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Factors Affecting the Bacterial Community in Pigs' Digestive Systems

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Abstract

Because microorganisms play such an important role in physiological processes, immunity, and nutrition utilization by the macroorganism, a thorough study of the dynamic distribution of the gut microbiota in pigs is crucial. Inflammation, oxidative stress, and a cytokine storm may result from changes to the gut flora. Short-term (environmental, dietary, and stress) or long-term (genetics) variables may all contribute to a dysfunctional gut flora. The intestine's microbiome plays a crucial role in the pig's health and well-being, from feeding to immunity. However, the qualitative and quantitative determination of the composition and function of a healthy microbial ecosystem that may be exploited to optimize animal health and performance is still lacking. The capacity of the gut microbiota to enhance disease resistance must be acknowledged while attempts are made to decrease the usage of antibiotics in pig farming. *Bacteroides*, *Escherichia*, *Clostridium*, *Lactobacillus*, *Fusobacterium*, and *Prevotella* are the most common types of bacteria found in pigs before they are weaned. After piglets are weaned, the genera *Prevotella* and *Aneriacter* predominate, whereas *Fusobacterium*, *Lactobacillus*, and Miscellaneous are much less common. More than 90% of pigs and three enterotypes - found in animals of the same species but different ages - may be tested positive for the presence of certain genera of bacteria. This indicates that healthy pigs have a microbial "core" in their digestive systems, which might be a target for dietary or health management. In order to evaluate and enhance the performance and health condition of pigs at various phases of development, scientists collect data to identify the "optimal" gut microbial makeup. Despite the fact that external and stochastic variables contribute to the uniqueness of the microbiota, the basic principles controlling how environmental factors and host genetic factors interact to build this complex ecosystem remain mostly understood and need systematic research.

Keywords: pigs, intestinal microbiota, gut, bacteria, microflora composition, health.

1. Introduction

Pigs, like humans, have a GIT teeming with bacteria that are crucial to immune function, physiological activities, and nutrition metabolism. Diet, age, stress, and environment all have a role in shaping the composition and function of the gut microbiome (Benson et al., 2010). This creates what is known as "cross-talk" between the gut microbiota and the macroorganism (Wylensek et al., 2020), which may have direct or indirect effects on the host's metabolism, immunological response, and intestinal homeostasis (David et al., 2014; Zhang et al., 2017). Although the microbiota in the gut has been researched extensively in humans because of its importance as a metabolic "organ," less attention has been paid to the bacteria that live in the pig's

digestive system. Studies like the one conducted by Fohse J. M., Zijlstra R. T., and Willing B. P. (2016), which focused on a collection of cultured bacteria from the porcine gastrointestinal tract, showed that this microbiota is more complex than previously thought. That's why it's important to go further into this topic.

The study's overarching objective was to investigate the ways in which different variables (such as pigs' ages, the number of days since they were weaned, the diet they were fed, etc.) affect the make-up of their gut microbiota.

Scientific articles written by other scientists were mined for information.

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2. Results and discussion

2.1 Results

Age is an essential factor contributing to the maturation of the intestinal microbiota (Kim et al., 2012; Lin et al., 2018). The diversity of microbes in the gastrointestinal tract of pigs changes over time (Soler et al., 2018), and it can be assumed that the dynamic distribution of intestinal microbiota in pigs is represented along the longitudinal age axis (Li et al., 2017). Newborn animals have a critical period during which microbial colonization occurs when the microbiota structure is unstable and sensitive to environmental conditions. There is growing evidence that early colonization of “appropriate” microorganisms can determine gut microbial composition and immunological maturation (Liang et al., 2018). Microbes are believed not to colonize the gastrointestinal tract of piglets before birth. However, bacterial populations immediately enter the gastrointestinal tract immediately after the animal is born. This process is mainly influenced by the sow (Slifkiewicz et al., 2015), colostrum (Li et al., 2020), skin and feces, etc. Therefore, the fecal microbial community of suckling piglets is similar to that of their mother (Huang et al., 2019). Recent studies show that the early establishment of a stable gut microbiome plays a fundamental role in the development of the physiological function of the gastrointestinal tract and the maturation of the innate immune system after weaning, which directly affects the growth performance of growing and finishing pigs (Mu et al., 2017).

