% of the 34,783 strains were ampicillin-resistant, respectively; 37.9% of 35270 strains were resistant to methicillin-sulfamethoxazole[6]. And the rate of tetracycline resistance in Salmonella was 79.52%; 82 strains were detected with tetracycline-resistant genes tetA[7]. The rate of resistance in Salmonella in South Asia has increased to 77% from 53% within 10 years[8]. In addition, the MDR rate of Salmonella is at a high level. Another example is that the MDR rate of Salmonella in Jilin City, China, was 54.07%[9]. Some strains have been reported to have strong drug resistance. One strain was able to develop resistance to four antibiotics (β-lactams, tetracyclines, sulfonamides, and quinolones) at the same time. It is evident that the current status of drug resistance in Salmonella is not optimistic.

Common medications used to treat Salmonella are primarily antibiotics, including penicillin and cephalosporins. Data from the U.S. Centers for Disease Control and Prevention (CDC) indicates that most people can be cured of Salmonella infections without the use of antibiotics, but antibiotics continue to be heavily misused globally, leading to a yearly increase in the detection rate of drug-resistant strains, the spread of drug-resistant strains, contamination of the food supply chain, and a threat to human health. The mechanisms of resistance in Salmonella are relatively complex, including genetic mutations, cellular exocytosis, resistance caused by mobile progenitors (for example, transposons), and increased resistance of strains due to biofilm changes.

2.2. Genetic mutation leads to increased drug resistance in the strain

The most important cause of MDR triggered in bacteria is mutations in coding genes and the transfer of resistance genes. There are various genes associated with Salmonella resistance, including beta-lactamase genes (bla), sulfonamide antibiotic resistance genes (sul), etc. Salmonella can hydrolyze β-lactam antibiotics (penicillin, etc.) through the β-lactamase encoded by the gene of bla, resulting in the hydrolytic inactivation of the antibiotic molecules (for example, penicillin, first-generation cephalosporins, and third-generation cephalosporins). The sul gene produces a variant dehydrogenate synthase so that the folate synthesis pathway is not inhibited by sulfonamide antibiotics, and thus the strain can continue to synthesize folate. Mutations in antibiotic resistance in Salmonella are associated with DNA mismatch repair genes, for example mutations in MMR genes (mutS, mutT, mutL, uvrD, etc.) trigger antibiotic resistance, and the degree of resistance is related to the quantity of mutation sites[10]. The MMR system has the ability to repair DNA mismatches, and can recognize and repair insertions or deletions occurring in DNA synthesis. Four genes encode proteins that play a role in the MMR system in promoting the occurrence of mutations, each of which increases the frequency of mutations. Thus, a higher frequency of mutations may cause the emergence of drug-resistant strains.

2.3. Efflux by the cell leads to the development of resistance in the strain

Efflux refers to the process by which bacteria excrete macromolecules, and the cellular efflux system can mediate multidrug resistance in bacteria. This may be the most effective resistance mechanism for bacteria[11]. Gu have found that there are several large families of proteins comprise efflux pumps that play important roles, such as the Resistance-Nodulation-Division (RND family), the Major Facilitator Superfamily (MFS family), the ATP-binding cassette family (ABC family), and the small

multidrug-resistant family (SMR family), etc.[12] The hazards of efflux pumps include contributing to MDR, decreasing the effectiveness of antibiotic therapy, and increasing the difficulty of clinical prevention and control.

2.4. Effect of protein family-mediated cellular exocytosis on drug resistance in bacterial strainsprotein

2.4.1. The MFS protein family

The MFS protein family is widely found in bacteria, and the protein consists of 400 to 600 amino acids, which is mainly responsible for transmembrane transport in bacteria. In the mechanism of tetracycline resistance in Salmonella, the protein as efflux pump encoded by the tet gene belonging to the MFS family plays a major role. The efflux pump encoded by the tetA gene utilizes the concentration difference between the inside and outside of the cell membrane to drive the tetracycline out of the cell, and it can effectively reduce the intracellular concentration of tetracycline, thus alleviating the effect of tetracycline on Salmonella [13].

