

ROLE OF GUT MICROBIOTA MODULATION IN HEALTH AND PRODUCTION OF PIGS

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Abstract

The importance of pig as a livestock species contributing to the meat production is well known. However, in recent years, the gut microbiome of pig has received considerable attention, as pigs serve as excellent biomedical models for human health compared to other non-primates. The pig gastro-intestinal tract harbours a lot of microbes, including bacteria, fungi, protozoa, viruses and bacteriophages. These microbes form a complex symbiotic ecosystem with the host and play pivotal role in maintaining various physiological, nutritional and immunological mechanisms of pigs. However, factors including rearing and management, environmental and antimicrobials used affect the microbial population in the pig gut affecting their health and growth. So modulation of gut microbiota is required which not only help in improving the health of pigs leading to higher production but also generate more revenue for the pig industry. In recent days, extensive studies have been made on gut microbiota using probiotics along with other prebiotic and feeding highly fermentable carbohydrates and microbial transplantation to reduce anti-microbial dependence for growth, maintenance of pig-health in order to elevate production. The review highlights various factors affecting pig gut microbiota and their role in health maintenance leading to efficient production of pigs.

Key words: Gut microbiota, Health, Modulation, Pig, Production

Introduction

The pig gastro-intestinal tract harbours a lot of microbes, including bacteria, fungi, protozoa, viruses, and bacteriophages. Out of approximately 10^{10} - 10^{14} cells, more than 98% of isolated genetic sequences present in the gut come from bacteria (Turner, 2018). These microbes form a complex symbiotic ecosystem with the host and play pivotal role in maintaining various physiological, nutritional

and immunological mechanisms of the pigs (Lee and Mazmanian, 2010; Brestoff and Artis, 2013). These mechanisms help in maintenance of health and also uphold production aspects of the pigs in farms. Besides harbouring beneficial microbes, the gut microbiome also consists of various pathogenic bacteria like *Escherichia coli*, Salmonella, Clostridium etc. which are regarded as opportunistic pathogens.

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Any sort of shift towards abnormality causes pathogenicity exerted by those pathogens in the gut accounting for morbidity and mortality among the pig population. So, to combat that, antimicrobials are routinely being used as a prophylactic and health-managemental procedure to minimize the loss in animal husbandry sector and livestock industries. Besides, the antimicrobials are used during weaning of piglets and also as growth factors to meet the production goals in the industry. This not only results into deteriorative effects on the gut microbiome of the weaned piglets, but also disrupt the gut lumen environment leading to post-weaning diarrhoea (Lallès *et al.*, 2004; Konstantinov *et al.*, 2006). Excessive usages of the antimicrobials hamper the beneficial microbes and may cause hindrance in obtaining proper health of the pigs. Growth promoting antimicrobials also elevate the population of antimicrobial resistant bacteria which is a major health concern (Dibner and Richards, 2005). Extensive studies on gut microbiota, using probiotics along with other prebiotic and feeding highly fermentable carbohydrates and microbial transplantation, are the way-outs to reduce anti-microbial dependence for growth and maintenance of pig-health in order to elevate production. This review highlights various factors affecting pig gut microbiota and their role in health maintenance leading to efficient production of pigs.

Intestinal microbiota of pig

Pig gut microbiome is comprised of numerous bacterial and non-bacterial components. The population of these components depends not only on age, but also their feeding habits, rearing environment, management types etc.

Bacterial components of the microbiome: The microbial colonization in gut of the piglets starts just after the birth (Fouhse *et al.*, 2016). Initial colonization is made with *Escherichia coli* and

Streptococcus spp., yielding an anaerobic environment to help *Bacteroides* spp., *Bifidobacterium* spp., *Clostridium* spp., *Lactobacillus* spp. to colonize (Konstantinov *et al.*, 2006; Petri *et al.*, 2010). Among them, *Lactobacilli* are the major bacteria in the piglet gut during the pre-weaning phase (Konstantinov *et al.*, 2006; Petri *et al.*, 2010)

