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Influence of Sow Gut Microbiota on Colostrum and Piglet Performance

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Abstract

Colostrum being the sole source of immunoglobulin and energy plays an essential role for piglet survival and growth. Studies have shown that colostrum and milk intake also influence the gut development and maturation of piglets. The early life colonization and development of the gut microbiota primes the development of the adult microbiome and has long-term impact on the health of the pigs. Growing number of evidences suggest that certain microbial species can exert beneficial effect on the sow and piglets, and thus improve production performances like colostrum yield, colostrum quality, sow physiology around farrowing, piglet weight gain, and health during lactation and weaning. The gut microbiota of pig which is unique at suckling stage, largely acquired from the mother, shifts over time. Multiple factors like age, environment, production system, diet can influence the gut microbiota of sow and piglets. The improvement of the sow and piglets microbiota toward beneficial bacteria can also be done by probiotic, prebiotic, and different feed additive applications.

Keywords

Sow · Piglets · Production performance · Colostrum · Gut microbiota

7.1 Introduction: Colostrum Importance in Pig

Colostrum is essential for piglet survival and growth by providing essential immunoglobulins, and being source of energy. Among the main causes of piglets' mortality before weaning are: lower birth weight, inadequate colostrum intake,

hypothermia, and hypoglycemia (Le Dividich et al. 2005). Newborn piglets lack globulins, relying on colostrum as the main source of antibody for the first weeks of age, until they become capable to produce it themselves (Salmon et al. 2009). The main reason is that piglets at birth don't have yet an active adaptive immune system, due to intrauterine placental barriers, therefore they are dependent on innate immune responses and passive uptake of immunoglobulins (Rooke and Bland 2002; Salmon et al. 2009). However, this passive intestinal absorption of large molecules like IgG is possible only for few hours after birth, until gut closure which occurs 24–36 h after birth (Quesnel et al. 2012). Failure of piglets to achieve an adequate intake of colostrum is the primary cause of piglet deaths occurring within the first days after birth (Quesnel et al. 2012). The concentration of IgG in the plasma of piglets shortly after birth is positively correlated with their survival and, in addition, dead piglets have lower serum IgG concentration than their surviving fellow piglets, indicating low colostrum intake (Vallet et al. 2013). There is clear evidence that colostrum and milk intake influence not only piglets' immune system, but also their gut development and maturation (Salmon et al. 2009; Turfkruyer and Verhasselt 2015). Other than immunoglobulins, colostrum contains many biologically active factors, including leukocytes, enzymes, hormones, growth factors but also bacteria (Hurley 2015; Chen et al. 2018). Some studies have found evidences that the development of the gut microbiota during early life primes the development of the adult microbiome and has long-term impacts on the health of the host (Turnbaugh et al. 2009; Han 2015). Colostrum and milk are indeed one of the largest sources of microbiota for the gut of neonate piglets. Chen et al. (2018) found that the composition and diversity of the milk microbiota changed significantly in colostrum but was relatively stable in transitional and mature milk. They found that *Corynebacterium* and *Streptococcus* were significantly higher in sow colostrum than in milk, while the other four most dominant bacterial taxa (*Lactobacillus*, two unclassified genera in the families Ruminococcaceae and Lachnospiraceae, and an unclassified genus in the order Clostridiales) had higher relative abundances in transitional and mature milk than in colostrum. Firmicutes and Proteobacteria were the most dominant phyla in sow milk (Chen et al. 2018). Another study revealed that the gut mucosa microbiota was different in high weight gain piglets and in low weight gain piglets (Morissette et al. 2018). The microbiota of high weight growth piglets had higher levels of Bacteroidetes, Bacteroides and Ruminococcaceae, and lower proportions of *Actinobacillus porcinus* and *Lactobacillus amylovorus* when compared with those of low weight growth piglets (Morissette et al. 2018). When looking to different studies' results, often the bacteria found in colostrum and milk are typical skin bacteria (like *Staphylococcus* and *Streptococcus*), indicating that the skin might be an important source of the milk microbiota (Urbaniak et al. 2016; Chen et al. 2018; Morissette et al. 2018). However, the presence of many obligate anaerobic gut-associated genera such as *Bacteroides*, *Blautia*, *Lactobacillus*, *Ruminococcus*, and *Bifidobacterium*, indicates that bacterial communities in sow milk do not solely originate from the host skin or environmental sources (Hunt et al. 2011; Jost et al. 2013; Chen et al. 2018; Morissette et al. 2018). Rodríguez (2014)

hypothesizes that milk bacterial community can originate from the maternal gastrointestinal tract through a bacterial entero-mammary pathway. The recent findings on the role of colostrum as source of energy, passive immunity, gut developing factors and bacteria for the neonate piglets, show how fundamental is the balance between sow's nutrition and health, with the environment, in relation to successful piglets' growth.

