TITLE: HIGH SIMILARITY AND HIGH FREQUENCY OF VIRULENCE GENES AMONG *SALMONELLA* DUBLIN STRAINS ISOLATED OVER A 33-YEAR PERIOD IN BRAZIL

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ABSTRACT:
Salmonella Dublin is a strongly adapted serovar that causes enteritis and/or systemic disease in cattle with high rates of mortality in many countries. Despite the clinical and veterinary importance of this serovar, there is a lack of studies in Brazil, one of world's largest beef producers. The aims of this study were to characterize the genetic diversity of 112 *S*. Dublin strains isolated from humans and animals in Brazil between 1983 and 2016 by Multilocus Sequence Typing (MLST), Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR) and the variation CRISPR - Multilocus Virulence Sequence Typing (CRISPR-MVLST) and to determine the frequency of some important virulence genes using whole-genome assembled sequences of the strains studied. The strains studied belonged to nine different Sequence Types (ST10, ST3734, ST4030, ST4097, ST4098, ST4100, ST4101, ST4232 and ST4574), being six of these reported for the first time in the database. CRISPR discriminated the strains into 69 subtypes with a similarity ≥84.4% and CRISPR-MVLST into 72 subtypes with a similarity ≥84.7%. The virulence genes *ratB, lpfA, mgtC, avrA, sopB, sopE2, sifA, sseA, ssrA, csgA* and *sinH* were found in all the strains studied, while *spvB, spvC, sodCI, rpoS, sipA, sipD, invA* and *hilA* were detected in a frequency of ≥93.7% among those strains. In conclusion, the high genotypic similarity observed among the strains revealed by all the techniques reinforced the clonal nature of the *S.* Dublin serovar, that may have descended from a common ancestor that little differed over a 33-year period in Brazil, as previously described in other studies. MLST suggested that *S*. Dublin strains from Brazil were phylogenetically related to strains of other parts of the globe. Moreover, the high frequency of many virulence genes in the strains studied reinforced the capacity of *S*. Dublin strains to cause invasive disease in humans.

KEYWORDS: *Salmonella* Dublin, WGS, CRISPR, MLST, virulence genes

DEVELOPMENT AGENCY: FAPESP and CAPES