Some Multidrug Resistant Pathogens Isolated From Food of Animal origin
Reham, M. Abdel- Wahhab*; Rania, A. Abdel Kader*; Wafaa, F. Ahmed*; Hend, A. Mahmoud** and Soad, H. El-Sheikh*

*Food Hygiene Unit, Zagazig Branch, Animal Health Research Institute, (AHRI), Agriculture Research Center (ARC), Egypt.
**Chemistry Unit, Zagazig Branch, Animal Health Research Institute, (AHRI), Agriculture Research Center (ARC), Egypt.

Corresponding author:
Reham, Mohammed Abdel-Wahhab
dr_reham.mohammed@yahoo.com

Abstract
The food of animal origin such as Red meat, poultry meat, milk and their products have a great importance in human nutrition due to their contents of essential amino acids, But the danger lies in their content of pathogenic microorganisms especially if these organisms are multidrug resistant, the problem which arises from the overuse of antimicrobial drugs that happen during animal growth, either as a prophylactic or therapeutic treatment. It has been recorded that at least twenty five percent of the foodborne isolates expose drug resistance to one or more groups of antimicrobials. An analysis conducted on the antibiotic resistance of pathogens obtained from different food products reveals that the average frequency of their existence in food is ≥11%. Meanwhile, multidrug resistance pattern (MDR) has been noticed among ≥36% of pathogens, the most reported resistance is directed to β-lactam antibiotics. Some food poisoning microbes were discussed, with referring to the most important mechanisms of development of drug resistance

Introduction
Abundant pathogens may earn access in to food of animal origin from various sources and induce varieties of food borne diseases either via the microbe itself or via its toxins. Relied on the type of disease induced, these illnesses are classified as food infection, food intoxication and food toxi-infection. It's a major issue, but the most prominent is when the causative organism is resistant to antibiotics, shockingly on the off chance that it is multidrug resistant one. Multidrug resistance refers to bacteria's ability to resist three or more classes of antibiotics that target various microorganisms **Nikaido, (2009)**. The issue in the meat and dairy industry; is the broad administration of antimicrobial agents to evade, control, or treat contamination in animals and to render as growth enhancers. The uncontrolled administration of these drugs to cattle may develop resistance versus bacterial pathogens **Sharma et al., (2011).** The exchange of genes responsible for antimicrobial resistance from one bacterium to another is the result of this behavior. Resistant bacteria eventually end up in the food chain **Nisha, (2008) and Sharma et al., (2011)**. Resistant foodborne microbes have gotten to be a food safety defiance that requests a one-health concern based arrangement. Making it worse; several previously treatable bacterial contaminations have, over time, developed resistance to certain antimicrobial agents **Nyenje and Ndip, (2013).** Each day, the number of resistant microbes to all known antibiotics is in boost, leading to the expectation that by 2050, "humanity may re-

turn to an era without antibiotics" **Durão *et al.*, (2018).** The point of this article is to crystallize the problem of antibiotic-resistant organisms in foods of animal origin

Foodborne Pathogen Transmission

Meat from animals or birds can infect humans with foodborne illnesses in a number of ways. Numerous domestic and wild animals, particularly those raised for human consumption, have had their digestive tracts colonized by foodborne pathogens such as Salmonella, Campylobacter, and pathogenic *E. coli* **Zhao *et al.* (2001).** These bacteria have the ability to contaminate food at many different phases of the food supply chain, such as handling or preparation, processing, distribution, retail marketing, and production. Eating foods derived from animals increases the chance of contracting foodborne illnesses significantly, according to a number of epidemiological studies **Petersen and James (1998).**

It is believed that poultry is a significant asymptomatic carrier of several infectious illnesses. According to **Mir *et al.* (2015),** one of the main reasons for the cross-contamination of the carcass with Salmonella and Campylobacter is the removal of the gastrointestinal tract during slaughter. However, the predominant route of foodborne disease transmission from poultry to humans is through the ingestion of contaminated meat. Meat processing, storage, or slaughtering is the possible situations during which contamination happens **Hafez, (1999).** According to an African study, selling carcasses without cold storage or protection from dust and flies raised the risk of microbial contamination of meat, especially from foodborne pathogens like Salmonella and Campylobacter **Kagambèga *et al.*,(2018).** Poor hygienic practices of poultry meat handlers also contributed to this risk.   Furthermore, elements such as unsuitable storage conditions; such as storing meat for an extended length of time also encourage microbial growth in meat and render it unfit for human consumption **Taulo *et al.*, (2008).**

The dairy cow mammary gland can transmit pathogens directly, or indirectly, via body secretions that can fall, inflate, or splash into milk. Handlers play a crucial part in addition to coughing, sneezing, and talking when milking or handling milk on a farm, contaminated hands can spread illnesses like typhoid, infantile diarrhea, diphtheria, scarlet fever, and septic sore throat. Moreover, the environment pathogens may also be introduced into milk products by the dairy farm environment at various phases of production and processing. Contaminated water, feed, and milk-handling equipment, together with other unsanitary conditions at the farm and factory, may have a substantial impact on pathogens and microorganisms that cause spoiling in milk **Almashhadany *et al.*, (2022).**

Some resistant pathogens isolated from food of animal origin

1- *Staphylococcus aureus*:

In humans and other animal species, *S. aureus* is an opportunistic pathogen. The pathogen is the third leading cause of food-related illness worldwide and is primarily linked to food poisoning **Sasidharan *et al.*, (2011).** According to **Hennekinne *et al.*, (2012)** strains of coagulase-positive staphylococci, primarily *S. aureus,* are responsible for a range of infectious disorders; dermatitis, meningitis, osteomyelitis, pneumonia in humans as well as mastitis in cattle, and bumble foot illness in poultry. Since a few decades ago, *S. aureus* has been linked to 25% of all foodborne diseases in the USA. Due to ongoing antibiotic misuse; methicillin-resistant *S. aureus* strains have emerged realization as one of the most grave nosocomial bacteria that induce food poisoning. Despite the low prevalence of MRSA in food, the problem stems from the strains' multidrug resistance, which makes treating infections difficult **Sciezynska *et al.*, (2012).** Multiple antimicrobial resistance patterns have been shown to be regularly observed in *S. aureus* **Enright, (2003).** This could be because the overuse of antibiotics has resulted in the emergence of certain antibiotic resistances, making antibiotic therapy useless. In soil, water, plants, and animals, resistant microorganisms can be found. Both humans and animals come into contact with the resistant bacteria that exist in their surroundings. According to estimates, humans consume almost the same amount of antimicrobial drugs **Farzana *et al.*, (2004)**

Because resistant bacterial strains are constantly circulating in the environment and can contaminate food and water, antimicrobial resistance is a serious public health concern in many countries **Normanno *et al.,* (2007).** In the past, *S. aureus* strains were almost always sensitive to semi-synthetic penicillinase-resistant β-lactam antibiotics, such as methicillin and oxacillin, which are the most widely utilized class of antibiotics for skin infections. The strains were referred to as "methicillin-resistant *Staphylococcus aureus*" (MRSA) which suggested that they were resistant to all β-lactam antibiotics, such as penicillins and cephalosporins.

