Commentary

Enhanced Genomic Surveillance Is Essential for Effective *Salmonella* Outbreak Response

Yanan Wang[1,2,#]; Xuebin Xu[3]; Baoli Zhu[4]; George F. Gao[4,5,6]

On May 1, 2025, Gonzalez-Perez and colleagues (*1*) reported a multi-country outbreak caused by *Salmonella enterica* subspecies *enterica* serovar Mbandaka (*S.* Mbandaka) that resulted in over 200 cases across Europe. Finland reported the highest number of cases with 97 infections. Whole genome sequencing (WGS) and comparative genomic analyses revealed that the outbreak strains were genetically linked to previously identified strains in the United Kingdom and to pre-cooked, frozen chicken meat used in ready-to-eat products. Subsequently, on May 5, 2025, the United States of America (USA) Centers for Disease Control and Prevention (CDC) announced a *Salmonella* outbreak associated with backyard poultry (*2*). As of May 19, 2025, this outbreak had expanded to 104 confirmed infections, with at least 33 individuals contracting *Salmonella* following contact with backyard poultry. Tragically, one death has been reported in Illinois. Scientific evidence demonstrates that *S.* Mbandaka isolated from patient samples, and matched the strain found in shipping boxes used to transport poultry from hatcheries to agricultural retail stores. Although confirmed and suspected cases have been reported from 35 states, including Florida, Illinois, Missouri, South Dakota, Utah, and Wisconsin, the actual number of infections likely exceeds reported figures due to underdiagnosis and underreporting. The outbreak's severity prompted the recall of more than 1.7 million eggs due to potential *Salmonella* contamination. Interstate and international transportation of poultry and chicken meat products appear to be facilitating the pathogen's spread across the USA, European countries, and globally. However, our understanding of the genetic characteristics and transmission patterns of *S.* Mbandaka remains limited.

In response to the current outbreak caused by *Salmonella*, which has been listed in the 2024 World Health Organization Bacterial Priority Pathogens List (*3*–*4*) and increasing trends in antimicrobial resistance (AMR) (*5*–*7*), rapid genomic sequencing, together with the timely sharing of data, is vital for assessing the outbreak source tracing, clinical guidance, and formulating effective prevention and control policies (*8*). As of February 15, 2025, 2,814 genomes with clear metadata (including collection date, source, and location of collection information), serovar, and sequence type (ST) were publicly available from the National Center for Biotechnology Information (NCBI). Genomic data submitted to the NCBI were collected from 6 continents, and 66.45% of them were isolated from North America (mainly in the USA), followed by Europe (20.04%) and Asia (8.14%). We identified a clear gap in data from Africa (*n*=13) and Oceania (*n*=48) despite the onward transmission of *S.* Mbandaka in North America and Europe during this time. The majority of genomes were from humans (21.57%), cattle (19.47%), environment (19.40%), chickens (11.05%), food (9.70%), and pigs (6.15%). A total of 18 STs were identified; ST413 (*n*=2,611) was the most dominant, followed by ST1602 (*n*=112). Due to the lack of timely data-sharing and genomic surveillance during this period, the current outbreak caused by *S.* Mbandaka may be underestimated.

Our previous studies demonstrate that *S.* Mbandaka ranks 17th among human infections in China (*7*) and 18th globally among 208,233 *Salmonella* genomes with comprehensive metadata (*6*). Genomic prediction analyses revealed increasing AMR trends in *S.* Mbandaka. We identified 95 acquired antibiotic resistance genes (ARGs) across these genomes. Notably, 4 genomes carried the carbapenem resistance gene $bla_{\text{NDM-1}}$, while 22 carried the colistin resistance gene *mcr-9*. All 4 strains containing the carbapenem resistance gene $bla_{\text{NDM-1}}$ were isolated from human patients in China, with 3 recovered from blood samples and 1 were from fecal specimens. Moreover, we detected third-generation cephalosporin resistance genes $bla_{\text{CTX-M-65/55/14/1/8}}$ (*n*=16), the fosfomycin resistance gene *fosA7* (*n*=1), and the azithromycin resistance gene *mph(A)* (*n*=22). These comprehensive genomic analyses enlarge our understanding of AMR evolution in *S.* Mbandaka and provide a critical context for interpreting current outbreak patterns.

Salmonella infections represent a significant zoonotic threat, necessitating comprehensive bacterial genomic surveillance that encompasses diverse sources, including humans, animals, food products, plants, and environmental samples. Technological advances in WGS and artificial intelligence (AI) have revolutionized genomic surveillance capabilities, making comprehensive multi-source data collection essential for tracking outbreak origins and monitoring AMR evolution in *S. enterica* (*6*–*9*). A prime example of this approach, is the high-quality, open-access, Chinese local *Salmonella* genome database version 2 (CLSGDBv2, https://nmdc.cn/clsgdbv2) (*10*), which serves as a valuable resource for global genomic surveillance and demonstrates substantial public health impact, having been accessed around 170 thousand times across 6 continents. These developments underscore the urgent need for enhanced genomic sequencing capabilities and improved data-sharing protocols, while simultaneously strengthening public health and clinical laboratory surveillance networks. Consequently, expanding publicly available genomic data for *Salmonella* serovars, particularly Mbandaka, would significantly improve real-time outbreak assessment capabilities, and prioritizing WGS of *Salmonella* strains from food and animal sources in underrepresented geographic regions is essential for comprehensive global surveillance.

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[#] Corresponding author: Yanan Wang, wangyanan1001@henau.edu.cn.

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[1] International Joint Research Center of National Animal Immunology, College of Veterinary Medicine, Henan Agricultural University, Zhengzhou City, Henan Province, China; [2] Longhu Laboratory of Advanced Immunology, Zhengzhou City, Henan Province, China; [3] Division of Pathogen Testing and Analysis, Shanghai Municipal Center for Disease Control and Prevention, Shanghai, China; [4] CAS Key Laboratory of Pathogen Microbiology and Immunology, Institute of Microbiology, Chinese Academy of Sciences, Beijing, China; [5] The D. H. Chen School of Universal Health, Zhejiang University, Hangzhou City, Zhejiang Province, China; [6] Chinese Center for Disease Control and Prevention, Beijing, China.

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