7.2 Gut Microbiota in Sow and Piglets

Pig intestine harbors a complex and diverse ecosystem of the microbial population. In a symbiotic relationship with the host, gut microbiota plays a significant role in the health and wellbeing of the pigs by providing energy, volatile fatty acids (VFA), vitamins, cellulose fermentation, immunological functions, and resistance to pathogens bacteria (Kim and Isaacson 2015; Fouhse et al. 2016; Stokes 2017; Yang et al. 2017; Guevarra et al. 2019). The gut microbiota in pigs is dynamic and varies with time, age, environments, production system, diet, and many other factors (Kubasova et al. 2017; Hasan et al. 2018; Niu et al. 2019). With the advent of the new technologies and consumer demand to produce antibiotic-free pigs, researches on this field have been continuously growing, trying to find the relationship between the gut microbiome and production performances of sow and piglets. During the last three decades, litter size has been significantly increased, and in the so-called hyper prolific sows, for example, the farrowing process can be affected by the sow gut microbiota (Hasan et al. 2018). The discussion on gut microbiota of this chapter will be on sow late gestation, farrowing and lactation, and on piglet pre-weaning stage. It is believed that gut microbiota at late pregnancy plays a significant role in the health and the production of sows, the nutrient metabolism, the immune stimulation, and the metabolic regulation. However, this is particularly important also for the piglets, as they acquire their first gut microbiota colonization from the mother and their immune system development depends on the acquisition of the microbiota and the immunoglobulins from the colostrum (Hasan et al. 2018).

The total number of the adult pig colon bacteria has been estimated to be 10^{10} – 10^{11} per gram of gut content, with an average 500–1000 diversified species living in mammalian gastrointestinal tract (Gaskins et al. 2002; Isaacson and Kim 2012). Studies have shown that certain microbial species can exert beneficial effects on the sow and piglets, thus boosting production performance like colostrum yield, improving colostrum quality and sow physiology around farrowing (Tan et al. 2016; Hasan et al. 2018; Wang et al. 2019a, b). This study by Hasan et al. (2018) also showed that young piglets have a unique microbiome acquired either from the mother directly via suckling or from the farrowing environment.

7.2.1 Sow Gut Microbiota in Late Gestation, Farrowing and Lactation

The composition of gut microbiota is not static and shifts over time. In sows, at pregnancy both diversity and abundance of certain microbial population increased with progression of the pregnancy until weaning (Ji et al. 2019). A diverse gut microbiota provides many metabolic capacities and functional redundancy in sows, which ensures the sufficient supply of nutrients for fetal growth and development (Ji et al. 2019). In a recent study carried out by Hasan et al. (2018), during farrowing, from a phyla level perspective, most gut bacteria were classified in Firmicutes, Bacteroidetes, Proteobacteria, Actinobacteria, and Candidatus. The Firmicutes represent the most abundant proportion of the total population, followed by Bacteroidetes. These two phyla accounted for approximately 98% of all bacteria present (Fig. 7.1). Another comprehensive study published by Kim et al. (2011) reported the same, being 90% of total bacteria present in the sow gut Firmicutes and Bacteroidetes were the most abundant. On the other hand, however, the findings of the study by Ji et al. (2019) reported that Bacteroidetes increased linearly with the progression of the pregnancy and represent the most dominant (45.56%) on 110 days of pregnancy. Jost et al. (2014) reported that Firmicutes exhibited no detectable changes over perinatal period. Studies have demonstrated that gestational weight gain or increase in the back-fat thickness in the sow may be associated with an increase in the abundance of Firmicutes or an increase in the Firmicutes to Bacteroidetes ratio (Feng et al. 2015; Ji et al. 2019). In terms of phyla, the abundance of Tenericutes, Fibrobacteres, and Cyanobacteria has been shown to increase with the progression of the pregnancy (Ji et al. 2019). These phyla have some beneficial effects, for example Tenericutes increase intestinal cells' integrity and Fibrobacteres were characterized as having the potential to metabolize non-soluble polysaccharides, such as cellulose, hemicellulose, or pectin (Ji et al. 2019). During

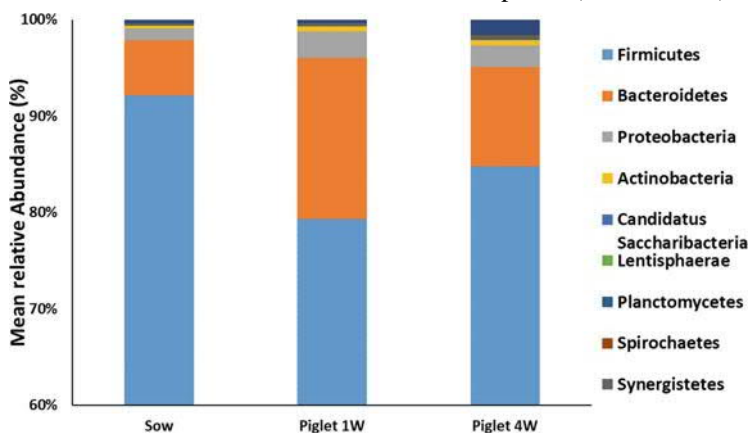


Fig. 7.1 The distribution of bacterial phyla in fecal samples of sows during farrowing, piglets 1 week (Piglet 1 W) and piglets 4 week (Piglet 4 W) ages. Figure adapted from Hasan et al. (2018)