2.4.2. The RND protein family

The cellular efflux caused by RND protein family form of the mainly relies on the efflux pump formed by its protein family, which RND family is mainly composed of three proteins, outer membrane protein, the membrane fusion protein, and secondary active exocytosis pump. Taking the AcrAB-TolC efflux pump of RND family as an example, AcrAB-TolC efflux pump is widely found in Gram-negative bacteria, which can assist in transporting antibiotics (aminoglycoside antibiotics, tetracycline antibiotics, chloramphenicol antibiotics, etc.) to the outside of the cell so as to reduce the level of intracellular antibiotics, and AcrAB-TolC efflux pump consists of three proteins which is AcrA, AcrB, and TolC. AcrA is served as inner membrane protein. The AcrB is served as transmembrane protein, membrane fusion protein, and membrane fusion protein. TolC is served as outer membrane channel protein[12]. The protein of TolC is an important constituent protein in the pump, which not only helps Salmonella to increase the chance of survival within the environment to help invade the host cell[14]. In addition, proteins of TolC are involved in making up seven types of Salmonella efflux pumps, and Horiyama found that the lack of these proteins disables seven types of Salmonella efflux pumps and enhances sensitivity to antibiotics[15], if strains lacking the tolC gene were 16 to 32 times less resistant to antibiotics than wild strains 16 to 32 times[12]. It suggests that the protein encoded by this gene is more linked to Salmonella resistance and directly helps Salmonella to develop resistance. Gene transfer leads to spread of Salmonella drug resistance in colonies.

2.5. Salmonella drug resistance mediated by Mobile genetic elements

Mobile genetic elements (MGEs) are genetic material that can be moved within a bacterial genome or between different bacteria, including plasmids, transposons, and so on. Mobile elements play a key role in bacterial genetic variation and the spread of drug resistance. Bacteria can pass drug resistance genes to other bacteria through splicing, transformation, and transduction.

2.5.1. Transposon

A transposon is an element located on DNA that can replicate and transfer autonomously and can carry genes that can move from one location to another in the genome. Recognition sites for transposases and recombinases are present on transposons. Frech found that transposons carrying tetracycline resistance genes have been identified in Salmonella, transposon Tn1721 can carry the tetracycline resistance gene, tetA, which has been successfully extracted from animals in Germany, and in a subsequent study The gene has also been extracted in different regions worldwide[16].

2.5.2. Plasmids

Plasmids, widely found in bacteria, are circular DNA molecules outside of the bacterial chromosome that are capable of replicating autonomously, with several copies present. Since plasmids can carry resistance genes for one or more antibiotics, and can move and pass them from one bacterial

individual to another, resistance can be transferred from one individual to another. For example, R plasmids can carry resistance genes to aminoglycosides, β-lactams, chloramphenicol, and tetracyclines; Inc-type plasmids can carry multiple resistance genes (for example, bla, qnr, tet, sul). The plasmids can carry and transmit multiple resistance genes, the phenomenon of MDR in Salmonella has become increasingly serious. Zhou found that places, in food, show that there is a rate of 48.49% which the portion of strains were resistant to three or more antibiotics, and among them, those that carried typeI complex integrators were extremely resistant, and they could be resistant to the five major classes of antibiotics simultaneously[17]. Oluwadare found that traS genes can hinder other exogenous plasmid splicing through the Entry Exclusive (EE) mechanism, reducing bacterial acquisition of resistance genes, which may become a future concept of governance of slowing down the antibiotic resistance in Salmonella [18].

2.6. Biofilm-mediated Salmonella resistance

Biofilms are extracellular polymeric substances (EPS) secreted by Salmonella accompanying its growth process, mainly including extracellular proteins, structural proteins, cellular debris, and nucleic acids. The EPS can promote the formation of multicellular aggregates and biofilm formation by Salmonella [19]. Biofilms are associated with the ability of bacteria to survive and produce resistance to antibiotics. It is believed that there are three main reasons why biofilms help bacteria to develop resistance: due to the uneven texture of biofilms, the oxygen and pH step concentration produced, a physical barrier is formed for Salmonella, which can impede the penetration of antibiotics[20].

