Determination of the prevalence of *Salmonella* spp. in three Colombian pig abattoirs

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Background

Salmonella spp. is one of the most important microorganisms in the pig industry, as well as in public health worldwide. This bacterium is responsible for causing salmonellosis, a foodborne disease, where pork is one of the main sources of infection. Pigs can be asymptomatic or symptomatic carriers of *Salmonella* spp. and can be infected from the farm and reach the abattoirs, where the carcasses can be contaminated; due to the complexity of the slaughter stages it is necessary to know how the pathogen behaves throughout this process, since the reports of the experts of the Committee for Safety Risk Assessment of the Food and Agriculture Organization of the United Nations (FAO) and the World Health Organization (WHO), have established that the reduction of *Salmonella* spp. at this stage of the production chain decreases cases of human salmonellosis. In Colombia, prevalence of *Salmonella* spp. has been reported, between 11% and 16% in pig carcasses. The aim of this study was to determine prevalence of *Salmonella* spp. in five stages of the pig slaughter process in three Colombian abattoirs.

Materials and Methods

To carry out this study, three pig abattoirs were selected, one in Bogotá (abattoir A) (handles the largest slaughter in the country (1500 animals per day)), another in the department of Meta (abattoir B) (highest level of technology in the country (1400 animals per day)) and the third in the department of Antioquia (handles the largest slaughter in the region (1400 animals per day)). Nine (9) samplings were performed (three in each abattoir), where carcass samples were taken by the sponge method (non-destructive method) according to the international standard ISO 17604:2015, in the stages of scalding, polish, gutting, decontamination and cooling (stage in each abattoir, 30 samples were taken and in cooling 60

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samples were taken, due to the difficult recovery of the microorganism after being exposed to disinfectants and low temperatures), in total, 540 samples of carcasses were processed and for the identification of *Salmonella* spp. was used the 3M-MDS Molecular Detection System. For the statistical analysis of the presence of *Salmonella* spp. analysis of variance and chi-square test were performed. The strains obtained were isolated, purified and identified by Maldi-TOF, serotyping was carried out by the Kauffmann-White scheme and whole genome sequencing (WGS) on the HiSeq platform of Illumina, Inc and its subsequent bioinformatic analysis for confirmation of the serotype through tools such as Pathogen Watch, SISTR, SeqSero 1.2.

Results

According to the microbiological mapping performed in abattoir A, prevalence of 56,7%, 36,7%, 43,3%, 53,6% and 16,7% were obtained in the stages of scalding, polish, gutting, decontamination and cooling, respectively, so there are statistically significant differences ($p < 0.05$) in the prevalence of *Salmonella* spp. in the analyzed stages. According to the genome sequencing of the strains obtained the predominant serotype in abattoir A was *S*. Typhimurium var. monophasic 1,4,[5],12:i:- (100%).

For the microbiological mapping performed in abattoir B, values of 46,7%, 26,7%, 16,7%, 6,7% and 0% were obtained in the stages of scalding, polish, gutting, decontamination and cooling, respectively, so there are statistically significant differences ($p < 0.05$) for the prevalence of *Salmonella* spp. between the analyzed stages, indicating that this abattoir, compared to the others, has an effective process for control and reduction of *Salmonella* spp., associated with the standardization of the process. According to the result of the genome sequencing of the strains the predominant serotype was *S*. Muenchen (67.6%). And in abattoir C, values of 20%, 6,7%, 13,3%, 0% and 1,7% were obtained for the prevalence of *Salmonella* spp. in the stages of scalding, polish, gutting, decontamination and cooling, respectively, with statistically significant differences ($p < 0.05$) between the different analyzed stages for the prevalence of *Salmonella* spp. According to the genome sequencing the predominant serotypes in this abattoir were, *S*. Panama (40%) and *S*. Uganda (40%).

Conclusions

Based on the results obtained in this study, the prevalence of *Salmonella* spp. is reduced or eliminated after the carcass cooling process. Taking this into account, in abattoir A the carcasses end with a prevalence of 16,7%, in abattoir B the prevalence ends at 0% being the abattoir with the best process for the control of *Salmonella* spp., and in abattoir C the carcasses end with a prevalence of 1,7%; showing that the combination of decontamination and cooling of the carcasses helps to reduce the prevalence of *Salmonella* spp. The serotypes of *Salmonella* spp. found in greater proportion in the three abattoirs were *S*. Typhimurium var. monophasic (1,4,[5],12:i:-), *S*. Muenchen, *S.* Panama and S. Uganda.