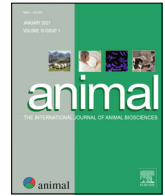


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Review: Can early-life establishment of the piglet intestinal microbiota influence production outcomes?

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ABSTRACT

The gastrointestinal tract microbiota is involved in the development and function of many body processes. Studies demonstrate that early-life microbial colonisation is the most important time for shaping intestinal and immune development, with perturbations to the microbiota during this time having long-lasting negative implications for the host. Piglets face many early-life events that shape the acquisition and development of their intestinal microbiota. The pork industry has a unique advantage in that the producer has a degree of control over what piglets are exposed to, providing conditions that allow for optimum piglet growth and development. An influx of publications within this area has occurred in recent times and with this, interest surrounding its application in pork production has increased. However, it can be difficult to distinguish which research is of most relevance to industry in terms of delivering repeatable and reliable production outcomes. In this review, we describe the literature surrounding research within pigs, predominantly during the preweaning period that has either provided solutions to industry problems or is generating information targeted at addressing relevant industry issues, with the focus being on studies demonstrating causation where possible. This review will provide a basis for the development of new studies targeted at understanding how to better support initial intestinal microbiota colonisation in order to improve piglet health and survival.

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Implications

The gastrointestinal tract microbiota has an essential role in many body processes. This review explores relevant literature in preweaning piglets tailored at generating solutions to industry problems. It is evident that early-life events shape the piglet's gastrointestinal microbiota and subsequent health and as such, further research into the long-term effects of normal husbandry practices on piglet intestinal microbiota, health and survival is needed. This will enable the development of strategies aimed at ensuring optimal microbiota colonisation on-farm for the improvement of sow and piglet health.

Introduction

A microbiome is a collection of microorganisms (bacteria, archaea, fungi and viruses), including their genomes and extra-

chromosomal elements present in and on the host (Dominguez-Bello et al., 2019), while the term "microbiota" refers to the microbial taxa associated with the host (Ursell et al., 2012). The gastrointestinal tract (GIT) contains the largest number and greatest diversity of microorganisms of all body systems (Patil et al., 2020). The GIT microbiota has received considerable attention in recent times due to its essential role in many body processes. Work in humans has demonstrated links to irritable bowel syndrome, obesity, autoimmunity, asthma and even mental health (Arrieta et al., 2015; Maruvada et al., 2017; Borba et al., 2018; Carlson et al., 2018). Interest in this work, as well as a growing appreciation of the roles and importance of the microbiota in 'gut health' (Pluske et al., 2018), has led to an increasing number of studies investigating applications within production animals. In particular, research in pigs has shown links between the intestinal microbiota and performance (Mach et al., 2015; Dou et al., 2017; Gaukroger et al., 2020a) and the ability to manipulate it for improvements in feed efficiency and average daily gain (Heim et al., 2015; Li et al., 2018b; McCormack et al., 2019), while other studies are focussed on the microbiota as a tool for improving herd health and reducing the industries' reliance on antimicrobials,

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predominantly in the postweaning period (Hu et al., 2018; Maradiaga et al., 2018; Mukhopadhyaya et al., 2019; Nowland et al., 2020b).

Nevertheless, with the growing number of publications in this field, it is often difficult to distinguish which research is of most relevance for generating industry applicable solutions to, for example neonatal and postweaning diarrhoea. Limited studies exist that directly demonstrate the functionality of specific bacteria to an industry issue such as diarrhoea rather than simply documenting the absence or presence of different taxa. Challenges in this field include first, identifying when and how to establish and then maintain an appropriate (or optimum) intestinal microbiota, second, whether that microbiota will cause relevant production outcomes, and third, whether or not the microbiota needs to be different/adaptable depending on the production index being measured.