2- *Salmonella* spp.

There are 2610 distinct serotypes of Salmonella enterica subspecies enterica; the most well-known serotypes include *Typhi, Paratyphi, Enteriditis, Typhimurium, and Choleraesuis* **SuandChiu, (2007).** According to **Bronze and Greenfield (2005),** the three surface antigens that define the serotypes are the polysaccharide "Vi" antigen (present in the Typhi and Paratyphi serotypes), the oligosaccharide "O" antigen, and the flagellar "H" antigen. Salmonellosis is usually linked with consuming food products contaminated with Salmonella species, especially eggs, poultry meat products.

Contact with diseased pets or inadequate hand washing are two ways that contamination might happen **Munck *et al.,* (2020).** Salmonella spreads primarily through food handlers of "meat processing" and "ready-to-eat" foods **Ehuwa *et al.,* (2021).** The key origins of the disease's transmission are thought to be the sale of contaminated food items and goods made with inferior quality **FAO/WHO, (2004); Bettridge *et al.,* (2014).**Concern over antimicrobial tolerance in relation to human and animal salmonellosis is developing **Suetal., (2004)**. As reported, Salmonella strains resistant to antibiotics are prevalent in most regions of the world and have boosted obviously in the last decade **WHO, (2018).**

The frequency of animal-to-human transmission is rising quickly. According to **Shrestha *et al.* (2017),** the problem of antimicrobial drug resistance is particularly severe in underdeveloped nations. Salmonella strains that are obtained from food, particularly poultry products

Ehuwa *et al.,* (2021); **Gargano *et al.,*(2021); Raji *et al.,* (2021),** are the most common source of multidrug resistance. One of the main worries is that these bacteria have the capacity to spread their resistance genes to bacterial pathogens that affect humans **Musawa *et al.,* (2021).** Notably, multidrug resistant *Salmonella* serovars obtained from chicken embryos in Henan province, China, gave an alarm for the immediate lowering in the usage of antimicrobial therapy in chicken hatcheries. Furthermore, different patterns found by pulsed-field gel electrophoresis among the Salmonella serovars suggest the existence of many sources of contamination **Xu *et al.,* (2021).**

The study conducted by **Samy *et al.* (2022)** investigated the prevalence of multiple drug resistance (MDR) Salmonella in Egyptian food originating from animals. The results indicated that the bacteria were resistant to 100% erythromycin, 57% ampicillin, 50% cefradine, and 50% amoxicillin in milk and milk products. Additionally, the study found that a high incidence of multiple antibiotic resistances was found in poultry sources, where the highest was 100% versus oxytetracycline, persuaded by amoxicillin 73.3% and ampicillin 66.6%. On the other side, in meat and meat products, the highest incidence of *Salmonella* resistance was against cefradine, 53.7%, 50% ampicillin, and 31.4% oxytetracycline and amoxicillin. Food safety agencies need to consider these significant percentages in order to implement the required actions.

3- *Escherichia coli* spp.

Escherichia coli are commensal bacteria that present among large variety of hosts. They commonly exist in the atmosphere and are informed to be an indicator of water and food fecal pollution. *E. coli* from other species in the ecosystem may evolve, keep, and transfer resistance genes because of its ubiquitous existence and its attitude as a commensal or pathogenic organism in human and animal.

E. coli-related foodborne infections are a significant global public health concern that is primarily spread by eating contaminated food. The existence of *E. coli* in poultry and beef meat has important public health consequences **Sousa, (2008)**.

E. coli isolated from food of animal origin rec-

orded high resistance to ampicillin, amoxycillin-clavulanic acid, trimethoprim/ sulphamethoxazole, tetracycline, and streptomycin **Ahmed and Shimamoto (2013); Ahmed and Shimamoto (2015); Moawad *et al.* (2017)**.

4- Bacillus cereus

B. cereus is Gram-positive, aerobic-to-facultative, spore-forming, motile rod-shaped that is broadly found in food and the environment. It generates the enzyme lecithinase, spores, and enterotoxins. According to **Hwang and park (2015)**, it is mostly found in soil, milk, grains, spices, and other dried foods. *B. cereus* is one of the common bacteria found in the environment and the cause of food poisoning **Rasko *et al.*, (2005)**. Additionally, it has been discovered that *B. cereus* is extensively distributed in human intestine, food, and soil **Bottone, (2010)**. In seventy seven outbreaks and 17.1% of cases involving bacterial toxins, *B. cereus* has been identified as the causal agent of food-borne outbreaks, according to the European Food Safety Authority's report **EFSA, (2006).**

According to **Osama *et al.*, (2020)** study, 100% of *B. cereus* isolated from milk and milk products found to be resistant to ampicillin, amoxicillin and colistin persuaded by 83.01% resistant to ampicillin-sulbactum, 67.9% resistant to streptomycin, then resistant to spiramycin, lincomysin, tetracyclin, and erythromycin by 45.2, 35.8, 22.6, and 5.6% respectively. These data also harmonized with **Kim *et al.* (2011)** who found that all studied *B. cereus* strains were resistant to β- lactam group comprising ampicillin, amoxicillin and penicillin while were susceptible to vancomycin, tetracycline, gentamycin, and ciprofloxacin.

In addition, according to **Abd-El Tawab *et al.* (2020)**, *B. cereus* isolated from meat and meat products exposed a high level of resistance to penicillin-G (92.2%), methicillin (90.2%), followed by ampicillin, oxytetracycline, sulfatrimethoprim, and cefotaxime as 88.2, 82.3, 80.4, and 54.9% respectively. In the meantime, the strains exhibited high susceptibilities to gentamycin (82.3%), ciprofloxacin (74.5%), meropenem (72.5%), and florphenicol (62.8%), on the other manner, intermediate susceptibilities were shown versus streptomycin (62.8%), erythromycin (58.8%), and neomycin (56.9%).