In the post weaning phase, a study by Kim *et al.* (2011) classified the bacteria found in the pig-faeces into five phyla: Firmicutes, Bacteroidetes, Proteobacteria, Actino-bacteria and Spirochaetes. Among them, the largest proportion is made by the phylum Firmicutes, followed by Bacteroidetes, together accounting for 90% of all the bacterial population primarily at the 3 weeks aged pigs. Along with the time, the Firmicutes population increase with respect to that of the phylum Bacteroidetes. Surprisingly, non-classified groups of bacteria also increase their population. *Prevotella* spp. are the most predominant bacteria accounting for 30% of all classifiable bacteria when the pigs are aged 10 weeks, but, their concentration decreased to 3.5-4% only at the age of 22 weeks (Kim *et al.*, 2011). The most abundant species are: *Prevotella* spp., *Anaerobacter* spp., *Streptococcus* spp., *Lactobacillus* spp., *Coprococcus* spp., *Megasphaera* spp., *Subdoligranulum* spp., *Blautia* spp., *Oscillibacter* spp., *Faecalibacterium* spp., *Dialister* spp., *Sarcina* spp., *Butyricoccus* spp. (Table 1).

Non-bacterial components of the microbiome:

In a bid to find the non-bacterial components in pig gut, Urubshurov *et al.* (2011) screened pig faeces using 26S rRNA gene coupled with denaturing gradient gel electro-phoresis (DGGE) and DNA sequencing. The researchers isolated yeast, such as *Kazachstania slooffiae*, *Galactomyces geotrichum*, *Candida catenulate* and *C. glabrata* using cultural technique

Table 1. Major bacterial population in different intestinal portions

Portion of the Intestine	Major bacterial species/phylum
Jejunum	Firmicutes, Proteobacteria, Cyanobacteria, Actinobacteria
Ilium	Firmicutes, Proteobacteria
Colon and caecum	Firmicutes, Bacteroidetes

Adapted from Isaacson *et al.* (2011)

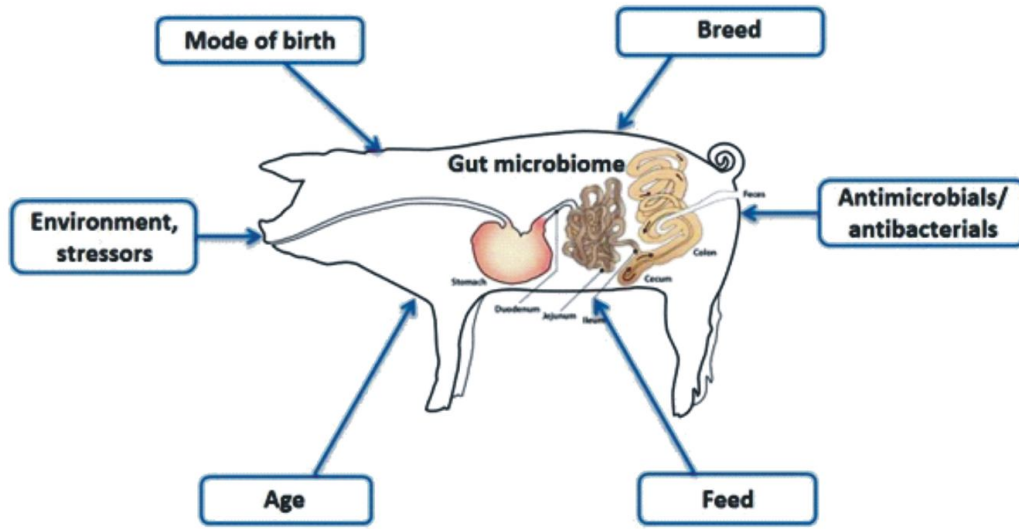


Fig. 1. Various factors affecting gut microbiome of pigs (Picture-Holman *et al.*, 2017)

(Urubschurov *et al.*, 2011). In a separate study, Shan *et al.* (2011) showed that the pig faeces contained (99%) RNA viruses from the families: Picornaviridae, Astroviridae, Coronaviridae and Caliciviridae. The DNA viruses present are of the Circoviridae and Parvoviridae families.

