



Evolution of *Salmonella* excretion by sows during gestation in link with the faecal microbiome

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Abstract

Pork meat is estimated to be responsible of 10 to 20% of human salmonellosis cases. Control strategies at the farm could reduce contamination at the slaughterhouse. One of the targeted sector of the production is the maternity, where sows could be *Salmonella* reservoirs. The aim of this study was to characterize the faecal microbiome of sows excreting or not *Salmonella* during gestation phases. A total of 76 sows were selected and fecal matters were analysed at the beginning or the end of gestation period. *Salmonella* detection was conducted using a method including two selective enrichment media (MSRV and TBG). Nine (9) isolates per positive samples were collected. Among the 76 sows tested, 31 were shedding *Salmonella*. The sows in the first third of their gestation shed significantly more frequently *Salmonella* (22/29) than those in the last third (9/47) ($\chi^2 P < 0.05$). The shedding status of 19 of the sows that were previously sampled in the first third of their gestation was followed, this time in the last third, confirming reduction of the shedding. Association between changes in the intestinal microbiome and this evolution of *Salmonella* shedding will be explored. MiSeq sequencing is currently being conducted on the feces to identify shifts in the composition or diversity in the microbial community that could be associated to these variations. A large number of *Salmonella* isolates that were collected were genotyped by a high resolution melt (HRM) technique. These results showed the presence of a major HRM profile (136 isolates / 169) and two minor profiles (24 and 9 / 169).