Genomic traits of a strain of Salmonella Heidelberg isolated in broilers in Brazil and related phenotypic tolerance to organic acids and antibiotics.

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Salmonella enterica serovar Heidelberg (SH) is found in broilers worldwide with isolates from Brazil (SHBR) increased since 2011 and showing greater tolerance to control measures. A previous trial showed that a probiotic composed of 3 Bacillus subtilis strains was effective vs. SHBR in broilers. Herein, we aimed at sequencing the genome of SHBR and relate genomic differences with SHBR tolerance to some organic acids (OA), antibiotics (AB); and clinical signs in broilers. Two trials used 1d old chicks housed for 21d in 8 sterilized isolated negative pressure rooms with 4 battery cages (reps) of 12 birds each. In both trials, birds were challenged or not with 107 cfu/bird of SHBR orally, and exposed, or not, to OA in a factorial 2x2 design. Challenge to SHBR occurred at 1 or 7d of age; and OA tested consisted of either formic + propionic acids in drinking water at 0.05% from 1 to 7d and 15–21d; or calcium butyrate fed at 2kg/ton of feed from 1 to 21d in trial 1 or 2, respectively. Nine AB were titrated in an in vitro MIC model using Mueller-Hinton agar as in CLSI[PM1] /NCCLS guidelines, to test SHBR-AB tolerance. SHBR DNA was sent to the High Throughput Sequencing Facility (University of North Carolina). The library was prepared using PacBio 20Kb template prep protocol PN_100–286–000–06, a size-selected range of 8000bp - 50,000bp, and the PacBio native pipeline for De novo assembly. The genome was deposited at NCBI genome database (No. CP020101) and compared with SH SL476 strain. Performance and immune response traits were unaffected by SHBR ($P > 0.05$). The use of OA did not reduce Salmonella counts found in cecum and liver of challenged birds ($P > 0.05$). SHBR was susceptible to amoxicillin-clavulanic acid, cephalosporin, ciprofloxacin, enrofloxacin, penicilin and trimethoprim-sulfamethoxazole and tetracyclin with mild resistance to gentamycin and ceftiofur. Several DNA fragments were missing in the SHBR genome which were associated with the codification of proteins involved with cell cycle regulation, virulence, drug resistance, cell adhesion, salt efflux, and various transposases and integrases that may relate to those deletions. These genomic findings relate to the phenotypic observations of low pathogenicity, OA tolerance and AB susceptibility of SHBR.

Key Words: Brazilian Salmonella Heidelberg, antibiotics, organic acids, resistance, comparative genomics