The development of intestinal microbiota in piglets is gradual and consistent (Li et al., 2020). In the first week after birth, *Bacteroides*, *Escherichia*, and *Clostridium* are the three most common genera of microorganisms. A marked shift from *Bacteroides* to *Prevotella* was observed as piglets aged/grew (Huang et al., 2019). Just two weeks after birth, *Prevotella* becomes the third dominant genus in the gut of piglets and increases to become the most abundant genus at weaning (21 days). In modern pig farming, piglets receive commercial feed 3–5 days after birth. The transition from the sow to solid feed helps to form the microbiota of the gastrointestinal tract of piglets.

Prevotella is associated with increased long-term carbohydrate intake (Kaevska et al., 2016) and can metabolize complex dietary polysaccharides (Liu et al., 2017). In solid feed consumption, bacteria such as *Prevotella* gradually take a dominant position. In addition, other genera such as *Blautia* (Mu et al., 2017; Liang et al., 2018), *Paraprevotella*, *Oscillibacter*, *Roseburia*, *Ruminococcus*, *Oscillospira*, *Co-prococcus*, *Faecalibacterium* and *Treponema* (Kaevska et al., 2016; Liang et al., 2018)

increase in large quantities in the intestines of piglets in the period from birth to weaning. However, such genera of microorganisms as *Bacteroides* (Kaevska et al., 2016; Liang et al., 2018), *Parabacteroides* (Zhang et al., 2016), *Fusobacterium* (Kaevska et al., 2016; Mu et al., 2017; Liang et al., 2018), *Lactobacillus* (Looft et al., 2014), *Anaerotruncus* (Liang et al., 2018), *Butyrivibrio* (Liang et al., 2018), *Streptococcus* (Kaevska et al., 2016; Liang et al., 2018), *Clostridium* and *Escherichia* – decrease (Kaevska et al., 2016).

As pigs grow, the diversity and richness of microbiota in the intestines increase. According to a large number of studies, *Prevotella* spp. are the most common bacteria in the gastrointestinal tract of pigs at the age of 28 to 91 days, but their number decreases at the age of 91 to 154 days (Looft et al., 2014; Li et al., 2017) – the proportion of bacteria *Anaerobacter* spp. increases when pigs grow, becoming the most common type of bacteria in the GIT at 154 days (Looft et al., 2014). Over time, other bacteria such as *Lactobacillus*, *Fusobacterium*, *Oscillospira*, *Escherichia*, *Roseburia*, *Faecalibacterium*, and *Bacteroides* are also part of the dominant microbiota in the pig gut during the growing period. During this period, feed consumption and the body weight of pigs increase sharply. At the same time, this functional composition of the intestinal microbiota can reduce the risk of infectious intestinal diseases and ensure the full realization of the growth potential of animals. Defining the “core microbiome” in the pig gut has been the focus of numerous publications (Poulsen et al., 2018), which is intriguing as it may provide new targets for medical, dietary, or therapeutic interventions. Based on mean relative abundance, microbial representatives with high abundance throughout life can be accepted as part of the “core” microbiome of the pig gut. On the other hand, microbial species that appear in pigs' gastrointestinal tract only at specific growth stages are proposed to be considered a “stage-associated” microbiome (Kaevska et al., 2016).

Although a “core” microbiota may not exist in pigs according to a strict definition, the scientists still found several types and genera of bacteria, in more than 90 % of the samples, at all stages of growth. Bacteria of the genus *Firmicutes* and *Bacteroidetes* accounted for the majority of total sequences (72.93 % in weanling piglets, 89.32 % in post-weaning piglets, 89.78 % in rearing piglets and 87.42 % in fattening piglets).

It has been established that more than 90 % of pigs contain bacteria of 19 genera, defined as “main”. Accordingly, *Bacteroides*, *Escherichia*, and



Lactobacillus predominate in weanling piglets, while *Prevotella*, *Lactobacillus*, and *Oscillospira* predominate in post-weaning piglets. In growing animals, the three most common genera are *Prevotella*, *Lactobacillus*, and *Faecalibacterium*, and in fattening animals, *Prevotella*, *Lactobacillus*, and *Streptococcus*.

These dominant bacterial taxa may be potential functional microbiota not only because of their relatively high abundance but also because of their greater frequency of contact with the host's intestinal mucosa. Further studies of these “main” microbes and their dynamic distribution, as well as the associated function, are of great importance for pig farming, as they impact the daily weight gain of animals and their physiological state (Looft et al., 2014).