late gestation *Romboutsia* was the dominant genus in sows which is from the phylum Firmicutes, followed by *Clostridium sensu stricto*, *Lactobacillus*, *Oscillibacter*, *Intestinimonas*, *Sporobacter*, *Christensenella*, *Barnesiella*, *Flavonifractor*, *Terrisporobacter*, *Acidaminobacter*, *Lachnospiraceae incertae sedis*, and *Turcibacter*, other genera being much less 1% (Hasan et al. 2018). In a similar study sample collected at 109 days of gestation reported that *Clostridium sensu stricto* was the most dominant genus, also from the phylum Firmicutes. In the same study the nine most abundant genera, in more than 1% of the total DNA sequences, were *Treponema*, *Lactobacillus*, *Gemmatimonas*, *Prevotella*, *Barnesiella*, *Gp7*, *Lachnospiraceae incertae sedis*, *Flavisolibacter*, and *Clostridium* cluster XI (Tan et al. 2016). However, the findings of these studies differed from those of Ji et al. (2019), who reported an overall increase in abundance of *Prevotella* linearly with the progression of pregnancy being most dominant with 14.02% of the total microbiota followed by *Lactobacillus* (6.91%).

7.2.2 Piglets Gut Microbiota in Pre- and Post-Weaning

In recent years, due to increased attention on reduction or ban of the use of antimicrobials and zinc oxide, the intestinal microbiome of piglets received a lot of attention for its essential role in the immune system development and function. Recent studies report that the suckling piglet has a unique microbiota, largely acquired from the mother (Tan et al. 2016; Li et al. 2017; Hasan et al. 2018). The piglets acquire mainly fecal microbiota from the sow, but also microbial communities present in the birth canal, on the skin of the mother and from the environment. Furthermore, the chemical and microbial composition of colostrum and milk might also influence the intestinal microbiota of the progeny (Mach et al. 2015; Chen et al. 2018).

The diversity of the piglet gut microbiota increased over time with dietary changes from sow's milk to plant based starter diet. At phyla level, in pre-weaning piglets (at 1 week and 4 week of age) Firmicutes and Bacteroidetes accounted for more than 90% of the bacteria (Hasan et al. 2018). Even though Firmicutes is the most abundant in pre-weaning piglets but over the time the proportion of Bacteroidetes increased post-weaning (Pajarillo et al. 2014a). In suckling piglets *Bacteroides*, *Balutia*, *Dorea*, *Eschericia*, *Fusobacterium* were the most abundant genus. In several reports the dominance of *Bacteroides* in suckling piglets was mentioned as it is not common in adult piglets (Pajarillo et al. 2014a; Kim and Isaacson 2015; Kubasova et al. 2017). The greater amount of the *Bacteroides* in the pre-weaned piglets could be due to their ability to utilize monosaccharides and oligosaccharides from sow's milk. In post-weaning the most predominant genus was *Prevotella*, which is in the phylum Bacteroidetes and *Lactobacillus* from the phylum Firmicutes. The genus *Prevotella* in the post-weaning piglets justifies the ability to degrade plant derived cellulose and hemicellulose by producing specific enzymes. Kim et al. (2011) mentioned that *Prevotella* represented up to 30% of all classifiable

bacteria when the pigs were 10 weeks of age. However, by the time these pigs were 22 weeks of age, *Prevotella* accounted for only 3.5–4.0% of the bacteria. As the levels of *Prevotella* decreased, there was a pronounced increase in *Anaerobacter* (in the phylum Firmicutes). In another study, Looft et al. (2012) reported on gut microbiome of 18 and 20 weeks piglet, the majority of the bacteria were classified in the phyla Bacteroidetes and Firmicutes and most predominant genera were *Prevotella*, *Anaerovibrio*, *Succinivibrio*, *Oscillibacter*, *Parabacteroides*, *Hallella*, and *Coprococcus*.