Factors affecting the gut microbiota in pigs

Several factors potentially affect the microbial population in the pig gut affecting the health and growth of the pigs, starting from the breed of the pig, management practices adopted, effect of host genetics and environmental factors (e.g., pen, kinship), age, body weight, obesity, diet, types of enrichment and antimicrobials used (Turner, 2018; Crespo-Piazuelo *et al.*, 2019; Wang *et al.*, 2019)

Birth: Studies have shown that the pig

microbial community is primarily influenced by the microbial encounters happened in the early stages of life i.e. the act of birth (Patil *et al.*, 2020). In fact, porcine gut microbial composition is heavily dependent upon the mode of the delivery (vaginal/normal delivery or caesarean section) along with the nutrition provided to the piglets (Patil *et al.*, 2020). It has also been reported that maternal transfer of gut microbial population is possible during parturition via umbilical cord (Patil *et al.*, 2020). Pigs born via normal mode of parturition have higher gut bacterial density and higher concentrations of acetate, propionate and butyrate, in comparison with the pigs born via caesarean section (Wang *et al.*, 2013).

Breed: Breed of the pig may also affect gut microbiota composition. On examining the faecal microbial community, Bian *et al.* (2016)

reported a different bacterial community structure in breeds of Meishan (a Chinese domestic obese breed) and Yorkshire (lean-type breed) piglets on day 14 and day 49. The Meishan sows had relatively higher abundances of Firmicutes but lower Bacteroidetes than Yorkshire sows, this may potentially affect postnatal development in piglets. Further, the authors (Mu *et al.*) concluded that *Prevotella*, a Gram-negative bacterium, was less abundant in Meishan breed compared to Yorkshire piglets (Mu *et al.*, 2019). In studying the gut microbiota profile of different pig breeds viz. Tibetan pig (TP), Yorkshire pig (YP) and Rongchang pig (RP) based on high-throughput pyrosequencing; Diao *et al.* (2016) opined that YP exhibited a lower Firmicutes/Bacteroidetes ratio whereas TP had higher levels of bacteria from *Spirochaetes* compared to other breeds. More diverse gut microbiome composition has been reported in Landrace pigs compared to the other two breeds, Duroc and Large White/Yorkshire (LWY) (Bergamaschi *et al.*, 2020).

In general, two major types of bacteria, Firmicutes and Bacteroidetes found in the pig gut and faecal materials, are also present in different proportions in different pig breeds (Patil *et al.*, 2020). Like, in Chinese Jinhua pigs, 70.4% faecal bacterial population is of the Firmicutes while the Bacteroidetes comprises 14.4% (Yang *et al.*, 2018a). In western breeds, the scenario changes quite drastically (Table 2).

Age: Microbial colonisation within the pig gut is also influenced by age of the pigs too (Zhao *et al.*, 2015; Holman *et al.*, 2017). The earliest colonisers (between birth and 2 days of age)

are *Escherichia* sp., *Clostridium* sp., *Fusobacterium* sp., *Streptococcus* sp. and *Enterococcus* sp. (Dowarah *et al.*, 2017). About 34% of the total microbial population of the gut is seen to be comprised of *Clostridium* spp. at the 6 hours age, which reduces to 1% when the pigs become 20 days (Petri *et al.*, 2010). Bacteria from the family *Enterobacteriaceae* are not found during those early days (Petri *et al.*, 2010). In the first 5 days after birth, strict aerobic and facultative anaerobic bacteria are seen which are replaced by the strict anaerobic bacteria gradually by the age of 22 days (Inoue *et al.*, 2005).

Likewise, analysing the gut microbiomes of newborns to 10 years old micro-pigs, Lim *et al.* (2019) found sequential changes of the gut microbiome in relation to age. With an increase in age, *Bacteroides* increased whereas beneficial microbes, including probiotic bacteria and short chain fatty acids (SCFA) producers, were found more in younger pigs (Lim *et al.*, 2019).

In a study by Mach *et al.* (2015), the composition of faecal microbiomes of healthy piglets at 14, 36, 48, 60 and 70 days after birth together assessed by 16S rRNA gene 454-pyrosequencing revealed *Bacteroides*, *Oscillibacter*, *Escherichia/Shigella*, *Lactobacillus* and unclassified *Ruminococcaceae* genera as the microbiota of suckling piglets. On the other hand, *Acetivibrio*, *Dialister*, *Oribacterium*, *Succinivibrio* and *Prevotella* genera were more dominant in piglets after weaning (Mach *et al.*, 2015).

