

Whole-genome sequencing analysis of *Salmonella enterica* serovar enteritidis isolates in Chile provides insights into possible transmission between gulls, poultry, and humans

Toro M.

Retamal P.

Ayers S.

Barreto M.

Allard M.

Brown E.W.

Gonzalez-Escalona N.

Salmonella enterica subsp. *enterica* serotype Enteritidis is a major cause of human salmonellosis worldwide; however, little is known about the genetic relationships between *S. Enteritidis* clinical strains and *S. Enteritidis* strains from other sources in Chile. We compared the whole genomes of 30 *S. Enteritidis* strains isolated from gulls, domestic chicken eggs, and humans in Chile, to investigate their phylogenetic relationships and to establish their relatedness to international strains. Core genome multilocus sequence typing (cgMLST) analysis showed that only 246/4,065 shared loci differed among these Chilean strains, separating them into two clusters (I and II), with cluster II being further divided into five subclusters. One subcluster (subcluster 2) contained strains from all surveyed sources that differed at 1 to 18 loci (of 4,065 loci) with 1 to 18 single-nucleotide polymorphisms (SNPs), suggesting interspecies transmission of *S. Enteritidis* in Chile. Moreover, clusters were formed by strains that were distant geographically, which could imply that gulls might be spreading the pathogen throughout the country. Our cg-MLST analysis, using other *S. Enteritidis* genomes available in the National Center for Biotechnology Information (NCBI) database, showed that *S. Enteritidis* strains from Chile and the United States belonged to different lineages, which suggests that *S. Enteritidis* regional markers might exist and could be used for trace-back investigations. © 2016, American Society for Microbiology. All Rights Reserved.