Title: Update of the genetic diversity of *Salmonella* Enteritidis strains isolated in Brazil: new data with old strains

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Abstract *Salmonella* Enteritidis emerged as the most frequent isolated serovar from gastroenteritis cases in many countries since the 80's. In Brazil, this upsurge was observed during the 1990s and it is believed that an epidemical and more virulent clone has been inserted in the country through the exchange of chickens with other countries. Previous studies using MLVA and strains isolated in Brazil after mid-90's showed little genetic diversity among those strains. In contrast, the only strain isolated before the 90's showed to be more genetically diverse. However, the use of only one strains isolated before the 90's in those studies may have compromised the results found. The aim of this study was to molecularly type more *S.* Enteritidis strains isolated in Brazil before 1990 and compare them to strains previously typed and isolated in this country after this period. For this, 22 *S.* Enteritidis strains isolated between 1968 and 1990 in Brazil were typed by PFGE using the protocol described by the Pulsenet using the enzyme *XbaI*. Moreover, we also typed four strains isolated in 1993, one strain isolated in 2012 and two isolated in 2013 in order to update our previous studies that typed strains isolated between 1986 and 2010, totaling 217 strains isolated over a 48-year period in Brazil. PFGE divided the strains in two main clusters named A and B. Cluster A grouped 12 strains isolated between 1968 and 1988 with a similarity above 57.1%. Cluster B grouped 205 strains isolated between 1989 and 2013 with 58.3% of similarity. The similarity between the two clusters was of 47.8%. The results showed that strains isolated before 90's and, consequently, before the pandemic period, differ genetically of strains isolated after this period. Moreover, these data suggest the introduction of a new and prevalent subtype of *S.* Enteritidis in Brazil after the 90's.

Keywords Salmonelose, *Salmonella* Enteritidis, Pandemic, Molecular typing, PFGE.

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