Genome Sequences of Multidrug-Resistant *Salmonella enterica* Serovar Paratyphi B (dT+) and Heidelberg Strains from the Colombian Poultry Chain

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*Salmonella enterica* is a pathogen of significant public health importance that is frequently associated with foodborne illness. We report the whole-genome sequences of four multidrug-resistant *Salmonella enterica* serovar Paratyphi B and Heidelberg strains, isolated from the Colombian poultry chain. The isolates contain a variety of antimicrobial resistance genes for aminoglycosides, β-lactams, fluoroquinolones, sulfonamides, tetracycline, and trimethoprim.

Salmonella spp. continue to be one of the most important causes of foodborne gastroenteritis globally, affecting mainly infants under 1 year and children between 1 and 4 years of age (1). *Salmonella* serovars Paratyphi B and Heidelberg have been determined to be causative of morbidity and mortality in humans (2, 3). Recently, *Salmonella enterica* serovar Paratyphi B and Heidelberg multidrug-resistant (MDR) strains have also been reported as the two most prevalent serovars in Colombian poultry (4–7). The four *Salmonella* isolates described here are part of a comprehensive prevalence survey from the Colombian Integrated Program for Antimicrobial Resistance Surveillance (COIPARS) (8) and were recovered from retail stores, slaughterhouses, and cecal contents during 2012 to 2013 in important poultry production regions (Cundinamarca and Santander) as well as Bogotá, Colombia. These *Salmonella* isolates are resistant to several families of antibiotics including β-lactams, quinolones, fluoroquinolones, aminoglycosides, tetracyclines, nitrofurantoin, in addition to folate pathways and β-lactamase inhibitors.

Here, we report the whole-genome sequences of four *Salmonella enterica* serovar Heidelberg (FSAN332CC, UG1286CA) and Paratyphi B (FCUN156CA, FSAN236CA) strains. Genomic DNA from each strain was isolated from overnight cultures using the Paratyphi B (dT+) and Heidelberg strains from the Colombian poultry chain. Genome Announce 3(5):e01265-15. doi:10.1128/genomeA.01265-15.

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Salmonella enterica is a pathogen of significant public health importance that is frequently associated with foodborne illness.
[strA, aph(3')-Ia, aadA1, and strB], β-lactams (blaCMY-2, blaCTX-M-2, and blaTEM-1B), fluoroquinolones (QnrB19), sulphonamides (sul1 and sul2), tetracycline [tet(A)], and trimethoprim (dfrA1,dfrA7). Future comparative analyses will advance national surveillance programs and our understanding of genome evolution and multidrug resistance in Salmonella.

**Nucleotide sequence accession numbers.** This whole-genome shotgun project has been deposited in DDBJ/EMBL/GenBank under the accession numbers listed in Table 1. The version described in this paper is the first version. The BioProject accession is PRJNA289090.

**ACKNOWLEDGMENTS**

This research was supported by Corporación Colombiana de Investigación Agropecuaria (CORPOICA) and the Intramural Research Program of the NIH, NLM, NCBI.

The results of this research are a product of the Colombian Integrated Program for Antimicrobial Resistance Surveillance (COIPARS). This study utilized the high-performance computational capabilities of the Biowulf Linux cluster at the National Institutes of Health, Bethesda, MD.

**REFERENCES**