7.3 Factors Affecting Sow and Piglet Gut Microbiota

7.3.1 Environment and Housing Effect

Even though piglets get the initial colonization during the birth, the management and production conditions, the maternal environment and the environmental microbiota sources complement the development. Source Tracker analysis showed that the microbiota from the slatted floor, sow's milk, and nipple surface were most likely the earliest to pass into the neonatal gastrointestinal tract, but did not have a long permanence during lactation. The sow's fecal microbiota were the easier to colonize in newborn piglet's guts by the cooccurrence with former colonized microbial communities (Chen et al. 2017). This study suggests that microbes from the maternal and surrounding environments may play an important role in the microbial succession of newborn piglets after birth. In pig production, the cleaning procedures applied in the farrowing unit prior to entrance of the sows decrease the occurrence of environmental microbiota. PCA analysis revealed that piglets at 1 week of age have unique microbiota (Hasan et al. 2018). Many studies, however, report similar results that the suckling piglet has unique microbiota acquired from the mother. The maternal dietary treatment had an impact on the composition of the microbiota in piglets, which was distinct from the sow's fecal microbial alterations. This was also observed when feeding sows with inulin, prebiotics, or probiotics (Tan et al. 2016; Hasan et al. 2018; Li et al. 2020). Nevertheless, piglets cohabiting the same pen have similar microbiota composition differently than separated siblings, proving the environmental effects (Thompson et al. 2008). Alternative sow enriched rearing systems in deep straw bedding are getting popular in pig production, since these systems reduce stress and straw provides a non-digestible fiber source. Microbiota of sows from enriched rearing system contained significantly more *Prevotella*, *Parabacteroides*, CF231, *Phascolarctobacterium*, *Fibrobacter*, *Anaerovibrio*, and YRC22 (Kubasova et al. 2017).

7.3.2 Diet Effect

The changes in the diet can result in differences in the composition of the microbiome and in its potential functionality, which are linked with feed efficiency

in the pigs. Recent research demonstrates the importance of dietary microbial modulation. Dietary supplementation of hydrolyzed yeast (Hasan et al. 2018), resin acid-enriched composition (Hasan et al. 2019a, b), probiotics (Menegat et al. 2019), and prebiotics (Tan et al. 2016; Li et al. 2020) in sow's late gestation diet significantly changes microbial populations. Different levels and types of protein and fiber in the diet are also modulating the gut microbial population both in gestating sows and weaning piglets. Due to the various physicochemical properties of dietary fiber and its physiological effects, the supplementation of pregnancy diet with soluble fiber effectively enhances the stability of gut microbiota structure and greatly changes the composition of gut microbiota in sow (Li et al. 2020). The representative changes in the composition of gut microbiota include a decrease in Proteobacteria and an increase in Ruminococcaceae, Oscillospira, and Eubacterium. Moreover, the increase of genus Eubacterium, after dietary soluble fiber supplementation during pregnancy, promotes propionate and plasma fatty acid production, which may be one of the potential mechanisms by which dietary fiber improves insulin sensitivity and systemic inflammation in perinatal sow (Xu et al. 2020). Studies were also conducted to investigate impacts of dietary protein levels on the gut bacterial community. A moderate dietary protein restriction (13% CP) could alter the bacterial community and metabolites, promote colonization of beneficial bacteria in both ileum and colon, and improve gut barrier function (Fan et al. 2017).

7.3.3 Genetic Effect

Genetics of the pig can play a role in shaping the gut microbiota. A study conducted by Pajarillo et al. (2014b), with 15 weeks piglets from purebred pig lines Duroc, Landrace, and Yorkshire, demonstrated that Landrace breed had the most diverse bacterial community composition. Prevotella, Blautia, Oscillibacter, and Clostridium were detected in all samples regardless of breed. On the other hand, Catenibacterium, Blautia, Dialister, and Sphaerochaeta were differentially detected among breeds. These bacteria may be linked to functional genes or characteristics unique to the breeds with which they are associated. In another study by Bian et al. (2016), piglets from two different breeds Meishan and Yorkshire had bacterial taxa difference during the suckling period. Piglets from the Meishan sows had higher population of Fusobacteriaceae family with a lower abundances of Bacteroides compared to the piglet from the Yorkshire sows. Genetic factors can also determine the susceptibility of the pig to certain infection in the gut and resulting in microbial shifts. For example, enterotoxigenic *E. coli* (ETEC) expressing F4 fimbriae causes severe diarrhea in piglets carrying F4 specific intestinal receptor (Rhouma et al. 2017). Therefore, existence and function of these receptors are crucial for the susceptibility of pigs to ETEC infections.

7.3.4 Antibiotic Effect (Antibiotic Growth Promoter)

Antibiotics have been one of the most cost-effective tools to improve the feed efficiency and health of the pigs. The usage of antibiotics in pigs as growth promoters is banned in several countries, and it's becoming important because of the growing concern of antibiotic resistance of bacterial pathogens. It is likely that antibiotics enhance the growth by alteration of the composition of gastrointestinal microbiome in pigs, especially in sub-therapeutic levels. A study by Kim et al. (2012) showed that the use of tylosin shifts the microbial population in both abundant and less abundant species. In particular, *Lactobacillus*, *Sporacetigenium*, *Acetanaerobacterium*, and *Eggerthella* were detected more frequently in the group of pigs receiving the tylosin compared to the non-treated group. In another study, simultaneous administration of chlortetracycline, sulfamethazine, and penicillin for 14 days showed an increase in Proteobacteria compared to the non-medicated piglets. This shift was driven by an increase in *E. coli* population (Looft et al. 2012). Antibiotics are also frequently administered during the early life stages of piglets to control respiratory and gastrointestinal problems. This treatment may have an immediate effect on colonization of gut microbiota in piglets. In a study conducted in a commercial piggery by Hasan et al. (2019a), piglets were marked if they received antibiotic (amoxicillin or florfenicol) treatment within the first 3 days of their life and equal number of piglets were selected from non-treated nearest litters as control. Fecal samples collected at 1 week of age were assessed to check microbial composition by 16S rRNA gene sequencing. The diversity (Shannon index) and Richness were significantly lower in antibiotic treated piglets compared to the non-treated piglets. Overall, the antibiotic treatment at an early age not only decreased the relative abundance of some opportunistic pathogenic bacteria like *Campylobacter*, *Pasteurella*, but it also reduced some beneficial bacteria like *Prevotella* and *Butyricimonas*. Moreover, individual assessment of each of the antibiotic revealed that treatment at an early age in piglets significantly decreased the relative abundance of *Clostridium sensu stricto*, *Butyricimonas*, *Flavonifractor*, *Romboutsia*, *Bacteroides*, and *Roseburia*.