There currently exist a number of excellent reviews describing the overall microbiota in pigs (e.g., Gresse et al., 2017; Guevarra et al., 2019; Nowland et al., 2019; Knecht et al., 2020). Our intention in this review is to describe the literature pertaining to the GIT microbiota of pigs in the period before weaning targeted at addressing some key pork industry issues, with the focus being on those studies demonstrating causation where possible.

Influence of the peripartum sow intestinal microbiota on sow and piglet performance

Initial microbial colonisation

It is unclear whether development of the microbiota begins during gestation as findings across species are contradictory, and no studies to date have observed *in utero* microbial colonisation within the piglet. Some authors have observed the presence of bacteria in the amniotic fluid and meconium of infants (Collado et al., 2016) while others refute these claims based on the approaches used (Perez-Munoz et al., 2017). In piglets, Nowland et al. (2021b) were able to identify the presence of bacteria within the spiral colon of stillborn piglets indicating that colonisation of the GIT occurred at least within the immediate prenatal period. Although the exact timing of initial colonisation has yet to be determined within pigs, research in humans indicates that initial microbial colonisation is driven by the mother and that perturbations during early life can have negative implications on long-term health (Brown et al., 2012; Cahenzli et al., 2013; Carlson et al., 2018). When investigating the literature within pigs, some studies indicate that the sow's microbiota influences the piglet's intestinal microbiota and, in turn, their immune system development, growth and survival (Ma et al., 2020; Liu et al., 2021), while others demonstrate that the rearing environment influences intestinal microbiota functionality and composition both in the suckling and weaning phases (Beaumont et al., 2021). In contrast, specific microbial changes within the sow are not always mimicked in their offspring. For example, Berry et al. (2021) observed numerous *Lactobacillus* species as well as *Clostridium clostridioforme* in piglet faeces; however, these bacteria were absent from the sow's faeces. This could be an artefact of the piglet's exposure to other factors such as the sow's vagina, pen environment, and sow antibiotic exposure (Chen et al., 2018b), or in the case of dietary treatments, the length of time between sow microbiota modulation and piglet exposure would be a contributing factor (Leblois et al., 2018). This example indicates the complexity of the interaction between the sow's microbiota and her progeny, and while research within this area is limited, it is reasonable to assume that the sow's microbiota prior to or during parturition would significantly influence the microbiota of her offspring.

Oxidative stress and sow microbiota

Sows experience oxidative stress during late gestation and early lactation as a result of the increasing metabolic demand from growing multiple young (Tan et al., 2016; Cheng et al., 2018; Wang et al., 2019). Oxidative stress can impair energy balance, body condition and milk production, and thus result in negative outcomes for sows and piglets (Wang et al., 2018b). Few studies have investigated the effects oxidative stress in sows may have on the intestinal microbiota in their progeny. Wang et al. (2018b) found that the relative abundance of the family *Bacteroidaceae* was positively correlated to antioxidant capacity and litter performance, while *Phascolarctobacterium*, *Cyanobacteria* and *Streptococcus* were correlated with lower piglet performance and higher oxidative stress in sows. Furthermore, Wang et al. (2019) observed that the relative abundance of *Lachnospiraceae_UCG-001*, *Marvinbryantia* and *Ruminococcaceae_UCG-004* was higher in sows with increased still-birth rate and reduced antioxidant capacity as demonstrated by lower serum total antioxidant capacity. Additionally, when observing differences between sows classified as high or low performers based on their reproductive output (litters/sow/year and litter size born alive), Uryu et al. (2020) observed an increase in the relative abundance of short-chain fatty acid producing and fibre-degrading bacteria *Ruminococcus*, *Fibrobacter* and *Butyrivococcus*, and higher concentrations of acetate, propionate and *n*-butyrate, in the faeces of higher performing sows. These studies demonstrate that the intestinal microbiota and oxidative capacity throughout gestation and lactation influence sow and piglet performance.