While studying the gut microbial community compositions in different age groups (from 25

Table 2. Western pig breeds and their major gut-bacterial composition

Western pig breed	Firmicutes present (%)	Bacteroidetes present (%)
Yorkshire	42.0	51.4
Duroc	39.6	57.0
Landrace	45.6	47.6

Adopted from Pajarillo *et al.* (2014, 2015)

to 240 days of age), Ke *et al.* (2019) found that the gut microbiota of pre-weaning piglets was predominated by two enterotypes, *Fusobacterium* spp. and p-75-a5, respectively whereas *Prevotella* spp. and *Treponema* spp. were the main enterotypes at later (> 80 days).

Diet and feed efficiency: Diet has significant impact on the gut microbial population and a proper and balanced diet to pig at different stages of growth also helps in preventing dysbiosis (Doré and Blottière, 2015), the reason behind numerous chronic diseases. On the other hand, any dietary changes or unbalanced rations coupled with low feed digestibility can change the richness of beneficial bacterial populations in favour of pathogenic bacteria in the gut, which may hamper the animal health and productivity.

Feed efficiency being an important economic and environmental parameter that is well-studied to find out the feasibility of the farm and swine industry is no exception to this. In fact, the gut microbiota plays an important role in carbohydrate metabolism and helps in nutrient uptake after metabolizing various food components, particularly indigestible polysaccharides (Yang *et al.*, 2017). Since the gut microbiota plays a pivotal role in nutrient digestibility, the differences in gut microbiome composition may impact feed efficiency among the swine breeds (Bergamaschi *et al.*, 2020), thereby affecting its production causing considerable economic loss to the sector.

Recent studies have shown that *Ruminococcus* spp. and *Lactobacillus* spp. lower the feed intake of pigs while the *Prevotella* spp. show just the opposite (Yang *et al.*, 2018b), justifying the role of *Prevotella* spp. as the keystone for appetite control of the pigs. When the pigs shift from milk-based diet to solid feed diet (during weaning), bacterial composition within the gut also changes (De Rodas *et al.*, 2018). Even

paternal (Duroc-DR) and maternal (Landrace-LR and Large White-LW) lines have significant effect on feed efficiency and gut microbiome composition. In a study, it was found that the microbial communities in DR breed had better proportion of the *Catenibacterium* and *Clostridium* genera than the other two breeds whereas LR pigs had significantly higher representation of *Bacteroides* than LW (Bergamaschi *et al.*, 2020).

Different researchers have even identified the relationship between gut microbiota diversity and feed efficiency in pigs. While the bacterial species belonging to the genera *Bacteroides*, *Cellulosilyticum*, and *Prevotella* are reported to be more abundant in pigs with low feed efficiency, *Oscillibacter* and *Rhodococcus* are described in feed efficient animals (McCormack *et al.*, 2017; Tan *et al.*, 2017).

Studying the gut microbiota of pigs from birth to market, i.e. lactation, nursery, growing and finishing, Li *et al.* (2020) found a dramatic change in gut microbiome structure during weaning, when solid food replaced sow milk. Even when on solid diet during different stages of growth, the change was gradual indicating the role of diet in influencing the composition of gut microbiota. A diet of weaning piglets supplemented with a cocktail of feed additives (cranberry extract, encapsulated carvacrol, yeast-derived products, and extra vitamins A, D, E, and B complex) and bovine colostrum has also been reported to modulate intestinal microbiota and improved the growth performance of piglets (Lo Verso *et al.*, 2020).

