

Genomic Epidemiology of *Salmonella* Infantis in Ecuador: From Poultry Farms to Human Infections



Lorena Mejía, José Luis Medina, Rosa Bayas-Rea, Carolina Satan Salazar, Fernando Villavicencio, Sonia Zapata, Jorge Matheu, Jaap A. Wagenaar, Fernando González-Candelas and Christian Vinueza-Burgos

BACKGROUND

Foodborne infections caused by *Salmonella enterica* are of primary importance worldwide. The WHO estimates that *Salmonella* causes more than 153 million illnesses, and 120,281 deaths annually. As foodstuffs can be contaminated in several parts of the food chain, a “from farm to table” approach is necessary to understand the epidemiology of *Salmonella*.

In the last years, *S. enterica* serovar Infantis has become an important emerging pathogen in many countries, often as multidrug resistant clones.

This research was aimed at describing by phenotyping methods and whole-genome sequencing, the antimicrobial resistance characteristics and genetic profiles of *Salmonella* isolates obtained from broiler farms, broiler carcasses and humans in Quito—Ecuador.

METHODOLOGY

Nov 2017 to Nov 2018

Poultry farms (n=69) - Caeca from 133 flocks

Chicken carcasses (n=335) - 125 supermarkets, 126 from small shops, and 84 from open markets

Human stool samples (n=302) - clinical samples from two health care centers

Culture, antimicrobial susceptibility testing and whole genome sequencing

Sequence data is available under **BioProject PRJEB37560**.



RESULTS

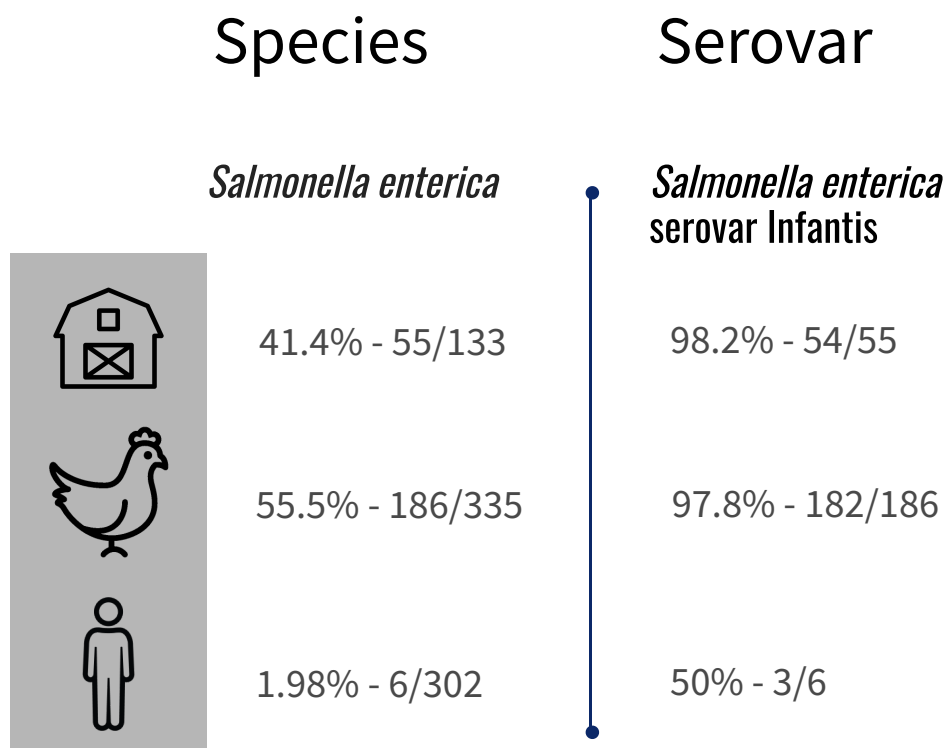


TABLE 1 | Number of *S. Infantis* isolates resistant to each tested antimicrobial.

