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Theme

Study of the antibiotic susceptibility of strains
of *salmonella* isolated from wild animals

Presented by:

BELLIL Dassine & TABET Anis Abdelghani

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Evaluation jury:

| | | |
|----------------------|-----------|------------|
| Mr. TOUATI Abdelaziz | Professor | President |
| Ms. MAIRI Assia | MCB | Supervisor |
| Mrs. ZENATI Karima | MCA | Reviewer |

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Dedicate

To my twine “CHALLA”

To my MOM and DAD

To my brothers and Sisters

To my glory Family BELLIL

To my friends

*It is a wish deep emotion that I dedicate this
memory:*

*To my dear parents to whom own so much and
who do not have has never ceased to show me
affection, for their love, support and
encouragement, by hoping to make them proud
and to my dear brothers and sisters for the
support and wise advice they have given me*

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List of Abbreviation

AMR: Antimicrobial Resistance.

CDC: Centers for Disease Control.

ELISA: Enzyme-Linked immunosorbent assay.

EUCAST: European Committee on Antimicrobial Susceptibility Testing.

HP: High pathogenicity.

INTS: Invasive No Typhoidal *Salmonella*.

LDC: Lysin decarboxylase.

LIA: Lysin iron agar

LP: Low pathogenicity.

MALDI-TOF MS: Matrix assisted laser desorption ionization – time of flight mass spectrometry.

MDR: Multi-Drug Resistance.

MIC: Minimal inhibitory concentration.

NTS: No Typhoidal *Salmonella*.

S. Tm: *Salmonella* Typhimurium.

SS agar: Shigella/ Salmonella agar.

TDA: Tryptophan deaminase

TSI: Triple Sugar Iron.

VIH: Human immunodeficiency virus.

XLD: Xylose-Lysine-Deoxycholate.

Introduction

Salmonella represent global public health significance and it is one of the leading causes of foodborne illnesses and zoonotic infections in humans and animals, which is responsible for thousands of deaths worldwide. It colonize almost all warm- and cold-blooded animals (Jajere, 2019; Nair et al., 2018). Although numerous animals are considered as a reservoir of great number of pathogens, they are also considered as the main vehicles of transmission and spreaders of these pathogen bacteria, especially wild birds (Elsohaby et al., 2021; Deguenon et al., 2019). Shedding light on wild birds, they are thought to be one of the common mechanisms responsible for wide geographic distribution of certain important new endemic foci of disease at great distances, from where an infection was acquired and along migration routes. Moreover, they can serve as vectors for disease dissemination between livestock, people, and the environment (Reed et al., 2003; Vogt et al., 2020; Hubálek, 2004).

Thus, those wild animals are considered most likely to transmit bacteria to humans by direct contact with the infected animals or with indirect environmental contact, and/or through food consumption (Chlebicz and Śliżewska, 2018). Furthermore, they are capable to introduce those bacteria into the farm or may acquire an infection already established in the farm (Andrés-Barranco et al., 2014). In fact, these birds could recycle the infection however, they are less likely to be the source of introduction (De Lucia et al., 2018). Interestingly, ingestion of infected carcasses of animals can serve as the source of foodborne infection for carnivorous animals (Hubálek, 2004), such as wild boar through their opportunistic feed types, they are the first line of *Salmonella* infection and transmission particularly humans consumers (Sasaki et al., 2013).

Furthermore, the emergence of several clones of *Salmonella* resistant to multiple antimicrobials worldwide underscores a significant food safety hazard (Nair et al., 2018). Until today, *Salmonella* including multi-drug resistant (MDR) strains remains one of the leading bacterial foodborne causes of deaths. Interestingly, many studies by molecular typing have provided some evidence that bird migration may play a role in the spread of

antimicrobial resistance (Reed et al., 2003). From elsewhere, the discharged AMR (antimicrobial resistance) bacteria find their way to the migratory wild bird habitats representing extra selective pressure for resistant bacteria in addition to the risk for long-distance dispersal to unexposed wildlife and free-range animals. The resulting proliferation and dissemination of AMR bacteria to the environment highlight the importance of integrating resident and migratory wild birds in OAMR epidemiology to better understand and manage this global public health (Elsohaby et al., 2021).