7.4 Improvement of Sow and Piglet Gut Microbiota

7.4.1 Probiotic and Prebiotic Concept

Probiotic and prebiotic or combination of both in swine diets stimulates the proliferation and metabolic activity of beneficial microbes, contributing to a stable microbial ecosystem. Probiotics are well-characterized bacteria, they can produce antimicrobial substances, modulate the host immune system, induce competitive exclusion of pathogenic bacteria, and modulate gut microbiota (Cammarota et al. 2014). From the perspective of probiotics in sow diets it is proposed to have a dual purpose, benefiting not only the sows but also their progeny. The probiotic application to sow's diet and the piglets' intimate maternal contact are important

determinants of gastrointestinal tract bacterial colonization in newborn piglets (Everaert et al. 2017). However, many obligate gut-associated genera in piglets such as *Bacteroides*, *Blautia*, *Lactobacillus*, *Ruminococcus*, and *Bifidobacterium* originate from sow milk (Hunt et al. 2011; Jost et al. 2013; Chen et al. 2018; Morissette et al. 2018). It has been speculated that these bacterial communities can be of maternal gastrointestinal tract through a bacterial entero-mammary pathway (Rodríguez 2014). Therefore, probiotic can have an effect on diet-driven modulation of milk bacterial population and influence the progeny intestinal microbiota during lactation. However, studies have demonstrated that provision of probiotics to sows can modify the sow fecal microbial population and carry over to progeny in pre-weaning and postweaning stages (Silva et al. 2010; Baker et al. 2013; Starke et al. 2013). *Bacillus subtilis* and *Enterococcus faecium*, a common probiotic species in sow diet during late gestation and lactation, were found to improve the population of beneficial bacteria, primarily *Lactobacillus* sp., and to reduce the population of potentially harmful bacteria, including *C. perfringens* and *Escherichia coli* (Baker et al. 2013; Starke et al. 2013). Feeding piglets with *Lactobacillus salivarius*, a commonly found probiotic, decreased the relative proportion of the bacteria from the phylum Spirochaetes with genus *Treponema*, *Anaerostipes*, and *Lactonifactor* while proportions of *Subdoligranulum*, *Oribacterium*, and *Hallella* increased (RibouletBisson et al. 2012). Several other probiotics *Lactobacillus* spp. like *Lactobacillus reuteri*, *Lactobacillus plantarum*, *Lactobacillus johnsonii* have been shown to improve piglet growth performance by regulating the gut microbiota and preventing diarrhea. Combination of probiotic and prebiotic, for example, lactulose with *Enterococcus faecium* NCIMB 11181 increases the relative proportion of *Lactobacillus* in the post-wean piglets (Chae et al. 2016). Prebiotics, for example, inulin, fructo-oligosaccharides, transgalacto-oligosaccharides, and lactulose are readily available fermentable source for the beneficial gut microbiota and protect the gut by lowering the pH and ensuring the cecal and colonic butyrate concentration (Fouhse et al. 2016).

7.4.2 Feeding Methods (Feed Additives Application)

Feeding sows with alternative compounds is a common practice in modern sow production with the hypothesis that feed additives are able to modulate gut microbiota of sow and piglets, improving their production performances and health. Although dietary components like fat, protein, and carbohydrate are explored for their impact on gut microbiota, however, to date, little attention has been paid to the studies related to supplementation of gestating sow diets with specific compounds, consequent gut microbiota modulation and their effect on sow and piglet performances. Sow and piglet feeding strategies mostly include functional fibers, yeast fractions and derivatives, essential oils, organic acids, medium chain and short chain fatty acids at different stages of productions. The mode of action of these feed ingredients relies on their ability to modify favorably the microbiota of the gut, which is of importance for sow's health and consequently piglets' health. Beneficial