Antimicrobial	Number (%) of resistant isolates		
	Poultry farms (farm)	Chicken carcasses (food)	Stool samples (human)
Nitrofurantoin	54 (100) ★	180 (99.4) ★	2 (66.7)
Tetracycline	54 (100) ★	176 (97.2) ★	3 (100) ★
Sulfamethoxazole + trimethoprim	44 (81.5) ★	158 (87.3) ★	1 (33.3)
Streptomycin	46 (85.2) ★	154 (85.1) ★	3 (100) ★
Gentamicin	45 (83.3) ★	155 (85.6) ★	2 (66.7)
Cefotaxime	51 (94.4) ★	150 (82.9) ★	1 (33.3)
Chloramphenicol	45 (83.3) ★	149 (82.3) ★	2 (66.7)
Ciprofloxacin	35 (64.8)	116 (64.1)	1 (33.3)
Fosfomicin	23 (42.6)	68 (37.6)	1 (33.3)
Azithromycin	10 (18.5)	31 (17.1)	0 (0)
Cefoxitin	7 (13)	11 (6.1)	0 (0)
Amoxicillin + clavulanic acid	7 (13)	7 (3.9)	0 (0)
Amikacin	0 (0)	0 (0)	1 (33.3)
Ertapenem	0 (0)	0 (0)	0 (0)

★ More than 80% of the strains are resistant

TABLE 3 | Comparison of phenotypic AMR with AMR genes obtained from WGS data.

Antibiotic family	Phenotype (%) ^a	Phenotype + AMR gene ^b (%)	No phenotype + AMR gene ^c (%)
Folate pathway inhibition	84.56	92.17	7.83
Aminoglycoside	97.06	100	3.03
Quinolone	58.09	1.27	0
Beta-lactams	84.56	94.87	4.27
Tetracycline	97.06	99.24	0.76
Phenicol	80.88	80.91	6.36
Nitrofurantoin	98.53	0	0
Macrolide	17.65	0	0
Fosfomicin	37.5	90.2	41.18

^aRate of isolates with phenotypic resistance.

^bRate of isolates with phenotypic resistance that presented a resistance gene by WGS analysis.

^cRate of isolates without phenotypic resistance that presented a resistance gene by WGS analysis.

CONCLUSIONS

- First report based on *Salmonella enterica* in Ecuador that uses phenotypic and WGS information to analyze the relatedness of strains isolated from poultry, food and human samples.
- Isolates from this study show **multidrug resistance patterns** highlighting the importance of a reduced and better usage of antimicrobials in intensive poultry farms settings.
- Presence of related megaplasmids together with the high similarity of the core genome suggest the **dissemination of *S. Infantis* through the food chain to humans**.
- The data presented here shows the importance of ***Salmonella enterica* serovar Infantis as a foodborne pathogen in Ecuador** and provides critical information about its clonality and circulating strains.

FUNDING

This project was funded by the **WHO Advisory Group on Integrated Surveillance on AMR** (AGISAR) grant AGISAR- JM/Ig and also funded by projects **BFU2017-89594R** from MICIN (Spanish Government) and **PROMETEO2016-0122** (Generalitat Valenciana, Spain). WGS was financed by the European Union through the **Operational Program of European Regional Development Fund (ERDF)** of Valencia Region (Spain) 2014–2020. LM was recipient of a predoctoral fellowship from **Fundación Carolina** and **Universidad San Francisco de Quito**.

