ANTIMICROBIAL RESISTANCE PROFILES OF Salmonella Mbandaka ISOLATED FROM DIFFERENT SOURCES IN BRAZIL AND ITS CORRELATION WITH PATHOGENIC POTENTIAL AND GENETIC DIVERSITY

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Introduction: *Salmonella* is one of the main agents of foodborne diseases worldwide. Among its serovars, *Salmonella enterica* serovar Mbandaka (*S*. Mbandaka) has stood out for its ability to adapt to different hosts and contaminate multiple food sources. In recent years, a concerning increase in antimicrobial resistance has been observed in strains of this serovar, which has been ranked among the ten most common in human sources and occupies the second position in non-human isolations in the state of São Paulo. **Objective:** To characterize the antimicrobial resistance profile of *S.* Mbandaka strains isolated over 15 years in Brazil, correlating with their pathogenic potential and genetic diversity. **Methods:** A total of 54 strains of *S.* Mbandaka isolated from food (n=35), humans (n=14), and the environment (n=5) between 2010 and 2025 were studied. Antimicrobial susceptibility tests were performed by the disk diffusion method for 14 antimicrobials, including screening for ESBL production. The virulence genes *invA*, *sopB*, *ssaR*, *sifA*, *sopE2*, *sipA*, *sipD*, *flgK*, *fljB*, *flgL*, and *spvB* were investigated by PCR. Molecular typing was performed by PFGE after digestion with 40U of the *Xba*I enzyme, with band patterns analyzed by BioNumerics software to generate a similarity dendrogram. **Results:** A total of 34 (63.1%) strains showed resistance to at least one antimicrobial, with gentamicin resistance being the predominant phenotype (30/54; 55.6). One isolate showed resistance exclusively to fluoroquinolones. Three strains were classified as multidrug-resistant (MDR), two of which were resistant to fluoroquinolones, including one ESBL-producing isolate with extended resistance to β-lactams. All virulence genes were found in frequencies above 76%, except for *spvB*, which was not detected in any of the strains analyzed. The PFGE analysis showed an overall similarity of ≥63.9% and discriminated the strains into 50 PFGE-types. Considering an epidemiological cutoff of 80% similarity, the strains were grouped into seven distinct clusters comprising strains from different sources and years. **Discussion:** Clinically, the detection of fluoroquinolone resistance and ESBL production phenotype (third- and fourth-generation cephalosporins) in isolates of food and environmental origin is alarming, since these profiles involve first-choice drugs and are classified by WHO as of high and critical priority, respectively. The high prevalence of SPI-1 and SPI-2 pathogenicity island genes reinforced the ability of *S.* Mbandaka for invasion and intracellular survival. PFGE was able to discriminate *S.* Mbandaka isolates and provided important epidemiological information **Conclusion:** The results obtained contributed for a better characterization of *S.* Mbandaka strains isolated in Brazil, and the identification of MDR profiles against clinically used drugs represents a serious public health alert due to

the risk of therapeutic failure. Furthermore, the pathogenic potential of the studied strains was highlighted while the observed genetic similarity among some strains suggested possible transmission of *S.* Mbandaka among different sources in the country, reinforcing the need for continuous surveillance and integrated control strategies under the One Health perspective.

Agradecimentos: FAPESP (2024/18739-7 and 2025/10016-9) and CAPES (Financial code 001)