5- Listeria monocytogenes

Listeria monocytogenes is a rod-shaped coccobacillus that is facultatively anaerobic, Gram-positive, and does not generate spores. Its normal dimensions are 0.5 to 2μm in length and 0.5μm in diameter **Acha and Szyfres, (2003)**. *L. monocytogenes* can proliferate at temperatures between 1 and 45°C and can thrive at a wide pH range (4.3 to 9.6) **Shamloo *et al.*, (2019)**. Globally, foodborne illness outbreaks and high hospitalization rates are linked to the foodborne bacterium *L. monocytogenes* **Osman *et al.*, (2020)**.

Various foods and dairy products contain *L. monocytogenes,* which is the cause of listeriosis in people and animals **Skowron *et al.*, (2019)**. The bacteria have also been linked to recent outbreaks and isolated cases of listeriosis **Kim *et al.*, (2018)**. It is also thought to be a possible source of contamination for cold and marine food products **Vinothkumar *et al.*, (2013)** as well as unpasteurized dairy products. According to research by **Abdeen *et al.,* (2021)** the antibiogram profile of *L. monocytogenes* revealed a high sensitivity to amoxicillin-clavulanic acid (76.4%), cefotaxime (70.5%), intermediate sensitivity to erythromycin, amoxicillin (64.6%), then gentamicin and vancomycin (58.7%). On the other hand, there was significant resistance to trimethoprim-sulfamethoxazole (76.4%), azithromycin (41.2%), levofloxacin (41.2%), doxycycline (64.6%), chloramphenicol (70.5%), and oxytetracycline (76.4%). *L. monocytogenes* strains gathered from 4 distinct sources; fish fillet, minced meat, raw milk, and sausage had generally comparable antimicrobial characteristics, moreover, all of the isolated *L. monocytogenes* were multidrug-resistant **Abdeen *et al.,* (2021)**.

6- Brucella spp.

Brucella is a Gram negative coccobacillus belonged to the family *Brucellaceae*. The currently recognized species involve *B. abortus, B. melitensis, B. ovis, B. suis, B. ceti, B. canis, B. neotomae, B. microti, B. pinnipedialis, and B. inopinata*. Humans contract the disease primarily by direct contact with the discharges of infected animals, consumption of unpasteur-

ized milk or dairy products, and undercooked meat or meat products **Nejad** *et al*., **(2020**).

According to **Hayoun** *et al*. **(2020),** there are more ways that Brucella can infect humans, including cutaneous abrasions, conjunctival inoculations, and aerosol inhalation. Human brucellosis symptoms are quite diverse and non-specific. The illness can produce fever, but its symptoms are similar to those of other feverish illnesses, leading to incorrect diagnoses and inadequate treatment. Chronic brucellosis can result from Brucella infection in the genitourinary system, joints, parenchymatous organs, and bone. After therapy, many relapses were documented **Wang** *et al*., **(2020).**

Brucella has maintained, to some degree, its sensitivity to rifampicin, aminoglycosides (gentamicin), fluoroquinolones (levofloxacin and ciprofloxacin), new glycylcycline (tigecycline), and doxycycline, according to **Wareth** *et al*. **(2021)** Rifampicin remains the primary common treatment choice for human brucellosis, usually in conjunction with other drugs.

Otherwise, a different study conducted by **Khanetal**, **(2019),** 75.2%, 66.7%, and 4.8% of animal-origin *B. melitensis* strains tested positive were resistant to ciprofloxacin, rifampicin, and streptomycin, respectively. According to a prior investigation, 277 (64%) of the 355 *B. melitensis* isolates with human origin in Egypt were resistant to rifampicin **Abdel**-**Maksoud** *et al*., **(2012).**

Mechanisms of development of drug resistance

Anti-Microbial Resistance (AMR) takes place when bacteria, fungi, viruses, and parasites are presented for a long time to sub-therapeutic doses of drugs that modify the ecology of microorganism. In order to combat with the residues exhibit in their environment, microorganisms may gain genetic components that permit them to overcome these compounds and survive. In some cases, the use of poor quality drug, fraud products, faulty product, and sub-therapeutic dosage can boost the emergence of microbial resistance. Another relevant component for up-growth of AMR is the inconvenient disposal of waste output in the agricultural production, pharmaceutical and wastewater treatment plants as they can be disseminated via the environment **FAO, (2019**).

The effectiveness of antimicrobials is compromised by an increasing number of antibiotic resistant pathogens.

Resistance can be depicted in two ways:-

A). **Intrinsic resistance** whereby microorganisms naturally have not target sites for the antimicrobials so the antimicrobials cannot affect them.

B). **Acquired resistance** whereby a naturally susceptible microorganism earns mechanism to not be influenced by the antimicrobial. Mechanisms of acquired resistance comprise; the existence of an enzyme that inactivates the antimicrobial agent, post-transcriptional or post-translation modification of the antimicrobial agent's object, minimized uptake to the antimicrobial drug as well as the active efflux of the antimicrobial agent.
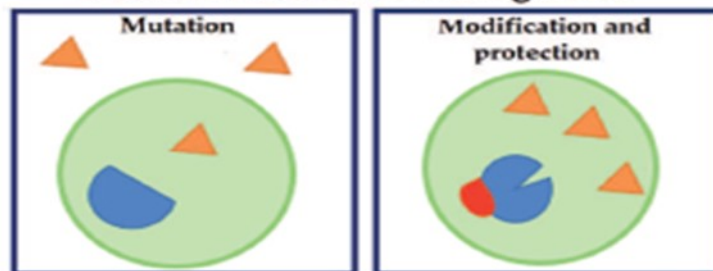
The intrinsic and acquired resistances are summarized by **Mancilla-Becerra** *et al***., (2019),** in figure 1.
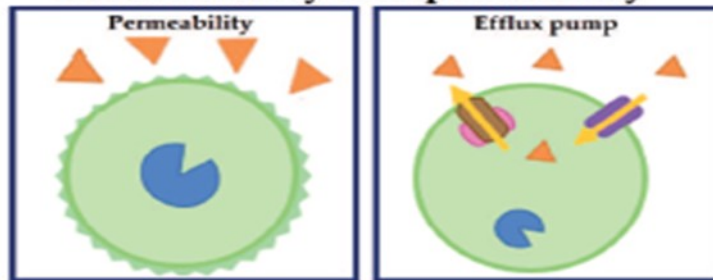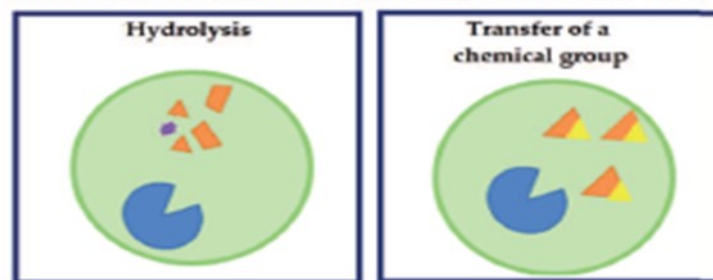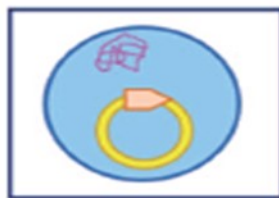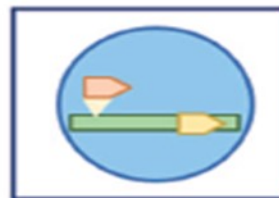
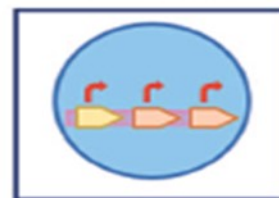**Figure (1).** Schematic representation of the mechanisms of MDR gaining in bacteria.