In recently studies found that some biofilms contain holdfast cells, and when they are in the environment of antibiotics[21], the antibiotics can instead be favorable to the biofilm formation, further hindering the entry of antibiotics into the bacteria[20]. This phenomenon has been demonstrated in a related study of A strain of Salmonella typhi from Slovakia[22]. Quorum sensing (QS) is a method by which bacteria utilize inducers to communicate among themselves. Salmonella expels antibiotics from its cells through an efflux pump and triggers group sensing, where the antibiotic acts as a signaling molecule that regulates the biofilm expression, efflux pump, and other antibiotic-resistant functions in other bacteria, ultimately increasing the resistance in the Salmonella population[23].

2.6.1. Constituents in biofilms have different roles in drug resistance

Table 1. Major Components in Biofilms

Ingredient	Corresponds	Impact on drug resistance
Exopolysaccharides (EPS)	A major component of biofilm formation, wrapped around bacteria	Forms a physical barrier that prevents antibiotics from entering the bacteria, causing the bacteria to enter a resting state and reducing their sensitivity to antibiotics
Extracellular Proteins	Involved in adhesion, signaling	Activation of efflux pumps, discharge of antibiotics,activation of group sensing
Outer Membrane Vesicles (OMVs)	Formation of small vesicles	Signaling for antibiotic degradation
Lipids	Formation of membrane structures	Involving in constructing EPS to form a barrier and form vesicles[24]
Extracellular DNA (eDNA)	Promoting gene exchange	Promoting the spread of drug resistance genes

3. Rapid Method FOR THE Detection OF Foodborne Salmonella SP.

In recent years, Salmonella contamination incidents have been frequent, especially in meat, aquatic products, egg products and dairy products with high detection rates, leading to a significant increase in the risk of foodborne disease outbreaks. More than millions of cases of foodborne illnesses due to Salmonella infections are reported globally each year, and some of these strains exhibit MDR, further increasing the difficulty of prevention and control. Traditional culture methods (for example, ISO-6579 and GB-4789) are the gold standard for bacterial detection, but due to their long detection period (usually 2-5 days), are difficult to meet the rapid response needs of the food industry, clinical diagnosis, and public health regulation. In response to the food industry. It is demand that the efficient detection of pathogenic microorganisms with high sensitivity and specificity, rapid detection technologies (for example, molecular biology methods, immunological detection, nanotechnology, and optical sensing technology) have been rapidly developed. In recent years, nucleic acid detection is based on the identification of specific nucleic acid sequences of Salmonella, based on a highly efficient detection means, has the advantages of high sensitivity, high specificity, fast detection speed, has become one of the most commonly used rapid detection technology. Compared with the traditional culture method, the molecular biology method can complete the detection in a few hours, which greatly reduces the detection time.

3.1. Rapid PCR-based detection

Polymerase chain reaction (PCR) utilizes the principle of DNA double-stranded replication to rapidly amplify specific nucleic acid sequences in a specific reaction system, with the advantages of short amplification time and recoverable detection products. In recent years, the rapid detection methods based on PCR reaction include traditional PCR and its derivatives of three PCR methods. Traditional PCR utilizes Taq DNA polymerase to amplify the target DNA and detects the amplified product by agarose gel electrophoresis to identify the presence of Salmonella by band comparison, which has the advantages of specificity, sensitivity, and simplicity of operation, but it is unable to analyze it quantitatively, and only determines the positive or negative. There is a detection limit of 102 CFU/mL by Lu who detected Salmonella Pullorum[25].