Usually, it can be stated that the epidemiology of *Salmonella* is caused specially by fecal pollution. It therefore represents a general pattern that is applicable to many more pathogens of zoonotic nature (Oosterom, 1991). In general, *Salmonella* epidemiology in industrialized world reports annually high numbers of cases of human salmonellosis, and it is generally accepted that there is a considerable underreporting, amounting up to 95% (Oosterom, 1991). On this rise was found in the USA, more than 1 million annual cases of food-borne salmonellosis were estimated by the CDC; they were associated with the largest number of hospitalizations and deaths compared with other food-borne microbial agents (Antunes et al., 2016). In Europe, salmonellosis has been the second most common zoonosis (82 694 confirmed cases and 20.4 cases per 100 000 population in 2013) and the most frequent cause of food-borne outbreaks, in spite the reported decreasing trend that has resulted from *Salmonella* control programmes (Antunes et al., 2016).

An interesting study carried out in French Guiana found a correlation between the *Salmonella* serotypes isolated in reptiles and those responsible of human salmonellosis in the same area. Two-thirds of the *Salmonella* serotypes isolated from reptiles were also isolated from patients in French Guiana. In particular, subspecies *houtenae* was isolated in 16.7% of the reptiles tested and this subspecies was responsible for 10% of human salmonellosis in French Guiana in 2011 (Lamas et al., 2018).

Although different serotypes have been associated with salmonellosis, a limited number are responsible for most human infections; *S. Enteritidis* being the most frequent one in the EU (39.5% in 2013) and USA (14.5% in 2012) followed by *S. Typhimurium* (Antunes et al., 2016). In the 21st century, a worsening situation is the increasing resistance to fluoroquinolones and third-generation cephalosporins in nontyphoid *Salmonella* (NTS). Although antimicrobial therapy is usually not indicated for uncomplicated *Salmonella* gastroenteritis. (Chen et al., 2013).

In this regard, few studies reported the prevalence of *Salmonella* in Algeria and none concerned wild animals, thus, the main aim of our survey was to report the prevalence of *Salmonella* in wild animals (proximity to humans) in Algeria. Besides, the antibiotic resistance patterns of these isolates.

Bibliographic Part

8. Taxonomy and Nomenclature of *Salmonella*

The first study of *Salmonella* began during the early 19th century by Eberth, who first recognized the organism. Gaffky isolated the bacillus responsible for human typhoid fever, in 1885 Theobald Smith together with Daniel Elmer Salmon discovered and isolated *Salmonella* from the intestines of pigs infected with classical swine fever (hog cholera). During this period, they thought that the bacterium was the etiological agent of hog cholera. Later, the bacterial strain was named *Salmonella* by Dr. Daniel Elmer Salmon. In recent years, the issue of nomenclature of the genus *Salmonella* has been complex, controversial, and still remains subject of debate, resulting in part from multiple independent investigators using phenotypic, serologic, and genotypic methods to characterize phylogenetic relationships within the genus, and in part from disagreements on nomenclature concerning the number of species and subspecies that form the *Salmonella* genus (Dekker and Frank, 2015).

Since the first Kauffmann-White serotype scheme based on surface molecular antigen variation published in 1934, serotyping has become the most important tool for identifying and classifying the *Salmonella* strains for more than 80 years. The serovars (serotypes), are differentiated by their antigenic composition, into serogroups based on the somatic (O), flagellar (H), and capsular (Vi) antigens (Holschbach and Peek, 2018). Besides, the recent whole-genome and metagenome sequence data allow the continuation use of traditional serovar nomenclature and enhance the ability to infer true phylogenetic relationships between isolates (Wang et al., 2020).

At present, most *Salmonella* reference centers in the world adopt the nomenclatural system of *Salmonella* as recommended by the World Health Organization (WHO) (Popoff et al., 2003). Since that point, this nomenclatural system classifies the genus *Salmonella* into two species, based on differences in their 16S rRNA sequence analysis, including *S. enterica* and *S. bongori* (Jajere, 2019).

The *Salmonella enterica* species is divided into six subspecies including *enterica* (I), *salamae* (II), *arizonae* (IIIa), *diarizonae* (IIIb), *indica* (IV), *houtenae* (VI) (Wang et al., 2020), Most serotypes are reported in *S. enterica subsp. enterica* (Chlebicz and Śliżewska, 2018) and they are responsible for 99% of salmonellosis cases in humans and warm-blooded

animals. In the other hand, *S. bongori* and the other subspecies of *Salmonella enterica* are rarely isolated in humans and are mainly found in cold-blooded animals and in the environment (Jajere, 2019). In fact, *Salmonella enterica* subspecies *enterica* represents more than 2600 serovars, with serotype Enteritidis and Typhimurium being the most common reported serotype (Tyson-Pello and Olsen, 2020; Jajere, 2019).