Indeed, research involving the use of feed ingredients as a means to manipulate the microbiota of sows in gestation and lactation has demonstrated some success in reducing oxidative stress during this time and improving piglet performance. Ingredients shown to reduce oxidative stress include konjac flour (Tan et al., 2016), inulin (Zhou et al., 2017), alfalfa meal (Liu et al., 2021) and differing ratios of soluble and insoluble fibre (inulin and cellulose) (Li et al., 2019). Often the proposed driver for how these substrates may influence oxidative stress is their prebiotic nature, favouring certain bacteria that could produce metabolites that in turn influence the animal's antioxidant capacity. However, given the lack of information surrounding the specific bacteria that are beneficial during this time, further research is warranted in order to identify the most appropriate way(s) for improving sow and piglet performance by this means.

Early-life events and strategies that influence intestinal microbiota development

Immediate postnatal factors influencing the piglet

Colostrum is the first milk produced by the sow and is provided during the first 12–48 h after the onset of parturition (Le Dividich et al., 2005). It provides the developing neonate with a source of energy and immunity (Le Dividich et al., 2005; Chen et al., 2018a). In addition, colostrum and milk contain a diverse array of bacteria and prebiotic compounds (e.g. oligosaccharides) that assist intestinal development (Bian et al., 2016; Chen et al., 2018a). The importance of colostrum and milk in relation to intestinal microbiota development and piglet health have been widely documented (Le Dividich et al., 2005; Borba et al., 2018; Chen et al., 2018a). Studies show that animals raised on formula rather than milk have reduced intestinal microbiota diversity and an increased susceptibility to disease (Inman et al., 2010; Iozzo and Sanguinetti, 2018). Hence, ensuring piglets receive optimal colostrum and milk in early life is important for intestinal micro-

biota colonisation and immune system development. Additionally, the mother's intestinal microbiota throughout lactation is important as studies in humans and mice suggest that the milk microbiota is controlled by selective luminal bacterial translocation from dendritic cells in the intestinal epithelium (Rescigno et al., 2001; Perez et al., 2007). Therefore, it could be presumed that if the sow's intestinal microbiota is not optimal, then the ability to expose the piglet to beneficial bacteria and establish an optimal microbiota for the piglet is limited.

Furthermore, studies have demonstrated that during the peripartum period, the sow's GIT microbiota composition shifts, with sows reaching their lowest level of bacterial richness and diversity in early lactation (day 3), as opposed to other time points investigated (gestation day 109 and lactation days 8 and 14) (Cheng et al., 2018; Gaukroger et al., 2020b). Additionally, Cheng et al. (2018) identified an increase in potentially pathogenic bacteria *Proteobacteria* and *Fusobacteria*, a decrease in potentially beneficial butyrate-producing bacteria *Ruminococcus_1* and *Lachnospiraceae_XPB1014*, and an increase in gut permeability and plasma endotoxin concentration in sows at day 3 of lactation, suggesting that early lactation would be a beneficial period to direct strategies targeted at supporting the GIT microbiota of sows.

Other factors that contribute to piglet microbiota community enrichment are the sow's vaginal and faecal microbiota, the environment the piglet is born into and reared in, and the bacteria present on and around the teat (Chen et al., 2018b; Maradiaga et al., 2018). Chen et al. (2018b) demonstrated that early in lactation, the piglets' GIT microbiota composition was similar to the bacteria found on the slatted floor, the sow's milk and nipple surface and, as lactation progressed, the faecal microbiota of piglets became more similar to the sow. Additionally, Bian et al. (2016) found that the nurse sow influenced the piglet during lactation by altering the bacterial species that colonise the GIT. However, the influence of the sow diminished with the introduction to solid feed and weaning (Bian et al., 2016). Choudhury et al. (2021) did not investigate the effect of the sow on GIT microbiota development, but reported that piglets having access to a feeding trough containing mixed fibre feed from as early as 2 days of age tended to be heavier, had altered intestinal morphology and a higher abundance of fibrolytic and/or butyrate-producing bacteria groups *Ruminococcus*, *Lachnospira*, *Roseburia*, *Eubacterium* and *Prevotella* at 28 days of age (prior to weaning) compared to those with no access. In this regard, it may be assumed that piglet exposure to sow feed in lactation would also influence their GIT microbiota.