Real-time fluorescent quantitative PCR (qPCR) monitors the amplification process in real time by fluorescent labeled primers and achieves accurate quantitative analysis by Ct value calculation, minus the electrophoresis step. Sun showed that the detection limit of qPCR for plasmid standard samples of Salmonella avian origin was up to 1.4 copies/μl with higher sensitivity[26]. Multiplex PCR improves the detection efficiency and reduces the experimental time by adding multiple primers to amplify multiple DNA sequences simultaneously in the same reaction system. Based on poisson distribution, droplet digital PCR (ddPCR) divides the PCR reaction system into a large number of microdroplets, and detects the amplification of each microdroplet by fluorescence signal to realize absolute quantitative detection. Compared with traditional PCR, ddPCR has higher accuracy and sensitivity, and can be combined with multiplex PCR to realize rapid and accurate detection of foodborne pathogens.

Loop-mediated isothermal amplification (LAMP) is a new type of constant temperature nucleic acid amplification technology. LAMP is a new type of thermostable nucleic acid amplification technique, which uses four primers to catalyze the synthesis of new strands of target genes at six sites under constant temperature using Bst DNA polymerase. LAMP has been widely used in food testing, and can be used to detect different target genes (for example, invA, siiA, etc.) efficiently and accurately. The minimum detection limit is 5 CFU/ml in milk[27].

3.2. CRISPR-Cas system-based detection of Salmonella sp.

The CRISPR-Cas system (Clustered regularly interspaced short palindromic repeats and CRISPR-associated protein) was originally discovered as an immune defense mechanism for bacteria and archaea, and has now become a gene editing tool. The CRISPR-Cas system uses Cas proteins to

specifically recognize and excise DNA sequences tagged with CRISPR sequences, which bacteria use to remove foreign DNA. The CRISPR-Cas system detection principle, on the other hand, uses Cas proteins (for example, Cpf1 or Csm/Cmr complexes) to bind to specific guide RNAs, which can be detected using the CRISPR-Cas9 system or the CRISPR-Cas12 system. CRISPR-Cas12/13 system for gene recognition and cleavage. Once the Cas protein recognizes a specific target DNA or RNA sequence, it cuts near the target site and generates a detectable signal through its "side-cutting" property. Li used the CRISPER/Cas12 system to detect Salmonella typhimurium and obtained a sensitivity test result of 1 copy/μl, which proved that the CRISPR-Cas system can detect Salmonella with high sensitivity[28].

3.3. Immunology in Salmonella detection

Enzyme-Linked Immunosorbent Assay (ELISA) utilizes the principle of specific binding of antigen-antibody and is commonly used in food safety testing to qualitatively detect samples through the signals (color, fluorescence, etc.) generated by the specific binding. ELISA is a highly sensitive analytical technique utilized for the detection and quantification of specific biomolecules, such as proteins, through antigen-antibody interactions. It is simple and sensitive, and has a good detection rate. Niu used indirect ELISA to detect Salmonella pellagra (IPAJ) in chickens and obtained better specificity and sensitivity[29]. However, ELISA suffers from significant disadvantages such as longer consumption time and the need to prepare antibodies in advance.

Table 2. Comparison of Several Testing Methods

Detection Methods	Vantage	Drawbacks
Traditional PCR	Mature and widely used, equipment is widely available	Time-consuming, unable to quantify, complex analytical steps
Multiplex PCR	High efficiency, multiple detections at once	Complex reaction environment, interferences need to be considered
Microtitre Digital PCR (ddPCR)	Absolutely quantify	More costly and time-consuming
Loop-mediated isothermal amplification (LAMP)	Run at constant temperature with low equipment requirements	Poor specificity, difficult to quantify
CRISPER-Cas system	Ultra-high sensitivity, good specificity	Immature method
Enzyme linked immunosorbent assay (ELISA)	Simple operation, able to quantify, wide range of applications	Long detection time and low sensitivity

4. Summary

In recent years, the drug resistance problem of Salmonella has become increasingly serious, and its resistance mechanism is complex and variable, mainly involving gene mutation, cellular exocytosis, mobile elements and biofilm. The detection rate of MDR is increasing due to the misuse of antibiotics and the transfer of genes between bacteria. This phenomenon poses a great challenge to food safety and public health. At the same time, traditional detection methods can no longer meet the demand for testing. Rapid methods for Salmonella detection (for example, PCR, LAMP, CRISPER-Cas) are particularly important and will contribute to the safety and security of the food industry.