bacteria can act as a barrier against pathogenic bacteria, having the ability to lower the pH of the gastrointestinal tract and produce antimicrobial compounds (Lallès et al. 2009). Microbiota fermenting indigestible carbohydrates produce short chain fatty acids (SCFA) that are an important energy source for the sow. Butyrate, in particular, is a gut health-promoting compound that acts as the main energy source for colonocytes and exerts anti-inflammatory properties (Sassone-Corsi and Raffatellu 2015). It is thus of interest to modify favorably the microbiota toward fermentative butyrate-producing and anti-pathogenic bacteria. Studies show that the reduction in the number of pathogenic bacteria in response to dietary supplementation is associated with an increase in beneficial microbiota, which in turn may modify the substrate availability and physiological conditions of the gastrointestinal tract (e.g., fermentation products, luminal pH, and bile acid concentration) (Liu et al. 2008). In a study, dietary supplementation of yeast hydrolysate in the pregnancy influences beneficial and fermentative bacteria (Roseburia, Paraprevotella, Eubacterium), while some opportunistic pathogens, including Proteobacteria, especially the genera *Desulfovibrio*, *Escherichia/Shigella*, and *Helicobacter*, were suppressed. In the same study, piglets at 1 week of age from sows fed the yeast product had more beneficial microbial populations with significant diversity and fewer opportunistic pathogens (Hasan et al. 2018). Yeast hydrolysate can bind and inhibit pathogen bacteria like *Salmonella* spp., *Clostridium* spp., and *Escherichia coli*, thereby promoting growth of beneficial gut bacteria, better utilization of feed nutrients, and reduced spread of pathogens to piglets (White et al. 2002; Burkey et al. 2004; Castillo et al. 2008; Liu et al. 2008). In another study, resin acid-enriched composition (RAC) has been used in feed as a novel additive to improve performance in sow (Hasan et al. 2019b). RAC, a novel dietary product, typically comprises resin acids (RA) (~8%) and free fatty acids (~90%), and 2 to 3% neutral components naturally occurring in coniferous trees. RAC modulates the microbial population in the small intestine, changes the microbial digestion, and improves the feed conversion ratio and gut microbiota in monogastric species (Kettunen et al. 2017; Vienola et al. 2018; Hasan et al. 2019b). Feeding RAC in late gestation significantly increased Firmicutes, and conversely Bacteroidetes and Proteobacteria were less abundant. RAC in sow diet increases the abundances of genus *Romboutsia* and *Clostridium sensu stricto* and decreases the abundances of *Barnesiella*, *Sporobacter*, *Intestinimonas*, and *Campylobacter* (Hasan et al. 2019b).

7.5 Sow Gut Microbiota Influence on Production

Understanding the sow gut microbiota in the modern swine production is of interest as it is an important issue in improving feed efficiency, reducing oxidative stress, it helps in farrowing, and colonizing microbes to neonates (Hasan et al. 2018; Wang et al. 2019a, b). In hyper prolific sow line pregnancy and lactation often lead to substantial metabolic and physiological changes which resulted in lower feed intake. However, hyper prolific sows often have a longer farrowing duration, high number

of stillborn piglets, and oxidative stress (Hasan et al. 2019a, b). Therefore, production efficiencies of the sow quite often can be affected by those mentioned factors. Growing evidence suggests that the gut microbiota plays a vital role in sow reproductive and production performance.

7.5.1 Feed Efficiency

Modern sows are often characterized with large litter size, and during pregnancy and lactation the sow undergoes substantial hormonal and metabolic changes (Algers and Uvnäs-Moberg 2007). However, raising a large litter also requires higher feed intake by sow. Alteration in the gut microbiota during the pregnancy plays a significant role in maternal pregnancy-induced metabolic changes. Recent researches suggest that during pregnancy up to lactation, the sow undergoes a decrease in insulin sensitivity and increase in systemic inflammation, resulted in lower feed intake of sow (Mosnier et al. 2010; Xu et al. 2020). Bacterial species like *Eubacterium* (e.g., *Eubacterium hallii*) can help to improve insulin sensitivity and systemic inflammation by producing propionate in the intestine. This has been shown in a recent study where sows were fed with soluble fiber (Guar gum and maize starch) during the pregnancy, resulting in a remarkable increase in *Eubacterium* (Xu et al. 2020). The *Eubacterium* spp., which is a common genus of adult pig gut microbiota, plays a crucial role in intestinal metabolic balance due to its ability to produce butyrate from the fermentation intermediates lactate and acetate and utilizes 1,2-propanediol to form propionate (Duncan et al. 2004; Engels et al. 2016). Insulin sensitivity and higher feed intake in late gestation and at farrowing are also correlated with higher abundance of *Akkermansia* and *Roseburia*. These are also short chain fatty acids (SCFA) producing bacteria, which can modulate insulin sensitivity by reducing fatty acid flux (Tan et al. 2016). However, feed efficiency in piglet especially after weaning is very crucial, as feed accounts for approximately 70% of the total cost of production. In a study while piglets being divided into high and low feed efficiency based on residual feed intake (RFI), microbes associated with a leaner and healthier host (e.g., *Christensenellaceae*, *Oscillibacter*, and *Cellulosilyticum*) were enriched in low RFI (more feed-efficient) pigs. However, more feed-efficient piglets also had notably lower abundance of *Nocardiaceae* (*Rhodococcus*) in the ileum with higher ileal iso-butyric acid concentrations (McCormack et al. 2017). The potential relevance of higher feed efficiency includes positive feedback between certain microbes and mucin production, goblet cells along the villi, and upregulation of butyric acid production. Therefore, it has been suggested that the porcine intestinal microbiota could potentially be targeted to improve feed efficiency in piglet. This will increase profitability while also reducing the environmental impact of pig production.