Since the 1950s, antibiotics have been used as a growth factor in pigs and for therapeutic purposes. However, their effect on changing the microbial composition is variable: treatment with tiamulin and chlortetracycline for 14 days in newborns significantly increased the amount of IgA, while carbadox and oxytetracycline did not change

2.2 Discussion

Various scientists have debated the relationship between performance and gut microbiota in pigs in recent years. It has been reported that birth weight strongly affects the bacterial composition of the gastrointestinal tract of piglets from 7 to 21 days (Yu et al., 2017). In addition, a link between body weight and the microbial composition of the intestines of pigs was found. For example, the levels of *Bacteroides* (2.65 % vs. 4.54 %), *Anaerotruncus* (0.01 % vs.

0.03 %), and *Anaerococcus* (0.02 % vs. 0.01 %) were significantly different in guts with larger masses (from 16.70 to

22.75 kg) of pigs than with a smaller one (from 8.09 to

11.89 kg) (Liu et al., 2017). It was also found that the body weight of pigs at the age of 136 days is positively correlated with the number of the microbiota of the genus Firmicutes and negatively correlated with *Bacteroidetes* (Xu et al., 2016).

Increasing evidence suggests that the gut microbiota may play an essential role in regulating appetite and feeding behavior in pigs. A correlation was found between enterotypes and food consumption by animals of this species at the stage of completion of fattening (Looft et al., 2014). For example, pigs with a *Prevotella*-dominated enterotype consume more food than *Treponema*-dominated pigs (Kaevska et al., 2016). This

(Hazon, 2019). The use of antibiotics as a supplement did not cause significant changes in IgG or IgA E in fattening animals. Since 2006, the European Union has banned antibiotics as growth promoters. Furthermore, more recently, in 2018, he passed a law on reducing the prophylactic use of antibiotics. Indeed, due to the systematic use of antibiotics in animal husbandry, the problem of the development of antibiotic resistance has arisen (Fleury, 2015).

Scientist Mickaël Fleury, while studying the assessment of the effect of antibiotics on the intestinal microbiota of piglets (colistin and ceftiofur), established resistance to antibiotics that caused chromosomal mutations and changes in gene plasmids. In particular, colistin significantly reduced the population of enterobacteria but, at the same time, did not cause resistance in *E. coli*. The administration of ceftiofur to pigs affected the bacterial populations of the digestive ecosystem but, at the same time, led to the selection and diffusion of the plasmid gene encoding beta-lactamase in bacteria (Yu et al., 2017).

indicates that microorganisms of the genus *Prevotella* may be the key and a potential new target for increasing food consumption. How the gut microbiota affects appetite in pigs remains unknown, but studies in other animal models may provide valuable clues (Slifierz et al., 2015).

Various factors affect the gastrointestinal microflora. In particular, antibiotics that are currently used for therapeutic purposes. To better assess the impact and quality of antibiotic therapy on animals, international organizations publish recommendations to reduce the use of antibiotics (WOAH) and “continue monitoring the sale of antibiotics and exposure to them by creating an observatory of use within the framework of Anses-NAVAM (National Agency of Veterinary Medicine) to analyze the data on medicated feed further”, “introduce a regular survey of representative veterinarians and farmers and extend pharmaco-epidemiological studies to all sectors”. At the European level, this goal is part of an approach coordinated by the European Medicines Agency within the ESVAC (European Surveillance of Veterinary Antimicrobial Use) project. The problem of studying the effect of antibiotics on the microflora of the gastrointestinal tract of pigs and other animals still needs to be solved and relevant (Dewulf et al., 2022).



3. Conclusions

Thus, it was established that age and feeding are important factors influencing the intestinal microbiota of pigs. The most common genera of bacteria are *Bacteroides*, *Escherichia*, *Clostridium*, *Lactobacillus*, *Fusobacterium*, and *Prevotella*. These microorganisms dominate in piglets before

weaning. Over time, they change, depending on age and feeding, to the predominance of *Prevotella* and *Aneriacter*. After weaning, the genera *Fusobacterium*, *Lactobacillus*, and *Miscellaneous* are also the dominant microflora in piglets.

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