9. Bacteriology

Salmonella is a genus of Gram-negative gammaproteobacterial, rod-shaped, facultative anaerobe bacillus with flagella and mobility using the peritrichal flagellum, relatively non-spore forming, intracellular human and animal pathogens belonging to the *Enterobacteriaceae* family (Mares, 2017; Holschbach and Peek, 2018). The main reason for this attention is that *Salmonella* spp. is a worldwide foodborne pathogen and the second most responsible for gastrointestinal human infections after *Campylobacter* spp. (Lamas et al., 2018). Initially, the genus *Salmonella* was characterized by its ability to utilize citrate as a sole carbon source and lysine as a source of nitrogen as well as its ability to yield hydrogen sulfide (Gal-Mor, 2018).

They are intracellular facultative pathogens, the size of which ranges between 0.2-1.5 × 2-5 µm. The shape of the rod is maintained due to the bacterial cytoskeleton made of an actin-resembling protein. *Salmonella* spp. rods may survive in variable conditions. They are able to grow at temperatures ranging between 8 and 45°C (optimum temperature 37°C), at the pH from 4.0 to 9.5 (optimum pH 6.5–7.0), and in conditions of low water activity of 0.94. Those bacteria pose a great threat to the food industry because they are able to adapt to environmental conditions that are significantly different from their normal range of growth. Some strains are able to grow at 54 °C, and others even at 2–4 °C (Chlebicz and Śliżewska, 2018).

10. Isolation and Identification of *Salmonella*

Whole stools are the preferred specimen for culture, and examination of multiple specimens may improve the recovery of *Salmonella*. Most commonly used pH-buffered stool transport media are compatible with recovery of *Salmonella*, though cooler box transport is preferred by many labs, due to its compatibility with other common stool pathogens (Jajere, 2019).

Typically, isolation of *Salmonella* from swabs, food, and other environmental samples utilizing the traditional or conventional culture method that involves an initial non-selective pre-enrichment of a defined volume of the sample, followed by a selective enrichment step, plating onto selective agars, and then biochemical and serological confirmation of suspect presumptive colonies. International Organization for Standardization (ISO) have standardized different approaches of *Salmonella* enrichment utilizing its unique biochemical physical properties. The current ISO standard method, ISO 6579:2002 has been adopted by many *Salmonella* reference centers and is essentially similar to other standard detection methods for *Salmonella* standardized by other regulatory agencies (Jajere, 2019).

While, stool culture is the most common source from which non-typhoidal serovars of *Salmonella* are recovered (Eibach et al., 2016). Thus, because *Salmonella* organisms are easily and rapidly out competed by other fecal gram negatives, the majority of diagnostic laboratories use enrichment media such as tetrathionate or selenite broth, to enhance the chances of *Salmonella* growth. Indeed, this enrichment broth allow the elimination of the normal fecal flora growth while it improve the growth of *Salmonella*. Once isolated, *Salmonella* should be sub-cultured using standard techniques to obtain colonies for identification by biochemical procedures and susceptibility testing(Holschbach and Peek, 2018).

However, due to other enteric pathogens bacteria, such as *Shigella* spp. and *Proteus* spp. which neither ferment lactose, stool samples inoculation onto an additional differential and selective media is required. Typically, two differential and selective media, are inoculated with the stool specimen. Hektoen and xylose-lysine-deoxycholate (XLD) agars are highly selective and both detect H₂S production, facilitating identification and detection of *Salmonella* species. More highly selective agars, embedded Salmonella-Shigella, bismuth sulfite, and brilliant green agars could possibly inhibit some *Salmonella* spp. strains, therefore are often used in combination with a less selective agar(Gal-Mor, 2018).

For this reason, a less selective differential enteric medium, such as MacConkey or eosin methylene blue, and a nonselective medium, such as 5% sheep blood agar may be inoculated in addition as part of the stool culture work up, depending on lab preference (Dekker and Frank, 2015). Indeed, these selective media allow the growth of *Salmonella* organism, while simultaneously suppressing the propagation of other bacteria. The resulting presumptive colonies obtained on inoculating media may then inoculated and incubated in

both triple sugar iron (TSI) and lysin iron agar (LIA). Isolates that yield reactions characteristic of *Salmonella* on TSI agar and/or LIA are further confirmed to the genus level using either a manual identification tool, like the API 20E system, or an automated bacterial identification system, such as Vitek2, or matrix-assisted laser desorption ionization–time of flight mass spectrometry (MALDI-TOF MS) (Gal-Mor, 2018).