Further to this, Schmidt et al. (2011) assessed the primary effects of environmental exposure on GIT microbiota development. This was done by observing the effects of rearing 24-h-old piglets in high hygiene isolators versus being indoor- or outdoor-reared. Differences in microbial succession and stabilisation were observed, suggesting that the establishment and development of the GIT microbiota requires continuous microbial exposure in early life, and that this is compromised by excessive hygiene. In a similar study design, Mulder et al. (2011) observed delayed gut closure and morphological development between isolator-reared and indoor- or outdoor-reared piglets (Dou et al., 2017). Additionally, differences in a large number of immune-related genes were also observed. More recently, Tsai et al. (2018) demonstrated that when piglets were reared in an isolator and fed milk replacer and solid feed (starting at 10 days of age) from 4 days postpartum, they exhibited improved growth after weaning. However, these pigs did not experience pathogenic challenges as would be seen in a commercial piggery. This demonstrates the integral role early microbial exposure has on the microbiota and demonstrates the potential benefit of early exposure to feed for piglets. Furthermore, recent work within our research group (Nowland et al., 2021a) observed the effect of the maternal faeces being kept in the pen

or removed twice daily on piglet microbial colonisation, and found that removal of sow faeces from the farrowing crate for the first 10 days of life altered colonisation and improved piglet growth and survival. Collectively, these studies demonstrate that although diverse microbial exposure is important in early life, consideration needs to be given as to the type/form of exposure that is not detrimental to the piglet, especially in the postweaning period. Additionally, the large influence of sow and pen environment on the piglet microbiota offers a potential opportunity for improvement within production systems where the stockperson can control what each animal is exposed to, particularly when piglets are confined to pens with a sow for the first 18-35 days of their life.

Cross-fostering

Cross-fostering is an industry practice that involves the movement of piglets onto another sow to ensure they have access to sufficient milk (Huting et al., 2017). Cross-fostering is required when the number of piglets born is larger than the number of functional teats on a sow or is done as a way of size matching piglets within a litter (Huting et al., 2017). Despite this being a very common and routine practice, studies investigating the impact of cross-fostering on the intestinal microbiota in pigs are limited and somewhat contradictory. Maradiaga et al. (2018) observed no significant effects of cross-fostering on piglet microbiota development when cross-fostering piglets of the same breed. However, it is possible that no significant difference was observed as the variability between the foster sows was not large enough to cause a difference. In contrast, Mu et al. (2019) observed differences between piglets cross-fostered, or not cross-fostered, between Meishan and Yorkshire breeds in their immune status and colonic microbiota. Specifically, piglets nursed on Meishan sows had a higher expression of interleukin 10 and Foxp3-positive cells that may indicate improved anti-inflammatory function in the intestinal epithelium as a consequence of different microbiota. Another study demonstrated a significant improvement in growth and caecal microbiota from cross-fostering Jinhua piglets onto Yorkshire sows (Xian et al., 2014), although sample size was relatively small in this study. Therefore, it seems that cross-fostering may also be a method for altering the GIT microbiota to improve piglet performance, when appropriate animals are used, although much more work is required to ascertain the specific requirements to ensure benefits are observed.