In the future, research should be devoted to exploring the regulatory routes of drug-resistant genes, studying the key mechanisms of drug-resistance transmission, and developing more scientific and reasonable strategies for the spread of drug-resistance on this basis. At the same time, a more comprehensive gene database of drug resistance genes should be established to provide support for strain traceability analysis and prevention and control. On the other hand, rapid tests should be developed in the direction of portability, low cost, and high throughput, in order to facilitate the adaptation of testing needs with more flexible scenarios and greater demands. Eventually, the upstream gene library establishment and the study of resistance mechanism together with the downstream detection means will realize the control of the current situation of Salmonella with high drug resistance rate as well as multi-drug resistance.

References

[1] E. Y. Klein et al., "Global trends in antibiotic consumption during 2016–2023 and future projections through 2030," Proceedings of the National Academy of Sciences, vol. 121, no. 49, p. e2411919121, 2024.

[2] E. Y. Klein et al., "Global increase and geographic convergence in antibiotic consumption between 2000 and 2015," Proceedings of the National Academy of Sciences, vol. 115, no. 15, pp. E3463-E3470, 2018.

[3] K. Landstedt et al., "Antibiotic prescriptions for inpatients having non-bacterial diagnosis at medicine departments of two private sector hospitals in Madhya Pradesh, India: a cross-sectional study," BMJ Open, vol. 7, no. 4, p. e012974, Apr 8 2017. (in English)

[4] Q. Dong et al., "Cross-species transmission risk of livestock-associated MRSA: A systematic review and Bayesian meta-analysis of global data," Preventive Veterinary Medicine, vol. 194, Sep 2021, Art. no. 105429. (in English)

[5] A. Chlebicz et al., "Campylobacteriosis, Salmonellosis, Yersiniosis, and Listeriosis as Zoonotic Foodborne Diseases: A Review," Int J Environ Res Public Health, vol. 15, no. 5, Apr 26 2018. (in English)

[6] C. S. Marchello et al., "A Systematic Review on Antimicrobial Resistance among Salmonella Typhi Worldwide," Am J Trop Med Hyg, vol. 103, no. 6, pp. 2518-2527, Dec 2020. (in English)

[7] H. Ming-Yang et al., "Analysis of drug resistance characteristics of food-borne Salmonella in Wuhan area," Journal of Food Safety and Quality, vol. 12, no. 01, pp. 78-85, 2021. (in English)

[8] H. Talukder et al., "Prevalence and Antimicrobial Resistance Profile of Salmonella Isolated from Human, Animal and Environment Samples in South Asia: A 10-Year Meta-analysis," J Epidemiol Glob Health, vol. 13, no. 4, pp. 637-652, Dec 2023. (in English)

[9] Z. r. fei, "Analysis of the Contamination Status andDrugResistance of Salmonella in food in Jilin Provincefrom2021 to 2022," Jilin University, 2024.

[10] H. Sheng et al., "Genes and Proteomes Associated With Increased Mutation Frequency and Multidrug Resistance of Naturally Occurring Mismatch Repair-Deficient Salmonella Hypermutators," Frontiers in Microbiology, Original Research vol. 11, 2020-May-08 2020. (in English)

[11] M. Chitsaz et al., "The role played by drug efflux pumps in bacterial multidrug resistance," Essays Biochem, vol. 61, no. 1, pp. 127-139, Feb 28 2017. (in English)

[12] G. Rongzhao et al., "Structural insights into the AcrAB-TolC efflux pump of Gram-negative bacteria promote the development of pump inhibitors " Microbiology China vol. 49, no. 05, pp. 1863-1873, 2022.