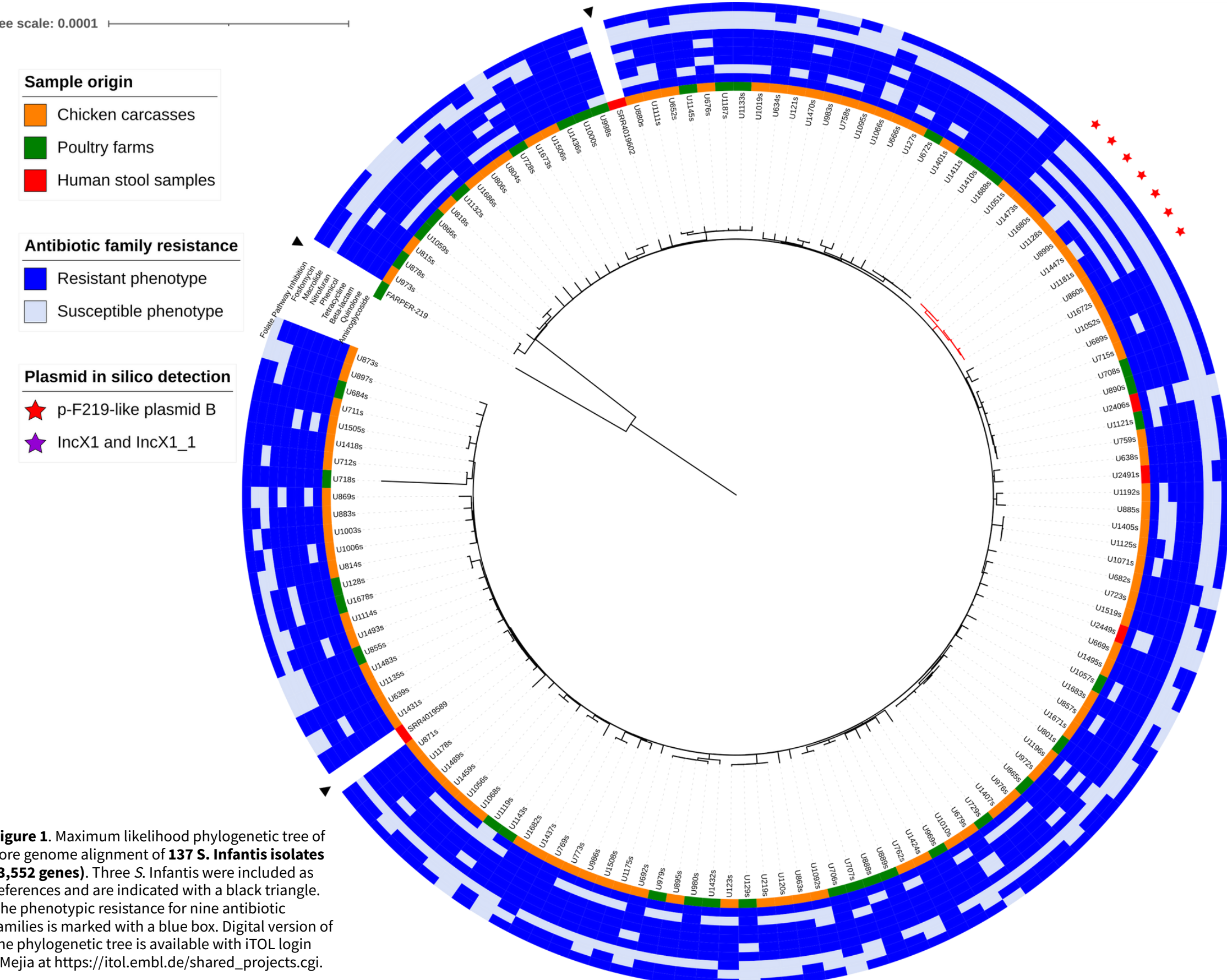


Figure 1. Maximum likelihood phylogenetic tree of core genome alignment of **137 *S. Infantis* isolates (3,552 genes)**. Three *S. Infantis* were included as references and are indicated with a black triangle. The phenotypic resistance for nine antibiotic families is marked with a blue box. Digital version of the phylogenetic tree is available with iTOL login LMejia at https://itol.embl.de/shared_projects.cgi.