The use of antibiotics in early life

Historically, the treatment and prevention of animal disease have largely revolved around the use of antibiotics for pathogen control. While antibiotics are effective at pathogen removal, they are non-selective and as a result impact the commensal microbiota (Nowland et al., 2019). The commensal microbiota has a major role in the development, maturation and maintenance of the immune system and a reduction in commensals can have negative health implications for the animal (Chase, 2018). As such, antibiotic use is often associated with a reduction in GIT microbial diversity and an increase in antibiotic resistant bacteria and, if their use is prolonged, can lead to enteric dysbiosis (Wlodarska et al., 2011; Looft et al., 2012). Studies in humans show that early antibiotic administration can have negative health consequences for infants, increasing their probability of developing asthma, necrotising enterocolitis and late-onset sepsis when they are older (Arrieta et al., 2014; Vangay et al., 2015).

In some countries, it is common practice to administer antibiotics to sows and (or) their young during lactation, to treat and (or) as a preventative measure to outbreaks of respiratory and intestinal disease. However, the impacts this has on the piglet

GIT microbiota and intestinal health long-term are unknown. When assessing the effect of maternal antibiotic administration on piglets, Xu et al. (2020) observed a negative effect on intestinal morphology, with decreased crypt depth in the ileum at 7 days of age and altered gene expression profiles in the ileum at 7 and 21 days of age. Similarly, De Greeff et al. (2020) observed differences in microbial colonisation and delays in intestinal development in piglets up to 5 weeks of age when sows were fed amoxicillin for the last 7 days of gestation. Although maternal administration is common, direct antibiotic administration to piglets is also often done within the first 5 days of life at piglet processing. When investigating the short-term effects of tulathromycin and stress on 4-day-old piglets, Schokker et al. (2014) found that the jejunal microbiota at 8 day of age had a higher microbial diversity, an increase in anaerobic bacteria *Bifidobacterium*, *Eubacterium*, *F. prausnitzii*, and *S. moorei*, and a decrease in *S. aureus*. Antibiotic administration also caused downregulation of immunological communication as reflected by the higher expression of chemokine and toll-like receptors as well as their respective ligands in non-antibiotic treated animals. Furthermore, Hasan et al. (2019) investigated the effects of administering amoxicillin and florfenicol to piglets in early life on their faecal microbiota and while a decrease in the relative abundance of potentially pathogenic bacteria *Campylobacter* and *Pasteurella* was observed, there was also a decrease in the abundance of potentially beneficial bacteria *Prevotella* and *Butyrimonas*. In contrast, Nowland et al. (2020a) observed no impacts on the faecal microbiota when piglets were treated with ceftiofur at 7 days of age. However, in that study, piglet faecal microbiota was not assessed beyond 11 days postantibiotic administration. In a longer-term study, Janczyk et al. (2007) showed that amoxicillin administration to a 1-day-old piglet altered its colonic microbiota composition up to at least 5 weeks of age. Similarly, Ruczizka et al. (2019) observed differences in the faecal microbiota of piglets at 12, 28 and 97 days of age when administered ceftiofur 12 h postpartum. Additionally, piglets treated with ceftiofur had reduced microbial diversity and long-term growth. From this, is it evident that antibiotics alter piglets' GIT microbiota, and that the timing of antibiotic administration and type of antibiotic used influence the outcomes observed. Nevertheless, it is clear that these alterations are not always beneficial with regard to microbial colonisation and immune system activation. However, further research is warranted to investigate the long-term consequences of early-life antibiotic administration to piglets, for example on survival and disease susceptibility, especially as it is currently a common industry practice.

Intestinal microbiota manipulation through faecal microbiota transplantation

The use of faecal microbiota transplantation (FMT) as a method for establishing an appropriate/optimum microbiota of the young pig is gaining some interest in the pork industry. Reviews on its use specifically in pigs include Niederwerder (2018), Canibe et al. (2019) and Nowland and Kirkwood (2020). Nevertheless, studies using FMT are contradictory, with some studies observing improvements in growth, reduced diarrhoea incidence and improved intestinal barrier and immune function (Xiao et al., 2017; Hu et al., 2018; Cheng et al., 2019; Zhang et al., 2020), while others either observed a negative effect on these parameters (McCormack et al., 2018; McCormack et al., 2019) or no effect (Nowland et al., 2020a). Collectively, the main contributing factors for positive or negative outcomes when using FMT can be attributed to three main characteristics; the donor used, the method of administration, and the age of the animal receiving the treatment. In its current form, FMT does not have direct industry application as it requires the use of multiple oral doses and is often paired with

