Characterization of *Salmonella* spp. serotypes isolated from Colombian pig farms.

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Introduction

Salmonella spp., is a zoonotic pathogen that causes salmonellosis in humans and other animals, associated with foodborne diseases and waterborne diseases. Foods of animal origin, including pork, are associated with food outbreaks caused by this bacterium. Infection of pigs often leads to meat contamination, for this reason it is important to reduce the infection burden from primary production to have a positive impact on human health with fewer cases of salmonellosis and thus reduce hospitalization and medicines costs that affect the public health systems of the countries, in addition to the economic impact that it represents for the pig chain. In pig farms, the entry of Salmonella into farms can occur through contaminated water or by the presence of other natural reservoirs such as rodents, birds, and insects, among others, in addition to contaminated feed and even from humans with contaminated work implements. In animals, infection can occur at any stage of the production cycle, affecting their welfare, health and representing a negative impact on production rates, as they are low weight animals with low feed conversion rates. Pigs has been described as the main reservoir of *Salmonella* Typhimurium and in recent decades the emergence of the serotype *S.* Typhimurium monophasic variant, having a high impact on public health due to its resistance to antimicrobials. In addition, serovars such as *S.* Typhisuis and *S.* Choleraesuis cause systemic disease in the animal affecting zootechnical parameters such as reduction in growth rate. On the other hand, serovars like *S.* Infantis, *S.* Agona, *S.* Anatum, *S.* Enteritidis and *S.* Heidelberg can be found in pigs, for this reason it is important to know the serovars that are circulating in Colombia, since there are no updated epidemiological records in pig farms, therefore, the aim of this study was to determine the circulating serovars in Colombian pig farms and establish their association with the type of sample.

Materials and Methods

To determine the prevalence of *Salmonella* spp. and circulating serovars, a stratified and proportional sampling of different water sources and rectal swabs was performed in 103 pig farms distributed in 26 Colombian departments. Between September and December 2020, 104 individual samples of catchment water, 103

of tank water, 103 of drinkers and 1025 individual rectal swab samples corresponding to 10 samples were obtained for each farm. The water samples were processed following the protocol A.P.H.A 9260-B and for the detection/identification of *Salmonella* spp., the Molecular Detection System 3M-MDS Salmonella-2® was used, the rectal swab samples were analyzed following the protocol of the ISO 6579:2017 standard; the isolates strains were serotyped following the Kauffmann-White-Le Minor classification scheme and were sequenced using Illumina® technology, once the genome assembly was done, bioinformatics tools were used to confirm serotypes by SISTR and PathogenWatch.

Results

The total number of samples collected and processed for rectal swab was 1025 and for water was 310; determining a total prevalence of *Salmonella* spp. of 9,9% (132/1329), the prevalence from rectal swab was 6,4% (66/1025) and in water 21,3% (66/310). The serotyping by the Kauffmann-White-Le Minor scheme performed to the 132 strains, showed a diversity of 40 serovars belonging to the different somatic groups, being *S*. Typhimurium var. monophasic (1,4,5,12:i:-) the predominant serovar in both water (15% (10/66)) and rectal swab (66% (44/66)) samples. Whole genome sequencing was performed on 119 strains of the 132 isolated strains, confirming that the predominant serovar was *S*. Typhimurium.var. monophasic, being 12,5% (7/56) in water and in rectal swab 69,8% (44/63). The total number of serovars found was 31, including *S*. Schwarzengrund (4,2%), *S*. Saintpaul (4,2%), *S*. Soahanina (3,4%), *S*. Derby (2,5%) and *S*. Anatum (2,5%) among others. The percentage of coincidence between Kauffmann-White-Le Minor serotyping and whole genome sequencing was 61,3% (73/119).