Dietary fibre: Dietary fibres are plant polysaccharides that are potentially available for bacterial fermentation in the large intestines of single-stomached animals (Bindelle *et al.*, 2008). The dietary fibre component of feed is reported to be beneficial for intestinal health and animal welfare, as it decreases the diarrhea

Table 3. Dietary components and their effect in improving the health and production of pigs

Components/Process	Usage	Effect on health and production	Reference
Dietary garcinol supplement	200mg/kg; 400mg/kg; 600mg/kg for 14 days	<ul style="list-style-type: none"> ▲ Increased daily feed intake ▲ Increased growth rate ▲ Reduced diarrhoea ▲ Elevated antioxidant activity ▲ Reduced intestinal barrier dysfunction ▲ Increased crypts depth of intestinal villi ▲ Decreased cytokine production ▲ Decreased pathogenic bacteria in the gut (<i>E.coli</i>) 	(Wang <i>et al.</i> , 2020)
Zinc oxide supplementation with peptide cocktail	Fish-porcine-microbial peptide cocktail: 0.05%; 0.25%; 0.5% Zinc oxide: 2500mg/kg Both to the nursery pigs	<ul style="list-style-type: none"> ▲ Increased body weight ▲ Restoration of growth performance of under-developed piglets ▲ Higher population of <i>Prevotella</i> sp. within the gut and rectal swab ▲ Increased <i>Streptococcus</i> sp. in the gut, leading to higher serotonin levels in piglets for better growth and body weight gain ▲ Lower systemic inflammation 	(Wei <i>et al.</i> , 2020)
Dietary copper	175mg/kg	<ul style="list-style-type: none"> ▲ Reduced population of <i>Lactobacilli</i> and <i>Streptococci</i> in the gut lumen of weaned piglets ▲ Higher unsaturated fatty acids leading to softer pork fat 	(Højberg <i>et al.</i> , 2005; Dębski, 2016; Patil <i>et al.</i> , 2020)
Probiotics	<i>Lactobacillus plantarum</i> strain JDFM LP11 (2.5X10 ⁷ CFU), 1% glucose, 1% molasses, 0.2% sea salt and 0.2% yeast extract: Liquid probiotic solution	<ul style="list-style-type: none"> ▲ Enhanced development of intestinal villi ▲ Elevated amino acid biosynthesis ▲ Enhanced butyrate metabolism ▲ Reduction in immune gene expression towards gut inflammation ▲ Increased commensal gut microflora diversity and population 	(Shin <i>et al.</i> , 2019)
Faecal microbiota transplantation (FMT) with dietary inulin supplementation	200ml of FMT (2.6X10 ¹¹ CFU): Pregnant sows of 70 days and 100 days of gestation	<ul style="list-style-type: none"> ▲ Better feed efficiency ▲ Lower concentrations of <i>Chlamydia</i> sp. and <i>Treponema</i> sp. in the ileum ▲ Lower butyric acid concentrations in the caecum 	(McCormack <i>et al.</i> , 2019)

Table 3, Cont.

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Components/Process	Usage	Effect on health and production	Reference
	2% Inulin: Adults/sows / pregnant sows	<ul style="list-style-type: none"> ▲ Higher no. of jejunal goblet cells ▲ Upregulation of duodenal cells lead to better glucose and volatile fatty acid homeostasis Increased platelet count 	
	3% Inulin: Weaned piglets	<ul style="list-style-type: none"> ▲ Reduced ileal propionate concentration, granulocyte counts and serum urea concentrations 	
Rapeseed based diet	20% rapeseed meal with common soybean meal diet as control: Growing finishing pigs weighing 25kgs	<ul style="list-style-type: none"> ▲ Abundant population of <i>Mucispirillum</i> spp. (immune-inducing bacteria) and <i>Lachnospira</i> spp. (anti-inflammatory stimulating bacteria) in ileum and large intestine. ▲ Upregulation of major amino acid fermenting microbes ▲ Higher population of amylolytic bacteria ▲ Enhanced carbohydrate and energy metabolism 	(Umu <i>et al.</i> , 2020)
Wheat bran diet	7% Wheat Bran (WB) diet: Day 3 to day 43 after AI in sows 250g/kg of DM WB: Pregnant sows 140g/kg DM WB: Lactating sows	<ul style="list-style-type: none"> ▲ Higher numbers of Proteobacteria, followed by the <i>Firmicutes</i> in the umbilical cord blood, depicting higher rate of maternal transmission of microbes to the offspring ▲ Lesser butyrate in the caecum of the piglets ▲ Lesser valerate in all the intestinal parts of the piglets ▲ Higher numbers of diversified microflora within the gut of the pregnant sows 	(Leblois <i>et al.</i> , 2017)
Bacteriophage cocktail (Phages of <i>Salmonella</i> , <i>E. coli</i> , <i>Clostridium perfringens</i> type A & C)	Up to 35 days age: Four groups of pigs given 0g/kg, 0.5g/kg, 1g/kg and 1.5g/kg cocktail bacteriophages (B); Afterwards: Three groups fed with 3g/kg of B, 1g/kg Probiotics (P) and 3g/kg B + 1g/kg P	<ul style="list-style-type: none"> ▲ Higher growth rate ▲ Higher feed intake ▲ Higher faecal concentration of <i>Bifidobacterium</i> sp. and <i>Lactobacilli</i> and lower coliforms 	(Kim <i>et al.</i> , 2014)