an intensive protocol aimed at reducing stomach acid secretions to ensure bacterial survival, making it less practical for use within young piglets and ineffective unless the timing and dose used are optimal. Further research on refinement of the technique to eliminate these issues is warranted, such as the efficacy of single doses either orally or via enema.

Nevertheless, if successfully developed, FMT has the potential to be used in multiple areas including improvement of growth and performance, as a preventative measure at times of high stress, or as an alternative to antimicrobials and the treatment or prevention of enteric diseases. Niederwerder et al. (2018) observed reduced morbidity and mortality in postweaned piglets treated with FMT before co-infection with porcine reproductive and respiratory syndrome virus and porcine circovirus type 2. More recently, Zhang et al. (2020) demonstrated that FMT from warthogs (*Phacochoerus africanus*) to commercial pigs conferred partial protection against attenuated African swine fever virus (ASFV) strains. However, the mechanisms for how this works needs to be investigated further. Given the significance of ASFV within the pork industry globally, with naïve pigs suffering a mortality rate of up to 100% (Sánchez-Vizcaíno et al., 2015), FMT as a potential preventative or treatment is encouraging.

In addition, promising applications of FMT are also occurring in other species, with potential implications for piglets. In humans, FMT has a greater than 90% success rate for the treatment of recurrent *Clostridium difficile* infections (Bakken et al., 2011) and has demonstrated success for treating inflammatory bowel disease (Fang et al., 2018). This is potentially important because disease caused by *Clostridium difficile* in sucking piglets can cause significant diarrhoea, requiring antibiotic use (Alvarez-Perez et al., 2009). In mice, FMT has been demonstrated to be able to both induce obesity and also reverse it (Ridaura et al., 2013), and has demonstrated efficacy in the treatment of experimental autoimmune encephalomyelitis (Li et al., 2020) and ulcerative colitis (Tian et al., 2016). Overall, this research is an emerging area of interest in all species and to date, the results are promising. Every new technique needs refinement before it can be utilised as a potential treatment in any capacity, whether that be for improving intestinal microbiota colonisation, as a method for improving production indices, as a preventative for enteric dysbiosis during times of high stress, or as a treatment for illness.

Microbial drivers of performance

Methods for improving pig health and productivity via intestinal microbiota manipulation have largely been through the use of dietary additives. There are a plethora of reviews in this area but, briefly, some of the methods investigated include phytochemical compounds (Walker et al., 2019), essential oils (Ruzauskas et al., 2020), organic acids (Oh et al., 2019), probiotics (Shu et al., 2001; Hayakawa et al., 2016), prebiotics (Tan et al., 2015; Liu et al., 2021) and minerals (Hojberg et al., 2005). It is evident that modulation of the microbiota is only one characteristic of how feed additives may function; however, when improved production outcomes are observed, there is generally a link with the colonisation of beneficial bacteria. Although the use of feed additives is a potential avenue for favourably manipulating the GIT microbiota and hence improving animal performance, the results in general are conflicting (for detailed reviews see: Bederska-Łojewska and Pieszka, 2011; Heo et al., 2013; Karásková et al., 2016; Tian et al., 2020). While the focus of these studies was to improve performance (e.g., growth, survival) through dietary additives, other studies have investigated the bacteria naturally present that are correlated with performance to better understand the key bacteria involved in optimal health and productiv-

ity. A list of some of the main bacteria involved in performance can be found in Table 1.

