FOODBORNE PATHOGENS AND DISEASE
Volume 22, Number 10, 2025
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DOI: 10.1089/fpd.2024.0036

Prevalence and Antibiotic Susceptibility of Nontyphoidal *Salmonella* from Food-Animal Products in Bejaia, Algeria

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Abstract

Nontyphoidal *Salmonella* presents a significant threat to animal and human health as a food-borne infectious agent. This study focused on the characterization of *Salmonella* isolates obtained from fresh animal products consumed in Bejaia, Algeria. In total, 495 beef products, 600 chicken products, and 355 dairy products were collected from retail outlets and slaughterhouses in the region. Out of the 1450 samples collected, a *Salmonella* positivity rate of 3.5% (51/1450) was observed. Traditional Algerian sausages exhibited the highest prevalence of *Salmonella* contamination (14.1%, 36/256). Fifteen different serotypes were identified, with *S.* Kentucky (n = 12), *S.* Anatum (n = 11), and *S.* Bredeney (n = 9) being the most prevalent. Antimicrobial susceptibility testing showed resistance to diverse antibiotics, particularly against tetracycline, ampicillin, nalidixic acid, and sulphonamides. Whole-genome sequencing conducted on 21 isolates enabled the comparison of phylogenetic links between isolates. We notably identified clones circulating across the region in different locations and food types, suggesting contamination at the early stages of the food chain (in the herd or slaughterhouses) that disseminated to numerous butcher shops in various cities. We also identified acquired antibiotic resistance genes and point mutations in the quinolone resistance-determining region genes, contributing to the observed resistance patterns. This study describes the genomic and phylogenetic characteristics of several *Salmonella* clones found in diverse food samples in Algeria. It suggests potential transmission dynamics that could better understand *Salmonella*'s contamination routes.

Keywords: *Salmonella*, serotype, food product, whole-genome sequencing, antimicrobial resistance

Introduction

Nontyphoidal *Salmonella* (NTS) is a leading cause of food-borne infections worldwide, primarily resulting in gastroenteritis. Although the morbidity rate is high, mortality remains low except among vulnerable populations such as newborns and immunocompromised individuals (Fleckenstein et al., 2021). Annually, NTS is responsible for approximately 93.8 million cases of gastroenteritis and 155,000 deaths (Mezali et al., 2019). The infection is often linked to consuming contaminated food products such as poultry, eggs, meat, milk, and seafood (Djeffal et al., 2021). In Africa, livestock and poultry serve as key protein sources, and in Algeria, the expansion of intensive husbandry systems has increased *Salmonella* contamination risks, with animals acting as reservoirs (Mezali et al., 2019; Murinda et al., 2002).

NTS contamination can occur at multiple stages of food production, including feed processing and meat handling. Cross-contamination in butcher shops further exacerbates contamination risks (Teklemariam et al., 2023). Improving detection methods is critical, particularly as antimicrobial resistance (AMR) in *Salmonella* strains continues to rise. The inappropriate use of antimicrobials, especially in developing countries, has contributed to the emergence of AMR

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