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Commentary

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Salmonella spp biochemical and molecular mechanisms for antibiotic resistance

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Description

Salmonella is a broad range of Gram-negative bacteria that is the leading cause of disease globally. *Salmonella* is one of the fourth most common causes of diarrheal illness worldwide, according to the WHO. *Salmonella* spp. is one of the microorganisms that might use antibiotic resistance to avoid the toxicity of antimicrobials, which is an issue for global health. Finding and releasing novel antibiotics is made more difficult by the evolution of antibiotic resistance to contemporary drugs. Antibiotic resistance is caused by a complicated molecular mechanism that modifies the structural and functional characteristics of bacterial cells. *Salmonella* serotype Typhi and drug-resistant non-typhoidal *Salmonella* have recently been labelled as "Serious Threats" because to their antibiotic resistance.

One of the pathogens associated with food that can cause diarrhoea anywhere in the world is *salmonella*. It is an Enterobacteriaceae family member and a flagellated, facultative anaerobic Gram-negative bacterium. *Salmonella enterica* and *Salmonella* bongori are its two main species. Based on the antigenic properties, *Salmonella* species are divided into several serotypes. They are categorised into about 2600 different serovars based on antigenic characteristics. Different *S. enterica* serovars can also result in typhoidal and non-typhoidal problems. *S. enterica* is a significant global burden. Its typhoidal serovars are well adapted to humans, including *S. enterica* serovar Typhi and *S. enterica* serovar Paratyphi A, B, and C. They are the enteric fever's etiological agents. According to the Centers for Disease Control and Prevention (CDC), there are between 11 and 21 million typhoid fever complications worldwide each year, leading to 200,000 fatalities. Enteric fever is brought on by typhoidal strains that are common in developing countries and spreads as a result of a lack of clean water, poor sanitation, and the fecal-oral pathway for pathogen transmission. On the other hand, *Salmonella* enteritidis and Typhimurium, two non-typhoidal serovars of *S. enterica*, are extremely common and cause salmonellosis all over the world. These serovars can spread through contact with people and animals, including cats, dogs, and rodents, as well as through food derived from animals. Nearly 77,500 people died as a result of non-typhoidal illnesses in 2017, which were projected to have been responsible for close to 535,000 cases.

Globally, gastroenteritis and systemic illness are primarily caused by *Salmonella*. The most prevalent *Salmonella* subspecies is *S. enterica* which causes 99% of *Salmonella* infections in warm-blooded creatures. S. bongori, on the other hand, primarily affects cold-blooded species and only rarely infects humans. Although salmonellosis is typically not serious, it can sometimes be. The severity of the disease is typically determined by the *Salmonella* serotype. It becomes more difficult to treat and manage an infection when drugs are used improperly. Human typhoidal disease and its non-typhoidal cousin are both classified as salmonellosis. A widespread health issue that mostly affects tropical and subtropical regions of poor nations is enteric fever. The growth of other organisms can be inhibited by antibiotics, which are low molecular weight microbial chemicals. These are produced either chemically or by naturally existing organisms. Antibiotics created chemically are referred to as synthetic antibiotics. In this covert battle against bacterial infec-

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tious diseases, antibiotics proved to be a society-benefiting invention. The use of antibiotic compounds, however, resulted in the emergence of antibiotic resistance just a few years after they were discovered. Sometimes the interaction of bacterial cells with the antibiotic leads to antibiotic resistance. This environmental antibiotic molecule permits bacteria to endure at particular concentrations and destroys the cells if their concentration goes above a predetermined limit. But frequently, the genes that cause antibiotic resistance already exist intrinsically, such efflux pump genes. Within a few years of the development of new drugs, antibiotic-resistant bacteria typically start to appear. *Salmonella* Multi-Drug Resistance (MDR) has been a serious public health problem, increasing the likelihood that antibiotics would not successfully cure infections. Third-generation antibiotics like cephalosporin and azithromycin were used to treat extremely drug-resistant enterica serovar Typhi when fluoroquinolone resistance increased and treatment failed.

These modifications either involve mutational changes or changes in the profile of genes involved in plasmid-mediated antibiotic resistance. The discovery of Anti-Microbial Resistance (AMR) variations from the available genetic data has thankfully been sped up by the creation of various online databases, such as Comprehensive Antibiotic Research Database (CARD). The most reliable platform for screening such variants in various bacterial species is made possible by the current information on antibiotic targets and their resistance genes, which is well-cited with the appropriate information. In order to create new antibiotic treatments, molecular scientists require an in-depth understanding of the molecular mechanisms that cause resistance. Prior to the administration of fresh antibiotics, the pre-existing resistance mechanisms of the target pathogen must be understood. Future efforts to prevent antibiotic resistance may involve the development of alternative medicines such as tailored probiotics, nanobiotics, stem cell-derived antimicrobial peptide therapeutics, and CRISPR-Cas delivery by temperate phages. The use of antibiotics is reduced due to engineered probiotics' effective management of *Salmonella* infection. To test for their efficacy and safety consequences, more research is needed on this issue. *Salmonella* spp Multi Drug Resistance (MDR) to different antibiotics complicates the management of *Salmonella* infection. Several contemporary antibiotics have molecular and metabolic mechanisms of resistance that are now understood. The ability of the *Salmonella* species to defend itself against potentially harmful antimicrobials, however, presents a challenge to the researchers to use a much more creative and long-lasting approach to deal with *Salmonella* infection.