Healthy weaner pigs on a farm in Germany. Photo: Henk Riswick

Tylosin administration in post-weaning pigs

The weaning period is a crucial time period in the life of pigs, as the gut microbial composition is still developing. The abrupt separation of the pigs from the sow can contribute to intestinal dysfunctions. A stable gut microbiome development is instrumental for maintaining piglet health.

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Piglets are frequently exposed to antibiotics early in life, to treat outbreaks of intestinal and respiratory diseases, thus it is important to understand how antibiotic administration affects intestinal microbiota.

Gut microbiome development in pigs

The microbiota diversity changes before and after weaning in healthy piglets. The major factor influencing the shifts in the microbiota in piglets at weaning is the transitioning from sow milk to solid feed with complex nutrients. Studies have shown that on bacteria family level relative abundances of Bacteroidaceae and Enterobacteriaceae decline, while over time those of Prevotellaceae, Ruminococcaceae, Lachnospiraceae, Succinivibrionaceae increase in weaned piglets.

Antibiotic use and effect on microbiota

Antibiotics are a critical tool for fighting bacterial infection in veterinary medicine. Pigs are post-weaning highly susceptible to a number of enteric diseases (*colibacillosis*, *ileitis*, *colitis*, *Cl.perfringens* infections). Practices that maintain the ability to treat animals but limit the disturbance to the gastrointestinal microbiota are an important component of antibiotic stewardship.

In the study below, the effect of tylosin (Pharmasin) water medication at treatment dose (5mg/kg bodyweight, 7-day treatment D0-D6) on the microbiome composition in healthy weaned pigs was investigated. Faecal samples were collected from non-medicated pigs (control) and from pigs prior (D0) and after (D3, D7, D14, D21, D28, D35, D42) tylosin treatment. All samples were analysed with 16S rRNA metataxonomics, to identify bacterial composition and diversity.

Bacterial profiles of tylosin-treated pigs differ from non-medicated pigs. Abundance levels of Prevotellacceae, Ruminococcaceae, Lachnospiraceae and Succivibrionaceae were constantly higher in tylosin-medicated pigs versus the control group (see *Figure 1*). Higher abundances of Prevotellacceae, Ruminococcaceae, Lachnospiraceae and Succivibrionaceae bacteria in the tylosin group are in line with the shift of the microbial composition observed post-weaning and linked to a carbohydrate fermenting microbiota. The decrease in Bacteroidaceae, Peptostreptococcaceae and Clostridiaceae bacteria abundances (see *Figure 2*) further confirms this microbiota shift post-weaning.

Stable and balanced gut microbiome

Treatment with tylosin does not negatively affect the physiological microbiota maturation post-weaning. Tylosin (Pharmasin) even seems to have a positive effect on the gut microbiota homeostasis and stabilisation of the intestinal microbial community.

Figure 1 – Abundances (in %) of *Prevotellaceae, Lachnospiraceae, Ruminococcaceae* and *Succivibrionaceae* in the tylosin and control groups.

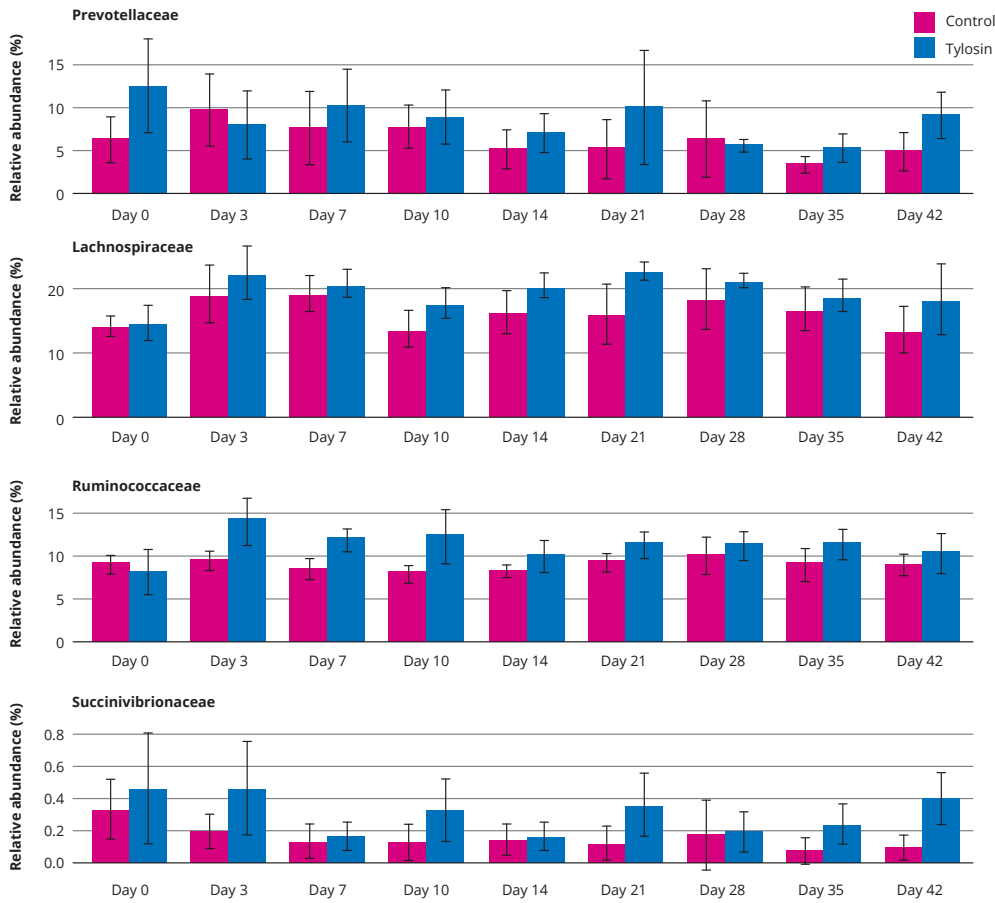

Figure 2 – Abundances (in %) of *Bacteroidaceae*, *Clostridiaceae* and *Peptostreptococcaceae* in the tylosin and control groups.