



Short Communication

Comprehensive Genomic Characterization of Antibiotic Resistance, Virulence, and Clonality in *Salmonella* Isolates from Wild Animals in Algeria

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Abstract: This study investigated *Salmonella* spp. in wild animals in Algeria, focusing on their prevalence, serotypes, antibiotic resistance, and virulence profiles. From fecal samples collected between May 2021 and June 2022, 1.9% showed *Salmonella* shedding. The identified serotypes included *S. Bredeney*, *S. Enteritidis*, *S. Altona*, and *S. Virchow*. Except for *S. Altona*, all isolates were resistant to quinolones, with *S. Bredeney* strains, exhibiting multidrug resistance. Whole-genome sequencing revealed various resistance genes and mutations in *gyrA* or *parC* genes. Additionally, plasmids IncX1 and ColpVC were detected in several isolates. A comprehensive analysis identified 201 virulence genes. These findings contribute to understanding *Salmonella* in wild animal populations and their potential impact on public health.

Keywords: *Salmonella*, wild animals, WGS, virulence factors, antibiotic resistance

Wildlife–livestock–human interfaces allow bacteria to spread, increasing the risk of pathogen transmission and disease outbreaks (Hassell et al. 2017). With numerous zoonotic pathogens among the 1400 known human pathogens, it is vital to comprehend the impact of these interfaces on public health. To effectively prevent and control disease outbreaks, a comprehensive understanding

of cross-species pathogen transmission mechanisms is essential (Woolhouse and Gowtage-Sequeria 2005).

Salmonella is a major public health concern, responsible for numerous foodborne and zoonotic infections resulting in global fatalities. It can colonize the intestines of both warm- and cold-blooded animals (Jajere 2019). Fecal contamination from various domestic and wild animals serves as the primary source of *Salmonella*, and humans can become infected through contact with contaminated farm animals or pets (Thomas et al. 2017) as well as the consumption of wild animal meat (Peruzy et al. 2022).

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