The mechanisms of action and resistance to antibiotic groups were tabulated in table (1) according to **Dowling *et al.,* (2017)**.

Table (1). Mechanism of action and resistance of prevalent used antimicrobial drugs.

Antimicrobial Family	Mechanism of Action	Resistance Mechanism
Beta-lactam antibiotics Cephalosporins Beta-lactamase inhibitors	Prohibits cell wall production. Binds enzymes (PBPs) that help form peptidoglycans. Inhibits/binds to beta-lactamase enzymes.	Beta-lactamase production primarily- bla genes. Changes cell wall protein enzymes to prevent binding to PBPs. Cephalosporinases Extended-spectrum beta lactamases (ESBLs). Class A-D.
Aminoglycosides	rRNA- binds to 30S subunit, causing genetic code misread. Inhibits protein production. Effect on cell membrane permeability	Phosphorylation, adenylation and acetylation of aminoglycoside stops them binding.
Fluoroquinolone	Interrupts DNA breakage-reunion step by binding DNA-gyrase or topoisomerase II and topoisomerase IV.	Target modification of DNA gyrase (gyrA and gyrB). Decreased permeability- outer membrane porins mutations (ompF). Efflux pumps.
Folate pathway inhibitors.	Purine synthesis for DNA. Interferes folic synthesis.	Chromosomal mutations but more commonly plasmid and integron-mediated resistance. Pathway blocked by resistant dihydrofolatereductase (dfr gene).
Tetracycline	rRNA- binds to 30S subunit and interferes with amino acid transfer. Prevents protein production.	Inducible efflux E. coli etc. (tetA, tetB, tetC). Binding site changes ($tetO$, $tetM$ genes).

Techniques for detection of antimicrobial resistance (AMR):

Although novel time-saving technologies have been introduced to gain antimicrobial resistance data, the classic, conventional technologies are still being used. These fundamentally comprise culture-based and molecular-based approaches. More recently, microscopy-relied and spectrometry-relied approaches have also been integrated in the tools for developing diagnostics.

1- Phenotypic Methods

A culture-based method relies on the phenotypic resistance detection by testing the bacterial growth in the existence of antibiotics, and can be categorized in two classes:

Manual tests were expressed as disk diffusion, minimum inhibitory concentration (MIC) determination and The E-test® or gradient test.

Disk diffusion method:
It is the process of an antibiotic diffusing over agar in a paper disc, with an inhibition zone forming around the disc. The results are categorized as resistant, intermediate, or susceptible using a qualitative method. It is a simple,

useful technique that works well for bacteria that grow quickly. However, there are several limitations, such as the usage of antibiotics that don't diffuse well in agar and challenging interpretation for anaerobic and fastidious microorganisms **Sejas *et al.*, (2003).**

Figure (2). Disk diffusion method

MIC detection
When testing in broth or agar, the goal of MIC determination is to measure the minimum antibiotic concentration that prevents detectable bacterial growth. Agar or broths with varying antibiotic concentrations are inoculated with solutions containing a specific number of bac-

teria. It is checked for microbial growth at the conclusion of the incubation time. It is an easy, low-cost procedure that doesn't need any specialist tools. However, because it uses a semi-quantitative approach, a precise MIC value might not be determined **Wiegand *et al.*, (2008)**.
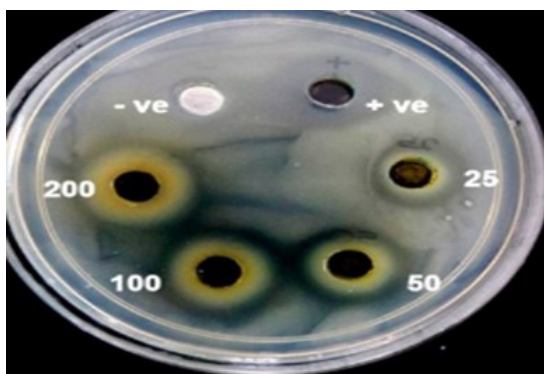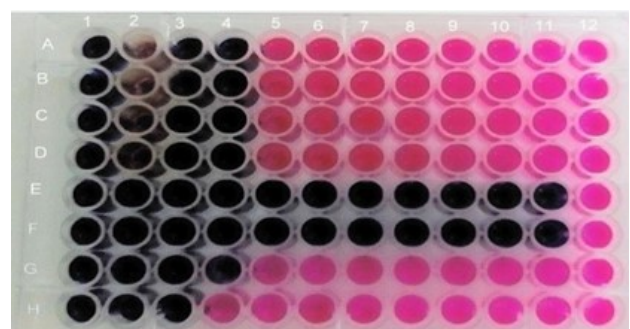