Finally, a range of chromogenic media for characterization of *Salmonella* in stool samples has been developed. These media utilize enzyme substrates that create a colored product following hydrolysis, hence resulting in colored colonies that can be easily recognized against the background of the commensal gut flora. Furthermore, Serotyping has wide acceptance as a method to differentiate *Salmonella* strains, and it is an important tool in public health. Immunology-based methods involving antigen-antibody bindings have been widely used for the detection of food-borne pathogens. Such as, immunology-based assays include ELISA, latex agglutination tests, immunodiffusion, and immunochromatography (dipstick). Moreover, direct hybridization (DNA probe) and amplification (PCR) methods are the two major techniques of the molecular assays that are used for the detection of *Salmonella* pathogens (Abebe et al., 2020).

11. Biochemical and Serological identification

Almost all serotypes do not produce indole, hydrolyze urea, and deaminate phenylalanine or tryptophan, either do not utilize lactose; most serotypes readily reduce nitrate to nitrite, ferment a variety of carbohydrates with acid production, and are negative for Voges–Proskauer reaction. With the exception of *S. enterica* subsp. *arizonae* and *S. subsp. diarizonae*, most serotypes utilize arginine, ornithine, decarboxylate lysine and hydrogen sulfide. Similarly, most serotypes utilize citrate with the exception of some few serovars of *S. Choleraesuis*, *S. Typhi*, and *S. ParatyphiA*. (Jajere, 2019; Lamas et al., 2018).

There are various methods available for identification and classification. Definitive identification ordinarily established by combining the phenotypic and serologic methods. The widely-used Kauffmann-White serologic typing scheme is established on the LPS O antigen, the H1 and H2 flagellar antigens, as well as the Vi antigen. While the O and H1 antigens are detectable in almost all strains of *Salmonella*, the H2 antigens are present only in certain strains and the Vi antigen is found predominantly in typhoidal strains. It should be noted that Vi, though useful for detection of serovar Typhi, may also be expressed in *Citrobacter* sp. (Dekker and Frank, 2015; Gal-Mor, 2018).

12. Transmission of *Salmonella* zoonoses disease

Foodborne transmission is recognized as the major cause of *Salmonella*'s infections (Ejo et al., 2016). In this sense, animal-origin food and their products such as milk, eggs, poultry, beef, and pork are the commonest vehicles of *Salmonella* to humans (Abebe et al., 2020). Besides, non-typhoid *Salmonella* NTS is most often transmitted to humans through contaminated food (Deguenon et al., 2019). Whereas, meat becomes infected with *Salmonella* spp. during the production process when the bacteria that are abundant in animal intestines of the carcasses or edible organs may become transferred onto meat as a result of careless processing or improper hygiene. Fresh meat is a good environment for the growth of pathogenic *Salmonella* spp. due to a high content of nutrients. Also, vegetables contaminated with animal fecal microbiota may constitute a reservoir for *Salmonella* spp. (Chlebicz and Śliżewska, 2018; Abebe et al., 2020).

In addition, the mode of transport of pathogenic agents by migratory birds are very important because it depends on the routes of transmission from one region to another through shedding their feces continuously and intermittently in a new geographic area (Reed et al., 2003).

Moreover, other important means of transmission include vertical and horizontal transmission. Vertical transmission, the former involves the transmission of the bacteria from parents to progeny and it is very important especially in poultry. On the other hand, horizontal transmission occurs either through the feco-oral or aerogenous routes, introduction of *Salmonella* from one individual to another by contaminated drinking water, contaminated feeds and dirty feeders, or asymptomatic carriers and feces from clinically infected animals in the farm (Jajere, 2019). Therefore, resulted by direct contact with infected animals or by indirect contact via their environment (Chlebicz and Śliżewska, 2018)

In addition, even flies act as mechanical vectors aiding transmission of the bacteria from one farm to another and transmission from animal to humans. Animals in the farm become infected through ingesting *Salmonella* infected flies. Besides, wild animals such as wild birds and wild boar are regarded as important reservoirs of *Salmonella* infection (Jajere, 2019). In summary, transmission is affected by overpopulation in areas of poor sanitary conditions (Chlebicz and Śliżewska, 2018).