7.5.2

Oxidative Stress, Longer Farrowing Duration and Stillbirth

In hyper prolific sows gut microbiota and their functions can influence stillbirth rate, while stillbirth rate and farrowing duration are correlated with the gut microbiota composition and oxidative stress status of sow (Wang et al. 2019a, b). The dramatic raise in the total born piglets in the modern swine production, with the introduction of hyper prolific sow line, increases the incidence of stillborn piglets with longer farrowing duration and reduced sow reproductive performances (Hasan et al. 2019a, b). Elevated oxidative stress reported to be associated with farrowing and lactation complication in the hyper prolific sow. Researches have outlined a significant correlation of oxidative stress status and the level of several genera in the intestinal flora of sow (Tan et al. 2016; Wang et al. 2018, 2019a, b). A study by Wang et al. (2018) reported that Ruminococcaceae and Coprococcus might prolong the farrowing process and increase the stillbirth rate by regulating oxidative stress status of sow. In another report by the same author it was found that the relative abundances of Blautia, Coprococcus_3, Lachnospiraceae_UCG_001, Marvinbryantia, and Ruminococcaceae_UCG-004 were negatively correlated with the total antioxidant capacity (T-AOC) concentrations of sows and positively correlated with the stillbirth rate of sow. The relative abundances of Prevotellaceae_UCG-001 and Ruminococcaceae_UCG-014 were correlated with the farrowing duration of sow (Wang et al. 2019a, b). Whereas,

Prevotellaceae_NK3B31_group might increase the antioxidant capacity and reduce the stillbirth of sows (Wang et al. 2018). In post parturition, Bacteroides can help sow to cope up with oxidative stress by improving the plasma concentration of T-AOC, while Phascolarctobacterium by preventing the production of reactive oxygen species (ROS), an inflammatory by-product (Wang et al. 2018). Sow suffer from oxidative stress in late gestation and early lactation found with an elevated level of reactive oxygen species (ROS), 8-hydroxy-deoxyguanosine (8-OHdG), and thiobarbituric acid reactive substances (TBARS). Increase in the abundances of butyrate-producing bacteria, butyrate being the main energy sources for colonocytes but also an anti-inflammatory compound, can help in this case to reduce oxidative stress in sows. For example, an increase in levels of Clostridium cluster XI was negatively correlated with 8-OHdG, which was resulted from feeding sow with soluble fiber konjac flour (Tan et al. 2016).

7.5.3

Colostrum Yield and Colostrum Quality

Feeding sows with alternative additives may modulate their natural ability to improve the colostrum yield. In hyper prolific sow some of the factors negatively influence the colostrum yield and quality are longer farrowing duration and higher blood progesterone at farrowing (Hasan et al. 2019a, b). Pearson's correlation analysis revealed that high colostrum yield, high colostrum proteins, high colostrum IgG, low blood progesterone level, and lower farrowing duration were positively correlated with the abundance of the bacterial families Lactobacillaceae,

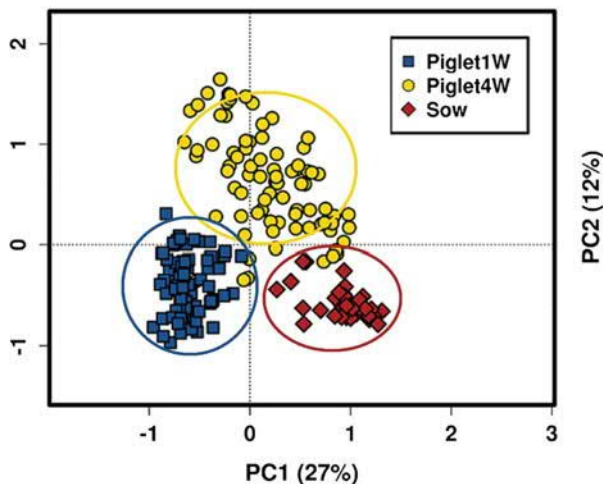
Ruminococcaceae, Acidaminococcaceae, Planctomycetaceae, Marinilabiliaceae, Veillonellaceae, and Prevotellaceae (Hasan et al. 2018). Improvement in beneficial gut microbiota increases the microbial protein synthesis in sow intestine and significantly altered the amino acid profile of intestinal digesta (McCormack et al. 2017). However, the beneficial fibrolytic bacteria increase the production of SCFA, which can influence the plasma concentration of acetic acid, butyric acid, and total SCFA (Tan et al. 2016). Thus, it can be speculated that the gut microbiota may contribute to the host metabolism, hydrolyze the feed, and promote nutrition absorption, which could have led to the increased colostrum yield and colostrum functional components and resulted in the positive correlation.