Figure (3). MIC on agar

Figure (4). MIC detection on broth by microtitre plate

E-test® or gradient test: This technique combines the last two approaches that were discussed. It calculates MIC but has disk diffusion-like processing. A rectangular device is set up on an agar plate with the interpretation scale and the antimicrobial concentration gradient on opposite sides. Despite the fact that the E-test® has the same execution time limitations as the two tests mentioned earlier, it offers a simpler method of directly quantifying the susceptibility of microorganisms, particularly those that are hard to culture (like *Mycobacterium bovis* and *Haemophilus influenzae*) or even anaerobes **Jorgensen, (1997)**. It also has an immobilized antimicrobial gradient indicated on the ruler
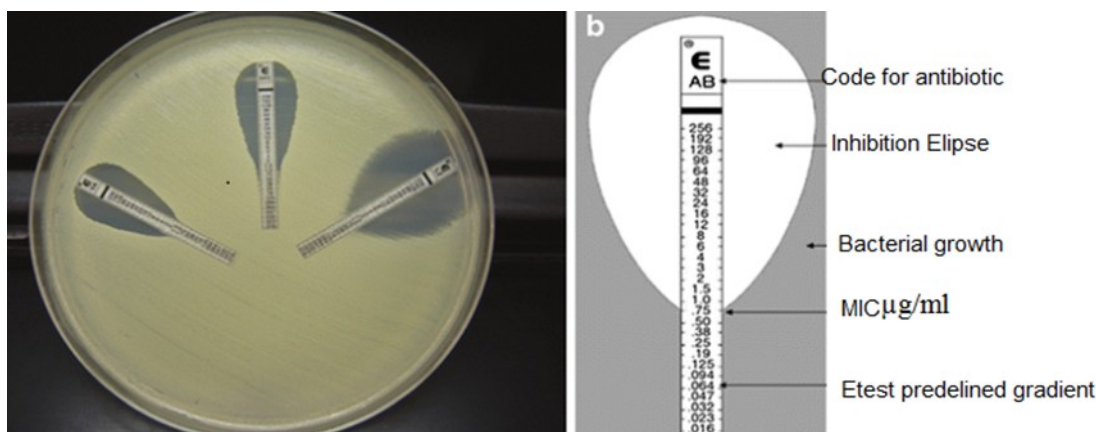

Figure (5). E-test® or gradient test for detection of antimicrobial resistance

Automated commercial platforms (VITEK® 2 COMPACT, Sensititre™ ARIS™ 2X, and Alfred 60AST system) use some of the aforementioned methods.

Automated MIC panel inoculation is the first step of an automated testing system. Computer-assisted incubation with reading, interpretation, and reporting features that eliminate the need for manual intervention follows **Evangelista and Karlowsky (2017)**.

2- Molecular Techniques

Molecular-based techniques have features over phenotypic assessments in detecting antibiotic resistance genes (ARGs), such as multiplex PCR, giving more precise identification and detection. These techniques display a viable alternative in certain taxonomic units where susceptibility breakpoints have not been realized. Non-purified polymicrobial samples can also be used in molecular-relied approaches, which can direct to faster response times to newly added resistance factors **Vasala *et al*., (2020)**.

However, due to their limited sensitivity and breadth, molecular-based approaches have limitations, including the inability to estimate MICs and the potential to overlook some ARGs. Furthermore, it can be expensive to create molecular-based assays that can identify the wide variety of AMR genes **Fluit *et al*., (2001)**. However, utilizing amplification and nucleic acid hybridization techniques to improve ARG expression and detection, molecular-based treatments are constantly being refined. In general, ARG may be detected quickly and sensitively using molecular-based methods **Sundsfjord *et al*., (2004)**.

3- Innovative Approaches

3-1. Mass Spectrometry-Based Methods

Antibiotic resistance can now be found via matrix-assisted laser desorption/ionization–time-of-flight mass spectrometry (MALDI-TOF MS), a quick and accurate technique for identifying microbes in clinical isolates and clinical samples. Three techniques are available for detecting AMR with MALDI-TOF MS: (1) measuring bacterial growth while exposed to an antibiotic, (2) evaluating antibiotic changes due to enzyme activity, and (3) identifying AMR by looking at pathogen peak patterns **Oviaño and Bou, (2018)**.

3-2. Bioinformatics Approach for Detection of AMR Determinants and Databases

Bioinformatics helps us assess the vast amount

of data gathered to choose specific approaches that are situation-specific and improve treatment, monitoring, and preventive strategies for infections caused by bacteria resistant to antibiotics **Seoane and Bou, (2021)**.

3-3. Microfluidics, Biosensors and Nanotechnology

Micro-Electro-Mechanical Systems (MEMS) biosensors were utilized by **Koydemir *et al*. (2011)** to effectively identify MRSA. In parallel, **Xue *et al*. (2018)** reported the development of a very sensitive electrochemical biosensor for identifying the *mec*A gene in MRSA strains.

Conclusion

In this review, we highlight the problem of antimicrobial resistance in food of animal origin With clarification of different mechanisms of antimicrobial resistance and the source of food borne resistant microbes, Referring to some examples of resistant bacteria in meat and milk products and the methods of detection of antimicrobial resistance, finally we would like to encourage some actions to Fight Antimicrobial Resistance by preventing the contaminations in food of animal origin by precise and continuous bacteriological examination. The aware use of antimicrobials, on all possible occasions, is the best way to mitigate the rise and dissemination of AMR among bacteria, particularly for drugs that are used in the remedy of both humans and animals. With greater alarming of the risks of indistinctive use of these antimicrobials, future issues in the treatment of pathogens can be controlled.

References

Abd El Tawab, A.A.; El Hofy, F.I.; Abou El Roos, N.A. and El- Morsy, D.A. (2020). Detection of virulence genes in *Bacillus cereus* isolated from meat products using PCR. J. World Poult. Res. 10(2S): 292-298, June 14, 2020.

Abdeen, E.E.; Mousa, W.S.; Harb, O.H.; Fath-Elbab, G.A.; Nooruzzaman, M.; Gaber, A.; Alsanie, W..F. and Abdeen, A. (2021). Prevalence, Antibiogram and Genetic Characterization of *Listeria monocytogenes* from Food Products in Egypt, MDPI, Foods 2021, 10, 1381. https://doi. org/10. 3390/foods10061381

Abdel-Maksoud, M.; House; B.; Wasfy, M.; Abdel-Rahman, B.; Pimentel, G.; Roushdy, G. and Dueger, E. (2012). In vitro antibiotic susceptibility testing of Brucella isolates from Egypt between 1999 and 2007 and evidence of probable rifampin resistance. *Ann. Clin. Microbiol. Antimicrob.* 2012;11:24. doi: 10.1186/1476-0711-11-24.

Acha, P.N. and Szyfres, B. (2003). Listeriosis, p. 168-179. Pan American Health Organization, Zoonoses and Communicable Diseases Common to Man and Animals, 3rd ed., Pan American Health Organization., Washington D.C.