13. Reservoir and host

Salmonella is ubiquitous and extremely persistent in the dry environment and in water for periods ranging from days to several months. *S. enterica* serovars have varied hosts and biological carriers, and can cause disease in both humans and animals. Thus, with the exception of a few serovars that are host-restricted, whereas, the majority of *S. enterica* serovars are host-adapted and specific (Jajere, 2019). According to the genetic differences between the host-restricted, host adapted, and generalist serovars provide insights into the bacterial characteristics that determine host range and depends on variety of host niches with a diversity of physiological requirements (Silva et al., 2014), an example is the serovar Choleraesuis considered a pig-adapted serovar because it persists in pig populations and not because it causes the severest disease in swine compared to man (Jajere, 2019).

In contrast, host-specific pathogens persist in a restricted environmental niche and have fewer selective constraint a lifestyle that sacrifices fast growth in a wide variety of environments for slower growth and persistence in a more protected environment. Therefore, the slower growth and more uniform metabolic requirements of host-specific *Salmonella* serovars eliminate the potential impact of genetic changes that invoke a fitness cost in fast-growth conditions with fluctuating metabolic demands (Silva et al., 2014).

It is believed that the process of host adaptation by *S. enterica* serovars involves two mechanisms namely, acquisition of novel genetic elements encoding specific virulence factors and loss of genes. Therefore, host adaptation or specificity is the ability of the particular organism to cause disease in a particular animal population regardless of the degree of pathogenicity it exhibits for a different animal host.

In addition, Common factors contributing to *Salmonella* disease include the infectious dose of the particular serovar, extremes in age of host, animal species infected, and immune response or the occurrence of immunosuppressive conditions, and other underlying comorbidities In addition, climatic conditions such as increased rainfall or drought that can result in food scarcity (Haselbeck et al., 2017). In fact, it has been demonstrated that a particular mechanism making a serovar virulent for one particular animal species could make the same serovar less or even avirulent for another animal species. This phenomenon is referred to as “serovar host specificity” or “serovar host adaptation” (Jajere, 2019).

14. Antibiotic resistance and role of wild animals in spread of MDR strains

The development of antimicrobial resistance (AMR) among foodborne pathogens such as *Salmonella* have been associated with an increased number of human and animal deaths,

longer duration of hospitalization, and high costs of treatment due to therapy failure. Several clones of multidrug-resistant (MDR) *Salmonella* have emerged during the late 1990s and early 2000s and since then, their prevalence both in humans, domestic animals and other wildlife species have expanded globally. Whereas, the risk of infection is high because of unhygienic living conditions, close contact and sharing of houses between animals and humans, and the traditions of consumption of raw or undercooked animal-origin food items(Abebe et al., 2020). In addition, the use of fecal waste as manure in agricultural lands also contributes to the spread of antibiotic resistance, especially in fresh produce, the contamination of waterways also contributes to the pool of resistant bacteria in agriculture and aquaculture.

Animal infectious diseases can greatly affect the cost of food production, with antimicrobial agents commonly used for a long-term in food animals or in their environment and on farms, creates ideal conditions for the development and spread of resistant strains in animals may directly (e.g. food; farm workers in contact with animals or the pig farm environment) or indirectly (animal waste handling, wind, surface and ground waters) routes reach humans through food, water, mud, and manure, which are used as fertilizers(Novais et al., 2013;Ma et al., 2021).

In fact, there is irrefutable evidence that foods from many animal sources and all food processing stages contain a large number of resistant bacteria. Although, several studies confirmed the transmission of antibiotic-resistant bacteria from animals to farm workers. The results revealed the prevalence of resistance among farmers before and after the introduction of antibiotics at their workplace. In addition, consumers may also be exposed to resistant bacteria via contact with or consumption of animal products. There is undeniable evidence that foods from many different animal sources and in all stages of processing contain abundant quantities of resistant bacteria and resistance genes(Ma et al., 2021).

Furthermore, the spread of clones of *Salmonella* can also be influenced by factors independent of antimicrobial usage, such as human foreign travel, the integrated structure of some animal production systems, animal movement and hygienic practices on farms. At this time, there is little data to support complex models and thus we need more molecular epidemiological research that will hopefully provide an improved understanding of the transmission dynamics occurring role (Greig et al., 2015).

Conclusion

Well, every effort was made to identify all relevant research on our topic, so this study showed 19 strains of salmonella, in which 5 strains were resistant to tetracycline. Although several factor such as the time given for the survey and the sampling, thus, we couldn't manage the serotyping test by consequence, we couldn't detect the serovars of *Salmonella* emerge in wild animals in North Algeria.

