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Evolution of the faecal microbiome of the sow during the gestation and its impact on *Salmonella* excretion

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Pork meat is estimated to be responsible of 10 to 20% of human salmonellosis cases. Control strategies at the farm could contribute to 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 at the end of gestation period. *Salmonella* detection was conducted. 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) (χ^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. The association between changes in the intestinal microbiome during time and the evolution of *Salmonella* shedding has been explored. MiSeq sequencing has been conducted on the feces of 46 sows to identify shifts in the composition or diversity in the microbial community that could be associated to these variations. The v3-4 rDNA of the bacterial and archaeal populations were targeted. A mean of 123 X 10^3 hits per sample was obtained and 289 bacterial and 15 archaeal genera or higher taxonomic rank were represented. Significant changes of composition of the microbiota were detected between sow at the beginning and the end of gestation (weighted and unweighted unifrac $p < 0.05$) but also between *Salmonella* positive and negative sows (weighted unifrac $p < 0.05$). On the taxonomic level three populations (*Rothia*,

Clostridium XIVa, Planctomycetia) were significantly associated with the beginning of the gestation and the presence of *Salmonella* and one population (*Ruminococcus*) was associated with the end of the gestation and the absence of *Salmonella*. Thus the stimulation of the *Ruminococcus* genus by feed additives could be interesting in the fight against *Salmonella*.