Ahmed, A.M. and Shimamoto T. (2015). Molecular analysis of multidrug resistance in Shiga toxin-producing *Escherichia coli* O157:H7 isolated from meat and dairy products. Int J Food Microbiol. 193:68–73.

Ahmed, A.M. and Shimamoto, T. (2013). Molecular characterization of multidrug-resistant avian pathogenic *Escherichia coli* isolated from septicemic broilers. Int J Med Microbiol.303:475–83

Almashhadany, D.A.; Mohammed, H.I.; Muslat, T.A.M.; Hassan, R.R.; Rashid, R.F. and Hassan, A.O. (2022). Milk-Borne Diseases, Health Risks of Food Additives - Recent Developments and Trends in Food Sector, DOI: 10.5772/intechopen.108796

Authority EFSA (2006). The Community Summary Report on Trends and Sources of Zoonoses, Zoonotic Agents, Antimicrobial resistance and Foodborne outbreaks in the European Union in 2006. EFSA J 2007;5. https://doi.org/10.2903/j.efsa.2007.130r

Bettridge, J.M.; Lynch, S.E.; Brena, M.C.; Melese, K.; Dessie, T.; Terfa, Z.G.; Desta, T.T.; Rushton, S.; Hanotte, O.; Kaiser, P. (2014). Infection-interactions in Ethiopian village chickens. Preventive Veterinary Medicine, 117(2): 358-366.

Bottone, E.J. (2010). *Bacillus cereus*, a Volatile Human Pathogen. Clin. Microbiol Rev 2010;23:382-98. https://doi.org/10.1128/CMR.00073-09

Bronze, M.S. and Greenfield, R.A. (Ed.). (2005). Biodefence Principles and Pathogens horizon bioscience.

Dowling, A.O.; Dwyer, J. and Adley, C.C. (2017). Antibiotics: Mode of action and mechanisms of resistance, Antimicrobial research: Novel bioknowledge and educational programs (A. Méndez-Vilas, Ed.),536-545.

Durão, P.; Balbontín, R. and Gordo, I. (2018). Evolutionary mechanisms shaping the maintenance of antibiotic resistance. Trends in Microbiol 2018; 26: 677-91.

Ehuwa, O.; Jaiswal, A.K.; and Jaiswal, S. (2021). Salmonella, food safety and food handling practices. Foods, 10(5): 907.

Enright, M.C. (2003). The evolution of resistant pathogen - the case of MRSA. Current Opinion in Pharmacol., 3: 474-479.

Evangelista, AT. And Karlowsky, J. (2017). Automated and Manual Systems for Antimicrobial Susceptibility Testing of Bacteria, CHAPTER 22Automated and Manual Systems for Antimicrobial Susceptibility Testing of Bacteria

FAO (2019). Food and Agriculture Organization of the United Nations. Antimicrobial resistence: What you need to know [Internet]. 2019. Available from: http://www.fao.org/fao-stories/ article/en/c/1056781/ [Accessed: June 4, 2019]

FAO (2018). Ethiopia: report on feed inventory and feed balance. FAO, Food and Agriculture Organization of the United Nations, Rome, Italy

Farzana, K.; Hussain Shah, S.N. and Jabeen, F. (2004). Antibiotic resistance pattern agent various isolates of *Staphylococcus aureus* from raw milk samples. Js. Res., 15: 145 -151.

Fluit, A.C.; Visser, M.R.; Schmitz, F.J. (2001). Molecular detection of antimicrobial resistance. Clin.Microbiol. Rev. 2001, 14, 836–871. [CrossRef]

Food and Agriculture Organization/World health organization (FAO/WHO) (2004). FAO/WHO regional conference on food safety for Asia and Pacific, in the national surveillance system for food-borne disease in China, FAO/WHO Seremban, Malaysia, pp. 24-27. Available at: https://www.fao.org/3/y5557e/y5557e.pdf

Gargano, V.; Gambino, D.;Migliore, S.; Vitale, M.; Sciortino, S.; Costa, A. and Vicari, D. (2021). Can human handling increase the presence of multidrug resistance (MDR) in Salmonella spp. isolated from food sources? Microorganisms, 9(10): 2018. DOI: https://www.doi.org/10.3390/microorganisms9102018

Hafez, H.M. (1999). Poultry meat and food safety: pre–and post-harvest approaches to reduce foodborne pathogens. World's Poultry Science Journal 55(3):269-80.

Hauge, S. (1955). Food poisoning caused by aerobic spore forming bacilli. J. Appl. Bacteriol. 18:591-595.

Hayoun M.A.; Muco E. and Shorman M. (2020). StatPearls Publishing LLC; Treasure Island (FL): 2020. Brucellosis.

Hennekinne, J.A.; De Buyser, M.L. and Dragacci, S. (2012). *Staphylococcus aureus*and its food poisoning toxins: characterization and outbreak investigation. FEMS Microbiol.Rev. 36: 815–836.

Hwang, J.Y. and Park J.H. (2015). Characteristics of enterotoxin distribution, hemolysis, lecithinase, and starch hydrolysis of *Bacillus cereus* isolated from infant formulas and ready-to-eat foods. J Dairy Sci 2015; 98:1652-60.

Jorgensen, J.H. (1997). Laboratory issues in the detection and reporting of antibacterial resistance. Infect. Dis. Clin. N. Am. 1997; 11:785–802.

Jorgensen J.H. (1997). Laboratory issues in the detection and reporting of antibacterial resistance. Infect. Dis. Clin. N. Am. 11:785–802. doi: 10.1016/S0891-5520(05)70390-1. [PubMed] [CrossRef] [Google Scholar]

Kagambèga, A.; Thiobodeau, A.; Trinetta, V.; Soro, D.K.; Sama, F.N.; Bako, E.; Bouda, C.S.;Fravalo, P and Barro, N. (2018). Salmonella spp. and Campylobacter spp. in poultry feces and carcasses in Ouagadougou, Burkina Faso. Food Science and Nutrition 66: 1601-1606.

Khan, A.U.; Shell, W.S.; Melzer, F.; Sayour, A.E.; Ramadan, E.S.; Elschner, M.C.; Moawad, A.A.; Roesler, U.; Neubauer, H. and El-Adawy H. (2019). Identification, genotyping and antimicrobial susceptibility testing of Brucella spp. isolated from livestock in Egypt. Microorganisms. 2019:7. doi:10.3390/

microorganisms7120603.