This study is the first national survey on the presence of salmonella in wild animals in Algeria particularly in wild boars, wild deer. According to the results of the present study suggest that the consumption of meat from these wild animals presents the risk that these bacterial infections could be transmitted to humans, and these animals are main potential vectors for the spread of antimicrobial resistant bacteria, especially wild boars and wild birds to farms and from one region to another by shedding fecal through species that act as carriers. Thus, its necessary to understand the mode of transmission of resistant bacteria and enzootic to wild animals and their ability to maintain and disseminate infection into the environment and human. Interestingly, the topic of zoonotic carriers is dynamic with many contributing factors and sources. Because neither pathogen nor animals respect political borders.

Prospects:

However, there are limited studies that have evaluated about these kinds of transmission of zoonotic for human safety by:

- The need for the use of antimicrobials in animal production should be reduced through disease prevention, supported by good animal husbandry and management practices, animal welfare and vaccination.
- limit and control farm visitors – people and vehicles
- keep farm access routes, parking areas, yards, feeding and storage areas clean and tidy
- know the health status of any animals or birds you are buying or moving
- Prevent animal entry through the use of fences, noise cannons, and other deterrents.
- Before each harvest, an assessment of the field should be done to ensure that there are no obvious signs of animal intrusion or fecal contamination.
- workers need to understand how to create buffers and follow the farm policy for leaving or removing the contamination. And they must also be instructed to wash their hands after handling contaminated produce or fecal material as manure.

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Background: *Salmonella enterica* are widely known as enteropathogenic bacteria and one of the most ubiquitous species causing foodborne infections. Although several animals suggested as it's the reservoir and the main vehicles of transmission of great number of pathogens bacteria. Currently, the emergence of multidrug-resistant zoonotic bacteria associated with consumption of contaminated animal products.

Aim of the study: This study was conducted to determine the prevalence and antibiotics susceptibility of *Salmonella* isolated from wild animals in Algeria.

Methods: This survey was carried out from 1 May to 30 June 2021. A total of 412 fecal samples were collected from different type of wild animals in Algeria. The suspected isolates were identified by using phenotypic methods, and were subjected to antimicrobial susceptibility tests wards 11 antibiotic agents.

Results: A total of 18 positive samples were reported giving an overall prevalence of 4,61%. A total of 19 strains of *Salmonella* were generated. All these strains were susceptible to all antibiotics except tetracycline, 5 strains were resistant to this antibiotic.

Conclusion: Fortunately, on the 19 strains obtained during this study, no multi-resistance to antibiotics were identified, however risks of an epidemic by a multi-resistant *Salmonella* are not to exclude. Thus, the prevalence and antimicrobial susceptibility of *Salmonella* in these wild animals should be monitored periodically.

Keywords: *Salmonella* spp. Antibiotic resistance, wild animals, Algeria.

Résumé :

Contexte : *Salmonella enterica* largement connue comme étant une bactérie entomopathogène et l'une des espèces les plus ubiquistes sur terre causant des infections d'origine alimentaire. Bien que plusieurs animaux suggèrent que c'est le réservoir et des principaux véhicules de transmission d'un grand nombre d'agents pathogènes. Actuellement, l'émergence de bactéries zoonotiques multirésistantes associées à la consommation de produits animaux contaminés.

Objectif de l'étude : Cette étude a été menée pour déterminer la prévalence et sensibilité aux antibiotiques des *Salmonella* isolées d'animaux sauvages en Algérie.

Méthodes : Cette recherche a été réalisée du 1er mai à juin 2021. Un total de 412 échantillons fécaux a été prélevé sur différents types d'animaux sauvages en Algérie. Les isolats suspects ont été identifiés par des méthodes phénotypiques, et ont été soumis à des tests de sensibilité antimicrobienne pour 11 agents antibiotiques.

Résultats : Un total de 18 échantillons positifs a été rapporté donnant une prévalence globale de 4,61 %, 19 souches de *Salmonella* ont été identifiées. Toutes ces souches étaient sensibles à tous les antibiotiques à l'exception de la tétracycline, cinq souches étaient résistantes à cet antibiotique.

Conclusion : Heureusement, sur les 19 souches obtenues au cours de cette étude, aucune multi-résistante aux antibiotiques n'a été identifiée, cependant des risques d'épidémie par une *Salmonella* multi-résistante ne sont pas à exclure. Ainsi, la prévalence et la sensibilité aux antimicrobiens de *Salmonella* chez ces animaux sauvages doivent être surveillées périodiquement.