A quantitative approach towards a better understanding of the dynamics of Salmonella spp. in a pork slaughter-line. - DTU Orbit (18/12/2018)

Pork contributes significantly to the public health disease burden caused by Salmonella infections. During the slaughter process pig carcasses can become contaminated with Salmonella. Contamination at the slaughterline is initiated by pigs carrying Salmonella on their skin or in their faeces. Another contamination route could be resident flora present on the slaughter equipment. To unravel the contribution of these two potential sources of Salmonella a quantitative study was conducted. Process equipment (belly openers and carcass splitters), faeces and carcasses (skin and cutting surfaces) along the slaughter-line were sampled at 11 sampling days spanning a period of 4 months. Most samples taken directly after killing were positive for Salmonella. On 96.6% of the skin samples Salmonella was identified, whereas a lower number of animals tested positive in their rectum (62.5%). The prevalence of Salmonella clearly declined on the carcasses at the re-work station, either on the cut section or on the skin of the carcass or both (35.9%). Throughout the sampling period of the slaughter-line the total number of Salmonella per animal was almost 2log lower at the re-work station in comparison to directly after slaughter. Seven different serovars were identified during the study with S. Derby (41%) and S. Typhimurium (29%) as the most prominent types. A recurring S. Rissen contamination of one of the carcass splitters indicated the presence of an endemic ‘house flora’ in the slaughterhouse studied. On many instances several serotypes per individual sample were found. The enumeration of Salmonella and the genotyping data gave unique insight in the dynamics of transmission of this pathogen in a slaughter-line. The data of the presented study support the hypothesis that resident flora on slaughter equipment was a relevant source for contamination of pork.

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