In this regard, Gaukroger et al. (2020a) observed that piglets with a higher average daily gain to 56 days of age had a higher abundance of *Lactobacillus*, unclassified *Prevotellaceae* and *Ruminococcaceae* UCG-005 at 4, 8 and 14 days of age, respectively, while those that were classified as poor performers were less abundant in *Ruminococcaceae* UCG-005 and more abundant in *Ruminococcaceae* UCG-014. This study also documented that differences in the GIT microbiota associated with performance were time-point specific, demonstrating the evolution of the intestinal microbiota as piglets aged. Additionally, Mach et al. (2015) observed an increase in abundance of *Ruminococcaceae* in piglets with better growth during lactation, while animals with higher abundances of *Prevotella* had lower growth rates during lactation

Table 1
Bacteria correlated with performance in young pigs.

Bacteria	Effects	References
<i>Actinobacteria</i>	A marker of diarrhoea resistance if present before weaning	Karasova et al. (2021)
<i>Bacteroidetes</i>	Increased abundance in diarrhoea resistant piglets and lighter pigs	Dou et al. (2017), McCormack et al. (2017)
<i>Bacillus</i>	Improved average daily gain and reduced feed conversion ratio	Wang et al. (2018a)
<i>Bifidobacterium</i>	Positively correlated with BW, improved average daily gain and reduced feed conversion ratio	Zhang et al. (2019), Wang et al. (2018a)
<i>Chlamydia</i>	A marker of diarrhoea resistance if present before weaning	Karasova et al. (2021)
<i>Faecalibacterium</i>	Present in non-diarrhoeic pigs after weaning	Karasova et al. (2021)
<i>Firmicutes</i>	Increased relative abundance in heavier and obese pigs	Cheng et al. (2018), McCormack et al. (2017)
<i>Fusobacterium</i>	Positively correlated with increased neonatal piglet diarrhoea	Cheng et al. (2018)
<i>Helicobacter</i>	A marker of diarrhoea resistance if present before weaning	Karasova et al. (2021)
<i>Lactobacillaceae</i>	Increased abundance in piglets that do not display postweaning diarrhoea	Dou et al. (2017)
<i>Lactobacillus</i>	Associated with increased feed efficiency and average daily gain, anti-inflammatory and antipathogenic activity against <i>Escherichia coli</i>	Gaukroger et al. (2020a), McCormack et al. (2017), Hillman (2001)
<i>Lachnospiraceae</i>	Increased abundance in piglets that did not display postweaning diarrhoea	Dou et al. (2017)
<i>Prevotellaceae</i>	Increased abundance in piglets with higher average daily gain and in those that did not display postweaning diarrhoea	Dou et al. (2017), Gaukroger et al. (2020a)
<i>Prevotella</i>	Reduced growth in lactation, but present in healthy pigs after weaning and improved average daily gain and feed conversion ratio	Mach et al. (2015), Karasova et al. (2021), Wang et al. (2018a)
<i>Roseburia</i>	Reduced feed conversion ratio and improved average daily gain	Wang et al. (2018a)
<i>Ruminococcaceae</i>	Improved lactation growth and higher in piglets not displaying postweaning diarrhoea	Mach et al. (2015), Dou et al. (2017), Gaukroger et al. (2020a)

but higher average daily gain after weaning. This may be because *Prevotella* produces enzymes that degrade complex dietary polysaccharides that would improve fibre digestibility and feed efficiency following weaning (McCormack et al., 2017; Le Sciellour et al., 2018).