incidence in pigs around the time of weaning. In fact, upon bacterial fermentation of the dietary fibres, short chain organic acids (acetate, lactate, propionate and butyrate) get formed, which help in digestive tract development by potentiating the gut epithelia (Montagne *et al.*, 2003). These acids also inhibit growth of *Salmonella*, *E. coli* and *Clostridium* (Pickard *et al.*, 2017). The non-starch polysaccharides stimulate the growth of commensals within the gut, increase the short chain organic acid production, lower the colon pH and increase the length of the intestinal villi (Bach Knudsen *et al.*, 2012; Lindberg, 2014). Some studies also suggest that the low fat and high fibre diet fed pigs have more numbers of *Lactobacillus*, *Bifidobacterium* and *Faecalibacterium prausnitzii* population within the gut whereas, the high fat and low fibre diet fed pigs contained more population of the bacteria under *Enterobacteriaceae* family (Heinritz *et al.*, 2016). The addition of guar gum or cellulose to a standard diet has also been reported to increase the ileal Bifidobacteria and Enterobacteria populations in growing pigs (Owusu-Asiedu *et al.*, 2006).

The levels of proteins or fibers and their source also influence the diversity and composition of the gut microbiota, particularly of weaning piglets (Rist *et al.*, 2013; Pieper *et al.*, 2015). For example, in weaning pigs, pectin enriched diets as well as a soybean meal is reported to decrease the relative abundance of *Lactobacillus* and increase *Prevotella* sp. in the colon (Tian *et al.*, 2017). On the other hand, a protein source from fish is often linked to an increase in *Escherichia/Shigella* group (Cao *et al.*, 2016).

Dietary copper: Copper is an essential micronutrient and if used in feed offer many biological functions in animals. It protects the animal from oxidative stress, helps in iron metabolism, improves the activity of digestive

enzymes, to name a few (Zhang *et al.*, 2019). Copper in feed of weaned piglets is reported to improve body weight gain and feed conversion ratio and reduce the frequency of diarrhoea. Therefore, copper supplementation with the feed is a tradition that pig industry practices due to its anti-microbial and growth promoting properties (Patil *et al.*, 2020). This practice helps to reduce the colonies of *Lactobacillus* and *Streptococcus* in the pig gut (Højberg *et al.*, 2005). High amounts of dietary copper increase the content of unsaturated fatty acids leading to production of softer pork fat (Dêbski, 2016).

Probiotics and prebiotics: Probiotics are a group of micro-organisms, when administered in adequate amounts, the individual gets overall health improvement (Linares *et al.*, 2017). Probiotics improve nutrient digestion and metabolism, resulting into a better growth of animals and thus the production performance of the animal gets improved markedly (Wang and Donovan, 2015). Probiotic supplementation increases beneficial bacteria within the pig gut (like *Lactobacilli*) and decrease the population of harmful bacteria (like *E. coli*, *Clostridia* spp. etc.) (Galdeano *et al.*, 2010) leading to much higher growth rate and body weight gain, meeting the production target in the pig industries (Wells *et al.*, 2005).