[13] Y. Lugo-Melchor et al., "Characterization of tetracycline resistance in Salmonella enterica strains recovered from irrigation water in the Culiacan Valley, Mexico," Microb Drug Resist, vol. 16, no. 3, pp. 185-90, Sep 2010. (in English)

[14] S. T. A. Dantas et al., "Environmental persistence and virulence of Salmonella spp. Isolated from a poultry slaughterhouse," Food Res Int, vol. 129, p. 108835, Mar 2020. (in English)

[15] T. Horiyama et al., "TolC dependency of multidrug efflux systems in Salmonella enterica serovar Typhimurium," J Antimicrob Chemother, vol. 65, no. 7, pp. 1372-6, Jul 2010. (in English)

[16] G. Frech et al., "Plasmid-encoded tetracycline resistance in Salmonella enterica subsp. enterica serovars choleraesuis and typhimurium: identification of complete and truncated Tn1721 elements," FEMS Microbiol Lett, vol. 176, no. 1, pp. 97-103, Jul 1 1999. (in English)

[17] Z. Yulei et al., "Detection of Multiple Drug Resistance and Complex Class I Integrons in Salmonella in Fresh Food," Modern Food Science and Technology, vol. 38, no. 01, pp. 73-80+288, 2022.

[18] M. Oluwadare et al., "The Role of the Salmonella spvB IncF Plasmid and Its Resident Entry Exclusion Gene traS on Plasmid Exclusion," Front Microbiol, vol. 11, p. 949, 2020. (in English)

[19] H. Ying et al., "Research progress in the mechanism and influencing factors of CsgD regulating the biofilm formation of Salmonella," Acta Microbiologica Sinica pp. 1-19.

[20] A. Aleksandrowicz et al., "Better together-Salmonella biofilm-associated antibiotic resistance," Gut Microbes, vol. 15, no. 1, p. 2229937, Jan-Dec 2023. (in English)

[21] C. A. Fux et al., "Survival strategies of infectious biofilms," Trends Microbiol, vol. 13, no. 1, pp. 34-40, Jan 2005. (in English)

[22] J. Majtán et al., "In vitro effect of subinhibitory concentrations of antibiotics on biofilm formation by clinical strains of Salmonella enterica serovar Typhimurium isolated in Slovakia," J Appl Microbiol, vol. 104, no. 5, pp. 1294-301, May 2008. (in English)

[23] J. Choi et al., "Implication of quorum sensing in Salmonella enterica serovar typhimurium virulence: the luxS gene is necessary for expression of genes in pathogenicity island 1," Infect Immun, vol. 75, no. 10, pp. 4885-90, Oct 2007. (in English)

[24] L. Yan et al., "Uncovering lipopolysaccharide regulation in bacteria via the critical lipid binding tunnel of YciS/YciM," Iscience, vol. 25, no. 9, Sep 2022, Art. no. 104988.

[25] L. Yao et al., "Establishment of a specific PCR method for detection of Salmonella Pullorum," Chinese Journal of Preventive Veterinary Medicine, vol. 43, no. 11, pp. 1178-1183, 2021.

[26] SUNShaodi et al., " Construction and Application of Fluorescent Quantitative PCR Method for Avian Salmonella," Hunan Journal of Animal Science & Veterinary Medicine, no. 01, pp. 41-45, 2024.

[27] B. H. Park et al., "An integrated rotary microfluidic system with DNA extraction, loop-mediated isothermal amplification, and lateral flow strip based detection for point-of-care pathogen diagnostics," Biosens Bioelectron, vol. 91, pp. 334-340, May 15 2017. (in English)

[28] L. Dan et al., "Establishment and application of CRISPR/Cas12a assay for the detection of Salmonella typhimurium," Journal of Food Safety and Quality, vol. 15, no. 12, pp. 143-150, 2024.

[29] N. Xiaojie et al., "Expression and Purification of IPAJ Protein of Salmonella Pullorum, Preparation oof Polyclonal Antibody and Establishing of ELISA Method," China Animal Husbandry & Veterinay Medicine, vol. 50, no. 03, pp. 1218-1228, 2023.