
COST Action FA1401PiGutNet

Open document on Develop a continuity concept in which the chain from sows to piglets to fattening pigs is considered and the GIT microbiota is optimized at each stage of production

It is currently widely accepted that in early life a fast and balanced settlement of the gut commensal microbiota, and its maintenance and programmed evolution, is the first requisite for the gut health along the different phases of growth.

Recent research in mice evidenced the relevance of the vertical transmission of bacteria from the mother to the new-borns. In fact, gut commensal bacterial lineages of wild mice from 17 inbred murine lines were vertically inherited for 10 generations in the laboratory¹. Conversely the transmission of pathogen bacteria tended to be horizontal¹, indicating the opportunistic behaviour of these organisms to spread around to different individuals. The relevance of natural mechanisms of vertical transmission is also clearly suggested by the difference between gut microbiota in human new-borns born with natural delivery, compared to those with caesarean delivery. This is also confirmed in pigs by the correlation between sow vaginal microbiota and the piglet microbiota². Overall, this stresses the practical relevance of reducing the risk of interference in this mechanism of adaptation, that is presumable a multifactor effect based on genetic background of the host and on acquired settlement. Thus, any measure taken on sows before or during the farrowing should be considered with this vision lens. In general, this concept is in favour of the careful use of sanitization measures. For example, a not aggressive washing of sows before the entrance into the farrowing rooms could reduce the transmission of environmental pathogens without affecting the transmission of the gut based microbiota to the new born. Conversely, trials in antibiotic-treated mice indicate that perturbation of the gut microbiota is later a favouring factor of pathogen multiplication, such as for Salmonella infection³.

In the suckling period, the milk provides a continuity base for the establishment of the gut microbiota. Some waves of microbiota development can be seen in pigs from birth to 21 – 28 days of age, with also a dependence on the intestinal site⁴. This can be also shaped by the evolution of milk composition from the colostrum phase to the full lactation milk. The systemic and gut immune history of the mother, reflected in the immunoglobulin profile of the colostrum and, for the gut component, of milk too, contributes to adapting the intestinal microbiota. Secondly, the evolution of the glycosylation from early milk secretion to the full lactation⁵ may affect the different foraging substrate of intestinal bacteria and explains the different waves of forming of the complex gut microbiota community and also their specific sugar digesting activity⁶. Also the high content of fat in milk affects the microbiota functional composition of suckling pigs (as compared to weaned)⁷. In the meanwhile, the porcine gut microbiota is starting to diverge in pigs to converge into different profiles, as indicated by the presence of at least two core microbiota structures evidenced in different pigs from currently available surveys, alternatively marked particularly by the genera *Prevotella* or *Ruminococcus*⁸. The relative importance of the genetic background and of the adaptation to environment is still matter of studies. Nevertheless, again, all this evidences the importance of gently favour the mixture of genetically and environmentally shaped adaptation mechanism. The decision of adopting the creep feed and its composition should be tuned to follow this process, helping to re-address and reroute it in case of failures and insufficiencies.

The weaning, with the removal of the constant presence of the mother, the shortage of feed substrates, the arrival of new feed chemical structures, creates a breach of this contiguity, time is required to partially restore the previous community, but data indicate that in general the connection between pre- and post-weaning is reduced⁴. However, management practices can try to minimize the gap. The frequent practice to keep the litter together in the post-weaning box is a way to consider this aim. This apparently will contrast later in the growing fattening phase with the need to feed males and females according to their different body growth natural, but the new techniques of precision feeding could contribute to solve this problem. Furthermore, this also implies that pigs of quite different weight should be kept together; again, it is possible that precision feeding tools could solve this problem. Nevertheless, there is still urgent need of more research comparing the long-term pros and cons of keeping most of the litter together all along the growing-fattening phases. This need is further confirmed by the risks that piglet stressed by mixing are lately more prone to Salmonella infection⁹.

Feeding measures can also contribute to reduce the gap between the pre- and post-weaning phase. Typically, the bovine milk whey has long been used to partially maintain the continuity with the maternal nutrition. Nevertheless, the oligosaccharide composition of bovine milk is quite different from the porcine. The provision of sources of oligosaccharides more similar to porcine composition should be considered. This in turn raises the topic of the possible variation of gut microbiota imprinted by the genetically determined variation of sugars in porcine milk. In studies on human milk oligosaccharide composition and on association with environmental factors, the genetically determined condition of secretor or not secretor mother for a specific sugar motif is considered to explain part of the variability¹⁰. Pigs present also genetic variability for blood antigen groups, associated with the ability to add a specific link to glycoproteins. Studies are under way to assess the relevance of breed on the glycosylation of colostrum, and this could in the future contribute to design more tailored post-weaning diets.

The post-weaning feed is frequently supplemented with probiotics. This can be used to attenuate the gap between the pre-weaning and the post-weaning microbiota. As an example, feeding a lactic acid bacteria (a *Lactobacillus amylovorus* strain, previously named *L. sobrius*) that is dominant in the pre-weaning pig could help to maintain its presence in the post-feeding and partially protect against the experimentally induced *E. coli* F4 infection¹¹.