Kim, J.B.; Kim, J.M.; Cho, S.H.; Oh, H.S.; Choi, N.J. and Oh, D.H. (2011). Toxin genes profiles and toxin production ability of *Bacillus cereus* isolated from clinical and food samples J Food Sci . 2011 Jan-Feb; 76 (1):T25-9.

Kim, S.W.; Haendiges, J.; Keller, E.N.; Myers, R.; Kim, A.; Lombard, J.E.; Karns, J.S.; Van Kessel, J.A.S. and Haley, B.J. (2018). Genetic diversity and virulence profiles of *Listeria monocytogenes* recovered from bulk tank milk, milk filters, and milking equipment from dairies in the United States (2002 to 2014). *PLoS ONE* 2018, 9, 13 (5): e0197053. [Google Scholar] [CrossRef] [PubMed]

Koydemir, H.C.; Külah, H.; Özgen, C.; Alp, A.; Hasçelik, G. (2011). MEMS biosensors for detection of methicillin resistant *Staphylococcus aureus*. Biosens. Bioelectron. 2011, 29, 1–12. [CrossRef].

Mancilla-Becerra, L.M.; Teresa Lías-Macías, Cristina L. Ramírez-Jiménez and Jeannette Barba León (2019). Chapter: Multidrug-Resistant Bacterial Foodborne Pathogens, Impact on Human Health and Economy,1:16

Mir, I.A.; Kashyap, S.K. and Maherchandani, S. (2015). Isolation, serotype diversity and antibiogram of Salmonella enterica isolated from different species of poultry in India. Asian Pacific Journal of Tropical Biomedicine 57: 561-567.

Moawad, A.A.; Hotzel, H.; Awad , O.; Tomaso, H.; Neubauer, H.; Hafez, H.M. and El-Adawy, H. (2017). Occurrence of Salmonella enterica and *Escherichia coli* in raw chicken and beef meat in northern Egypt and dissemination of their antibiotic resistance markers, Moawad et al. Gut Pathog 9:57,1:13.

Munck, N.; Smith, J.; Bates, J.; Glass, K.;Hald, T. and Kirk, M.D. (2020). Source attribution of Salmonella in Macadamia nuts to animal and environmental reservoirs in Queensland, Australia. Foodborne Pathogens and Disease, 17(5): 357-364. DOI: https://www.doi.org/10.1089/fpd.2019.2706.

Musawa, A.I.; Bashiru, G.; Al-Rasheed, A.; Yakubu, Y.; Jibril, A.H.; Ballah, F.M.; Sidi, S.; Lawal, N.; Bala, J.A. and Odhah, M.N. (2021). Prevalence and antimicrobial susceptibility profiling of Salmonella isolated from poultry products sold in Sokoto metropolis, Nigeria. Journal of Animal Health and Production, 9(2): 148-155. DOI: https://www.doi.org/10.17582/journal.jahp/2021/9.2.148.155

Nejad, R.B.; Krecek, R.C.; Khalaf, O.H.; Hailat, N. and Arenas-Gamboa A.M. (2020). Brucellosis in the Middle East: current situation and a pathway forward. *PLoSNegl. Trop. Dis.* 2020; 14 doi: 10.1371/journal. pntd. 0008071.

Nikaido, H. (2009). Multidrug resistance in bacteria. Annual Review of Biochemistry, 78: 119-146. DOI: https://www. doi. org/10. 1146/annurev.biochem. 78.082907.145923

Nisha, A. (2008). Antibiotic residues-a global health hazard. Vet World 2008; 1: 375-77.

Normanno, T.G.; La Salandra, G.; Dambrosio, A.; Quaglia, N.C.; Corrente, M.; Parisi, A.; Santagada, G.; Firinu, A.; Crisetti, E. and Celano, G.V. (2007). Occurrence, characterization and antimicrobial resistance of enterotoxigenic *Staphylococcus aureus* isolated from meat and dairy products. International J. Food Microbiol.115: 290-296.

Nyenje, M.E. and Ndip, N. (2013). The challenges of foodborne pathogens and antimicrobial chemotherapy: A global perspective. AJMR; 7: 1158-72. DOI: 10.5897/AJMRx 12.014

Osama, R.; Ahmed, M.F.E.; Abdulmawjood, A. and AlAshmawy, M. (2020). Prevalence and Antimicrobial Resistance of *Bacillus cereus* in Milk and Dairy Products, Mansoura Veterinary Medical Journal 21(2) 11-18.

Osman, K.M.; Kappell, A.D.; Fox, E.M.; Orabi, A. and Samir, A (2020). Prevalence, pathogenicity, virulence, antibiotic resistance, and phylogenetic analysis of biofilm producing *Listeria monocytogenes* isolated from different ecological niches in Egypt: Food, humans, animals, and environment. Pathogens 2020, 9,5.

Oviaño, M. and Bou, G. (2018). Matrix-assisted laser desorption ionization–time of flight mass spectrometry for the rapid detec-

tion of antimicrobial resistance mechanisms and beyond. Clin. Microbiol. Rev. 2018, 32, e00037-18. [CrossRef] [PubMed]

Petersen, K.E. and James, W.O. (1998). Agents, vehicles, and causal inference in bacterial foodborne disease outbreaks: 82 reports (1986-1995). Journal of the American Veterinary Medical Association. 1;212(12):1874-81.

Raji, M.A.; Kazeem, H.M.; Magyigbe, K.A.; Ahmed, A.O.; Lawal, D.N. and Raufu, I.A. (2021). Salmonella serovars, antibiotic resistance, and virulence factors isolated from intestinal content of slaughtered chickens and ready-to-eat chicken gizzards in the Ilorin Metropolis, Kwara State, Nigeria. International Journal of Food Science, 2021: 8872137. DOI: https://www.doi. org/10. 1155/2021/8872137

Rasko, D.A.; Altherr, M.R.; Han, C.S. and Ravel, J. (2005). Genomics of the *Bacillus cereus* group of organisms. FEMS Microbiol Rev 2005; 29:303-29.

Samy, A.A.; Arafa, A.A.; Hedia, R.H. and Ibrahim E.S. (2022). Multiple Drug Resistance Salmonella and Antibiotic Residues in Egyptian Animal Products. World Vet. J., 12 (4): 363-373. DOI: https://dx.doi. org/10. 54203/scil.2022.wvj64

Sasidharan, S.; Prema, B. and Yoga Ltha, L. (2011). Antimicrobial drug resistance of *Staphylococcus aureus* in dairy products. Asian Pcific Journal of Tropical Biomiedicine: 130-132.