7.6 Piglet Gut Microbiota Influence on Growth and Health

During fetal life, piglets are believed to be devoid of microbes until their birth, when they will encounter microbial population by the contact with mother's external mucosae and skin, and with the environment itself (Isaacson and Kim 2012; Pajarillo et al. 2014a, b, c). During this early phase after birth, the gut microbiota gradually shape toward adult like population (Fig. 7.2) and it is influenced by different factors like diet, use of antibiotics, probiotics, or prebiotics (Bian et al. 2016; Chae et al. 2016; Hasan et al. 2018).

Different studies found that the alpha diversity of piglet gut microbiota increased from birth to after weaning age. At the family level, relative abundances of Bacteroidaceae and Enterobacteriaceae decline from birth over time, while those of Lactobacillaceae, Ruminococcaceae, Veillonellaceae, and Prevotellaceae increase in weaned piglets (Kim et al. 2011; Pajarillo et al. 2014a, b, c; Frese et al. 2015). During early life, the shaping of the gut microbiota in piglets will affect also their health and growth. Hasan et al. (2018) found that piglets growing faster and larger in

Fig. 7.2 Spatial description of gut microbiota of 37 sows and their piglets (1 and 4 weeks old). At 1 week of age, piglets have a very distinct gut microbiota population than their adult mothers, but already at 4 weeks of age the piglets' gut microbiota is switching toward adult sow alike population (adapted by Hasan et al. 2018, PlosOne) size at 4 weeks of age had higher relative abundances of Lactobacillus,



Flavonifractor, Barnesiella, Gemmiger, Faecalibacterium, Roseburia and Anaerophaga at 1 week of age. On the other hand, piglets growing more slowly and with poor average daily growth (ADG) hosted more Desulfovibrio, Acidaminobacter, Dethiosulfatibacter, Fastiduisipila, Ruminococcus, and Anaerotruncus at 1 week of age. For instance, Desulfovibrio bacteria are responsible for inflammatory intestine syndrome in humans and animals, due to active hydrogen sulfide production, which has cytotoxic effects on the gut mucosa cells (Pitcher and Cummings 1996; Loubinoux et al. 2002). Hydrogen sulfite may act also through an inhibition of butyrate oxidation, the main energy source for colonocytes (Loubinoux et al. 2002). Impairing this energy function leads the intestinal epithelium cells to chronic inflammation and death (Loubinoux et al. 2002). Hasan et al. (2018) demonstrated that supplementation of a yeast hydrolysate to pregnancy diet in sows reduced the amount of Desulfovibrio bacteria in their feces. Zhang et al. (2016) showed that a diet rich in alfalfa during lactation period decreased the abundance of the pathogen known Streptococcus suis in feces of nursing piglets. In addition, the diet containing alfalfa increased the abundance of Coprococcus eutactus, a butyrate-producing microbe. Volatile fatty acids like acetate have been shown to be an anti-inflammatory metabolite maintaining gut homeostasis (Fukuda et al. 2011). Moreover, butyrate is beneficial for gut mucosal immunity and barrier function (Kelly et al. 2015). Suckling piglet showing diarrhea during lactation had lower abundance of Prevotellaceae, Lachnospiraceae, Ruminococcaceae, and Lactobacillaceae compared to healthy piglet of the same litter (Dou et al. 2017). Petri et al. (2010) found that colonization of the intestine by Lactobacillaceae species begins at 3 days of age and remaining the dominant group up to 20 days of age. Healthy piglets showed a steady decrease in Lactobacillus and Escherichia, as well as a gradual increase in Prevotella in the period from nursing to transition to solid food, therefore an altered relationship between Prevotella and Escherichia may be the main cause of diarrhea in pre-weaned piglets (Yang et al. 2019). The same authors indicate that a reduced number of Bacteroides, Ruminococcus, Bulleidia, and Treponema, which are responsible for the digestion and utilization of solid feeds, may be related to the onset of piglet diarrhea in the post-weaning phase. Recent findings report that high abundances of Selenomonas and Moraxella in ileum, and of Lactobacillus in both cecum and colon, were correlated with high weight gain in pre-weaned piglets (Ding et al. 2019). In conclusion, it is evident from many researches that different types of gut microbiota are correlated with piglets' growth. This correlation can be exploited because of the ability of certain gut microbiota to modulate intestinal homeostasis, nutrients digestion and absorption, production of energy sources from indigestible compounds (fiber), and ultimately protect gut mucosa from inflammatory processes. The focus of future research should be to identify specific microbiota correlated with health and growth, at different stages of the piglets' productive life. Subsequently, implement methods to improve the gut colonization of this particular microbiota, either with diet modulation or management and environmental conditions or by passive administration in form of pre- or probiotics.

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