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Présentation par affiche (poster)

To be or not to be *Salmonella* positive? That is the question we ask the pig's microbiota

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Many studies have investigated ways to eliminate *Salmonella* from pig production by alternative methods to the use of antibiotics. While some treatments do reduce *Salmonella* shedding, they also modify the rest of the fecal microbiota. The question is: Are these changes in the gut microbiota the cause or the consequence of the reduction of *Salmonella* shedding? It then becomes of interest to investigate the gut microbiota before the beginning of these treatments. To do so, the fecal microbiota of 96 pigs was investigated before the beginning of a diet presentation challenge to control *Salmonella*. Over the 21 days of treatment, the pigs could be either negative or positive at the beginning, and either negative or positive at end (day 21) of treatment, splitting them in 4 groups: (-,-), (-,+), (+,-), (+,+). The microbiota of pigs from the (-,-) and (-,+) groups were compared, as were the ones from the (+,-) and the (+,+) groups. Although some genus tended (0,05>p>0,005) to be different in these two comparisons (i.e. Roseburia, Schwartzia, Aeromonas, *Enterococcus*, *Lactococcus*, and others), one in particular was significantly different (p<0,005) for each comparison: *Propionibacteriaceae,* a family of bacteria known to produce propionic acid. *Propionibacteriacea* were in greater number in the (-,+) pigs compared with the (-,-), and bacteria from the *Sutterella* genus (linked to chronic and/or severe diarrhea in dogs and to kids with autism syndrome) were more represented in the (+,+) pigs compared with the (+,-) group. While small-chain fatty-acid (such as propionate) are often linked to control of potential pathogens, it must not be forgotten that this effect is strain-dependent and that some *Salmonella* Typhimurium strains have been proven to be able to use propionic acid as a source of energy. Further analyses will permit us to establish links with the long term fate of these groups of the microbiota and even with the impact of the feed presentation.