

Draft Genome Sequence of *Salmonella enterica* subsp. *enterica* Serovar Gallinarum Biovar Pullorum Strain FCAV198, a Brazilian Chicken Pathogen

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***Salmonella enterica* subsp. *enterica* serovar Gallinarum biovar Pullorum is a bird-restricted pathogen which causes pullorum disease. The strain FCAV198 was isolated from a pool of chicken ovaries in Brazil, and its genome may be helpful for studies involving molecular mechanisms related to pathogenesis and other related applications.**

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Pullorum disease (PD), which is caused by *Salmonella enterica* subsp. *enterica* serovar Gallinarum biovar Pullorum, was reported worldwide in 2012, but its occurrence was especially high in Asian countries (http://www.oie.int/wahis_2/public/wahid.php/Diseaseinformation/statusdetail). PD is known as a systemic disease responsible for high mortality in young birds (1). Some of the birds that recover from infection become persistently infected and transmit *Salmonella* biovar Pullorum vertically (2). The bird restriction and aspects of PD pathogenesis, mainly the persistence of infection, are thought to be associated with gene losses (O. C. Freitas Neto, personal communication). The genome decay in *Salmonella* biovar Pullorum, caused by pseudogene accumulation, has already been observed in other *Salmonella enterica* subsp. *enterica* genomes (3–5).

Genetic variability among *Salmonella* biovar Pullorum strains has been demonstrated by use of several different molecular approaches over the past few years (6–8), highlighting the need for more genome sequencing to reveal the core genes. In addition, genomic comparisons among the closely related pathogens *Salmonella* biovar Pullorum and *Salmonella* serovar Gallinarum biovar Gallinarum could be helpful to clarify the genome evolution and molecular basis of their distinct pathogenicity and epidemiology. The *Salmonella* biovar Pullorum strain FCAV198 was isolated in Brazil from a pool of chicken ovaries in 2008. This strain was serotyped and granted by the National Agriculture and Livestock Laboratory (LANAGRO), which is the official laboratory of the Brazilian Ministry of Agriculture, Livestock and Supply and gives support to the surveillance of animal diseases.

The whole genome was sequenced using the SOLiD 4.0 sequencing system, which produced 65 million mate-paired reads of 50 bp, with insert sizes from 1,000 to 2,000 bp. *De novo* assembly was carried out using the CLC Genomics workbench 6.5.1 (CLC bio, Aarhus, Denmark) and generated 128 contigs. The draft genome sequence has a G+C content of 52.2% and a total size of

4,783,588 bp, as expected for *Salmonella* spp. (4, 5). The annotation and metabolic reconstruction were performed using the Prokka pipeline version 1.7 (Prokaryotic Genome Annotation System) and Rapid Annotations using Subsystems Technology (RAST) server (9), respectively. With these methods, 4,652 coding sequences (CDSs; with an average length of 847 bp), 65 tRNA-encoding genes, and 27 rRNA-encoding genes were predicted. It is noteworthy that the last 182,819 bp (from contigs 48 to 127) corresponds to mobile genetic elements, plasmids, and other genomic sequences which had no matches to the closely related *Salmonella* biovar Pullorum strain CDC 1983-67 (NC_022221). Some of these regions may be acquired by lateral gene transfer and encoding of potential biovar-specific traits, such as were observed in other *Enterobacteriaceae* (10, 11).

Experimental studies by *in vivo* infection indicate that the strain FCAV198 is pathogenic for chickens and shows the typical biochemical profile observed in other *Salmonella* biovar Pullorum strains (12). Furthermore, the genetic variability observed among the strains of *Salmonella* biovar Pullorum (6–8) suggests that their genomes are under different evolutive forces. Indeed, the genome sequencing approach of several different biovars could shed light on the biology of *Salmonella* biovar Pullorum and on PD disease, which is still responsible for economic losses to the poultry industry worldwide.

Nucleotide sequence accession number. The annotated draft genome sequence was deposited in DDBJ/EMBL/GenBank under accession number [AZRG000000000](https://www.ncbi.nlm.nih.gov/nuccore/AZRG000000000). The version described in this paper is the first version.

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