Prebiotics are the compounds which help to upregulate the population of beneficial micro-organisms in the gut (Hutkins *et al.*, 2016). Prebiotics potentiate the works of probiotics also, leading to additive effect on that of the probiotics to help elevate growth rate of pigs, meeting the production target in the pig industry (Çetin *et al.*, 2005; Yin *et al.*, 2008). Also, prebiotic supplementation elevates interleukin production in the pig's body (Çetin *et al.*, 2005; Yin *et al.*, 2008). Prebiotics, such as lactulose, provided to the weaned piglets showed marked improvement in IgG, IgM and IgA production upon challenging with

Salmonella enterica subspecies *enterica* serovar Typhimurium (Pietà *et al.*, 2007).

Antibacterials: Antibacterials like penicillins, tylosin, sulfamethazine, tetracyclines are often used as growth promoters in the pig industry (Allen *et al.*, 2011; Kim *et al.*, 2012, 2016; Looft *et al.*, 2014). But these agents have negative impact on the commensals living in the pig gut (Dibner and Richards, 2005). Excessive usage of antimicrobials cause to increase immune-tolerance, leading to insufficient immune response against the anti-microbial-resistant pathogenic species infections in future (Schokker *et al.*, 2014). In recent days, the negative effects of antibacterials on gut microbiota and host health have been recognized. Further, long term uses of antibacterial not only decrease bacterial diversity and their relative abundance but also develop antibiotic resistance. So to minimise the effects of antibiotics on the intestinal microbiota, tailored antibiotic treatment is often advocated to avoid this collateral damage.

Stressors and weaning: It is well established that any form of stress like weaning, heat stress, etc affects the growth, reproduction, productivity and diseases susceptibility in livestock (Parkunan *et al.*, 2015). There are six phases in a piglet's life and weaning is considered as the critical phase among all. The stress caused as a result of weaning not only changes microbial composition and function but also alters the microbial metabolic profiles in the intestine (Li *et al.*, 2018). During this period, functional changes in the gut microbiome is observed when the host animal undergoes stressful conditions like confinements, weaning, heat etc. (Patil *et al.*, 2020). Due to the stress exerted because of weaning, the ileal *Lactobacilli* population undergoes marked changes, hampering the production criteria for pigs (Janczyk *et al.*,

2007). Post weaning periods depict uphold of *Bacteroidetes* population over Firmicutes in the pig gut (Pajarillo *et al.*, 2014).

Conclusion

The importance of pig as a livestock species contributing to the meat production is well known. However, in recent years, the gut microbiome of pig has received considerable attention, as pigs serve as excellent biomedical models for human health compared to other non-primates. Pigs have a relatively high degree of similarity index with humans in terms of the genome, protein sequences as well as immune responses. So swine as a model is more preferred over other species in studying the interaction of early gut microbiota and its impacts on health risks. With the development of modern analytical methods such as fluorescent in situ hybridization, temperature gradient gel electrophoresis, DGGE, molecular tools, particularly next generation sequencing, it is now possible to identify and analyse the composition of microbial communities of gut at different stages of growth. This helps in better understanding the gut microbial composition which could be used as a biomarker to predict health status of piglets, contributing better immunological protection to the host and thus, lesser diseases will occur. As transition through weaning is a crucial period in pig farm management, gut microbe modulation comes out handy. This not only elevates the population of the microbes within the gut, but also decreases the harmful, pathogenic microbes, so that the beneficial commensals get the upper-hand within the gut. So modulation of gut microbe not only helps in improving the health of the pigs leading to higher production but also generate more revenue for the pig industry. Formulating a commercial diet during this transition period is important for optimum gut health of pigs. As the intestinal microbiome is significantly affected by dietary changes (from milk to solid food), more research is needed

in this front to develop feed with non-antimicrobial alternatives such as pre- and probiotics, essential oils, enzymes, macro- and micronutrients etc. as additives to restore intestinal balance and overcome crucial weaning transition. This will not only ensure optimum composition of the gastrointestinal microflora in piglets by maintaining a balance

between beneficial and potentially pathogenic bacteria but also help the industry to get rid of the antibacterial/antimicrobial dependence to combat diseases or to promote growth. Further, research is also needed in understanding the impact of routine farm practices and farm environment having any role on a piglet's microbiome.

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