Large surveys indicate that on the average the microbiota composition is maintained along the growing fattening phase up to the slaughtering, with the constant dominance of fecal bacteria belonging to *Clostridium*, *Prevotella*, *Ruminococcus*, *Bacteroides*, *Lactobacillus*, *Fusobacterium*, *Eubacterium*, *Campylobacter*, *Escherichia* genera¹². There are also some microbial traits having a moderate heritability, such as alpha diversity and OUT richness, that have higher values in the growing fattening phase, than at weaning¹². This indicates that a further stabilization is in progress with the age and that there is a family derived component.

Evidences are also available showing that the transgenerational effect on gut microbiota can extend long over the growing fattening phase, and that this can shape the productive efficiency of the pig. The interaction with the host is nevertheless very complex. In fact, the faecal transplantation from highly efficient finishing pigs to gestating sows and/or to their offspring, changed consequently the gut microbiota composition¹³, in comparison with the control sows and offspring. However, the favourable gut-associated trait, that was feed efficiency, was not transferred, indicating that the characteristic of the receiving host, compared to the donor, where not irrelevant,

On the whole, it can be stated that the concept of continuity of the gut microbiota along the productive chain, from sows to piglet to finishing pigs received an important research attention, it has a sounded basis and it is supported by data. Nevertheless more research is need to detail how this is expressed with the

varying host genetic base and to suggest the best management ways to accompany this naturally programmed development along the pig life.

Literature cited

- 1) Moeller, A. H., Suzuki, T. A., Phifer-Rixey, M., & Nachman, M. W. (2018). Transmission modes of the mammalian gut microbiota. *Science*, 362(6413), 453-457.
- 2) Maradiaga, N., Zeineldin, M., Aldridge, B., & Lowe, J. (2014). Influence of maternal microbial communities on the mucosal microbiome of neonatal pigs. *AASV*, 2014, 1-39.
- 3) Sekirov, I., Tam, N. M., Jogova, M., Robertson, M. L., Li, Y., Lupp, C., & Finlay, B. B. (2008). Antibiotic-induced perturbations of the intestinal microbiota alter host susceptibility to enteric infection. *Infection and immunity*, 76(10), 4726-4736.
- 4) De Rodas, B., Youmans, B. P., Danzeisen, J. L., Tran, H., & Johnson, T. J. (2018). Microbiome profiling of commercial pigs from farrow to finish. *Journal of animal science*, 96(5), 1778-1794.
- 5) Wei, J., Wang, Z. A., Wang, B., Jahan, M., Wang, Z., Wynn, P. C., & Du, Y. (2018). Characterization of porcine milk oligosaccharides over lactation between primiparous and multiparous female pigs. *Scientific reports*, 8(1), 4688.
- 6) Salcedo, J., Frese, S. A., Mills, D. A., & Barile, D. (2016). Characterization of porcine milk oligosaccharides during early lactation and their relation to the fecal microbiome. *Journal of dairy science*, 99(10), 7733-7743.
- 7) Motta, V. (2018). PhD Thesis.
- 8) Ramayo-Caldas, Y., Mach, N., Lepage, P., Levenez, F., Denis, C., Lemonnier, G., ... & Rogel-Gaillard, C. (2016). Phylogenetic network analysis applied to pig gut microbiota identifies an ecosystem structure linked with growth traits. *The ISME journal*, 10(12), 2973.
- 9) Callaway, T. R., Morrow, J. L., Edrington, T. S., Genovese, K. J., Dowd, S., Carroll, J., ... & Nisbet, D. J. (2006). Social stress increases fecal shedding of *Salmonella typhimurium* by early weaned piglets. *Current issues in intestinal microbiology*, 7(2), 65-72.
- 10) Azad, M. B., Robertson, B., Atakora, F., Becker, A. B., Subbarao, P., Moraes, T. J., ... & Bode, L. (2018). Human Milk Oligosaccharide Concentrations Are Associated with Multiple Fixed and Modifiable Maternal Characteristics, Environmental Factors, and Feeding Practices. *The Journal of nutrition*, 148(11), 1733-1742.
- 11) Konstantinov, S. R., Smidt, H., Akkermans, A. D., Casini, L., Trevisi, P., Mazzoni, M., ... & De Vos, W. M. (2008). Feeding of *Lactobacillus sobrius* reduces *Escherichia coli* F4 levels in the gut and promotes growth of infected piglets. *FEMS microbiology ecology*, 66(3), 599-607.
- 12) Lu, D., Tiezzi, F., Schillebeeckx, C., McNulty, N. P., Schwab, C., Shull, C., & Maltecca, C. (2018). Host contributes to longitudinal diversity of fecal microbiota in swine selected for lean growth. *Microbiome*, 6(1), 4.
- 13) McCormack, U. M., Curião, T., Wilkinson, T., Metzler-Zebeli, B. U., Reyer, H., Ryan, T., ... & Gardiner, G. E. (2018). Fecal Microbiota Transplantation in Gestating Sows and Neonatal Offspring Alters Lifetime Intestinal Microbiota and Growth in Offspring. *MSystems*, 3(3), e00134-17.