Sciezynska, H; Mackiw, E; Maka, L and Pawlowska, K. (2012). The new microbiological hazards in food. Roczniki Panstwowego Zakladu Higieny 63(4): 397-402.

Sejas, L.M.; Silbert S.; Reis A.O.; Sader H.S. (2003). Avaliação da qualidade dos discos com antimicrobianos para testes de disco-difusãodisponíveis comercialmente no Brasil. *J. Bras. Patol. E Med. Lab.* 2003; 39:27–35.

Seoane, A. and Bou, G. (2021). Bioinformatics approaches to the study of antimicrobial resistance. Rev. Española Quimioter. 2021, 34 (Suppl. 1), 15.

Shamloo, E.; Hosseini, H.; Moghadam, A.Z.; Larsen, H.M.; Haslberger, A. and Alebouyeh, M. (2019). Importance of *Listeria monocytogenes* in food safety: A review of its prevalence, detection, and antibiotic resistance. Iran. J. Vet. Res. 20:241-254

Sharma, D.; Sharma, P.K. and Malik, A. (2011). Prevalence and antimicrobial susceptibility of drug resistant *Staphylococcus aureus* in raw milk of dairy cattle. Int Res J Microbiol 2011; 2: 466-70.

Shrestha, A.; Bajracharya, A.M.; Subedi, H.; Turha, R.S.; Kafle, S.; Sharma, S.; Neupane, S. and Chaudhary, D.K. (2017). Multi-drug resistance and extended spectrum beta lactamase producing Gram negative bacteria from chicken meat in Bharatpur Metropolitan, Nepal. BMC Research Notes, 10(1): 574.

Skowron, K.; Wałecka-Zacharksa, E.; Grudlewska, K.; Wiktorczyk, N.; Kaczmarek, A.; Gryń, G.; Kwiecińska-Piróg, J.; Juszczuk, K.; Paluszak, Z. and Kosek-Paszkowska, K. (2019). Characteristics of *Listeria monocytogenes* strains isolated from milk and humans and the possibility of milk-borne strains transmission. *Polish J. Microbiol.* 2019, *68*, 353–369.

Sousa, C.P. (2008). The Impact of Food Manufacturing Practices on Food-borne Diseases. Brazilian Archives of Biology and Technology, 51(4),815-823.

Su, L.H. and Chiu, C.H. (2007). *Salmonella*: clinical importance and evolution of nomenclature. Chang Gung Medical Journal, 30(3), 210-219.

Su, L.; Chiu, C.; Chu, C. and Ou, J. (2004). Antimicrobial resistance in nontyphoid Salmonella serovars: A global challenge. Clinical Infectious Diseases, 39(4): 546-551. DOI: https://www.doi.org/10.1086/422726.

Sundsfjord, A.; Simonsen, G.S.; Haldorsen, B.C.; Haaheim, H.; Hjelmevoll, S.O.; Littauer, P. and Dahl, K.H. (2004). Genetic methods for detection of antimicrobial resistance. Apmis 2004, 112, 815–837.

Tao, Q.; Wu, Q.; Zhang, Z.; Liu, J.; Tian, C.; Huang, Z.; Malakar, P.K.; Pan, Y. and Zhao, Y. (2022). Meta-Analysis for the Global Prevalence of Foodborne Pathogens Exhibiting Antibiotic Resistance and Biofilm

Formation. Front. Microbiol. 13, 906490. [Google Scholar] [Cross Ref]

Taulo, S.; Wetlesen, A.; Abrahamsen, R.; Kululanga, G.; Mkakosya, R. and Grimason, A. (2008). Microbiological hazard identification and exposure assessment of food prepared and served in rural households of Lungwena, Malawi. International Journal of Food Microbiology 1252: 111-116.

Vasala, A.; Hytönen, V.P. and Laitinen, O.H. (2020). Modern tools for rapid diagnostics of antimicrobial resistance. Front. Cell. Infect. Microbiol.2020, 10, 308.

Vinothkumar, R.; Arunagiri, K. and Sivakumar, T. (2013). Studies on pathogenic *Listeria monocytogenes* from marine food resources. Int. J. Curr. Microbiol. *Appl. Sci.* 2013, 2, 86–93. [Google Scholar]

Wang, W.; Lu, X.; Li, C.; Ri, M.J. and Cui, W. (2020). A man with recurrent fever, arthritis, and rashes-brucellosis? A case report. BMC Infect. Dis. 20:18. doi: 10.1186/s12879 -019-4746-0.

Wareth, G.; El-Diasty, M; Abdel-Hamid,N.H.; Holzer, K.; Hamdy, M.E.R.; Moustafa, S.; Shahein, M.A.; Melzer, F.; Beyer, W.; Pletz, M.W.; Neubauer, H. (2021). Molecular characterization and anti-microbial susceptibility testing of clinical and non-clinical *Brucella melitensis* and *Brucella abortus* isolates from Egypt.OneHealthVolume 13, 2021, 100255

Wiegand, I.; Hilpert, K. and Hancock, R.E.W. (2008): Agar and Broth Dilution Methods to Determine the Minimal Inhibitory Concentration (MIC) of Antimicrobial Substances. Nat. Protoc. 2008; 3:163–175.

World Health Organization (WHO) (2018). Drug-resistant Salmonella.

Xu, L.; Liang, W.; Wen, Y.; Wang, L.; Yang, X.; Ren, S.; Jia, N.; Zuo, X. and Liu, G. (2018). An ultrasensitive electro-chemical biosensor for the detection of mecA gene in methicillin-resistant *Staphylococcus aureus*. Biosens. Bioelectron. 2018, 9424–430. [CrossRef]

Xu, Y.; Zhou, X.; Jiang, Z.; Qi, Y.; Ed-Dra, A. and Yue, M. (2021). Antimicrobial resistance profiles and genetic typing of Salmonella serovars from chicken embryos in China. Antibiotics, 10(10): 1156.

Zhao, C.; Ge, B.; De Villena, J.; Sudler, R.; Yeh, E.; Zhao, S.; White, D.G.D.C.; Wagner, D. and Meng, J. (2001). Prevalence of Campylobacter spp., Escherichia coli, and Salmonella serovars in retail chicken, turkey, pork and beef from the Greater Washington, DC, area. Applied and Environmental Microbiology 6712: 5431-5436