Postweaning diarrhoea (PWD) is a major problem worldwide, hence there is interest in non-antimicrobial methods to try and control or mitigate this disease, for example, favourably manipulating the microbiota during lactation to reduce diarrhoea after weaning. Karasova et al. (2021) documented a correlation between specific faecal bacteria present before weaning and the incidence of PWD. Increased abundance of Actinobacteria 3 days before weaning was a marker for increased PWD, while increased abundance of *Chlamydia* and *Helicobacter* before weaning were markers for healthy and diarrhoea resistant pigs after weaning. Additionally, healthy pigs after weaning had a higher abundance of *Prevotella* and butyrate-producing *Faecalibacterium* in their faeces. Similarly, Dou et al. (2017) observed that piglets not displaying PWD (assessed 2 weeks after weaning) had a different microbiota compared to those with PWD when examined at 7 days of age, in lactation. Weaned pigs with less diarrhoea displayed a lower evenness and higher abundance of *Prevotellaceae*, *Lachnospiraceae*, *Ruminocaccaceae* and *Lactobacillaceae* at 7 days of age when compared to animals that presented with PWD. This may be due to the improved nutrient digestibility often associated with *Lactobacillaceae* (Le Sciellour et al., 2018), *Prevotellaceae*'s ability to degrade complex carbohydrates (Le Sciellour et al., 2018), and (or) the capacity to reduce intestinal inflammation and improve intestinal barrier function through the production of butyrate from the families *Ruminocaccaceae* and *Lachnospiraceae* (Wang et al., 2018b; Hall et al., 2021). This is supported by Jenkin et al. (2015) who demonstrated improved growth and reduced *E. coli* shedding with a higher abundance of butyrate-producing *Christensenellaceae*. Non-diarrhoeic piglets also had a higher abundance of *Bacteroidetes* 1 week prior to the onset of diarrhoea, at 30 days of age. Additionally, Luise et al. (2021) assessed the faecal microbiota of pigs before and after weaning across 16 farms and observed that those pigs less disrupted by weaning, as seen by less of a reduction in growth, had a more mature microbiota characterised by a greater abundance of *Prevotella*. All in all, these studies demonstrate that positive links occur between the piglet GIT microbiota, or a change in the piglet GIT microbiota, and production parameters. However, further studies are needed in order to more clearly elucidate how these bacteria have this effect and then how the microbiota can reliably and consistently be altered to establish young pigs for life-long benefits.

Impacts of microbiota-derived metabolites on the gastrointestinal tract

Another approach used to identify how different bacteria influence GIT structure and function is through the analysis of microbiota-derived metabolites. Beaumont et al. (2021) assessed the metabolite signature before (13 days old) and after (23 days old) weaning across different lactation rearing locations, and found that diet and rearing location influenced GIT microbial communities and their associated metabolites. The GIT microbiota composition drives metabolite production and hence, potentially, regulates GIT functionality. Bacterial metabolites that have been widely documented include short-chain fatty acids butyrate, propionate, and acetate. Butyrate is a common metabolite that represents a major energy source for intestinal epithelial cells and is known to enhance intestinal barrier function and attenuate intestinal inflammation (Bedford and Gong, 2018), while propionate has been demonstrated to reduce colitis by improving intestinal barrier

function and reducing inflammation and oxidative stress (Tong et al., 2016). Additionally, acetate has the capacity to restore mucosal barrier function and support immune health (Beaumont et al., 2021). When investigating the link between metabolites and bacteria in pigs, Beaumont et al. (2021) observed a correlation between the relative abundance of bacteria *Christensenellaceae*, *Ruminococcaceae*, *Oscillospiraceae* and *Prevotellaceae* after weaning and short-chain fatty acid production. Additionally, Li et al. (2018a) observed links with weaning stress-induced GIT microbiota dysbiosis and, relative to nursing piglets, the decrease in key metabolic pathways including phenylalanine metabolism, the citrate cycle, glycolysis or gluconeogenesis, propanoate metabolism, nicotinate and nicotinamide metabolism. This area of research is still relatively new, and to our knowledge, no study has assessed the specific metabolites most beneficial for GIT health in piglets during lactation. As this area expands, it has the potential to provide knowledge that is beneficial for understanding how microbial communities influence GIT function, enabling the development of nutritional strategies targeting the production of bacterial metabolites for the improvement of GIT health.

Conclusions

A review of the existing literature in pigs and other species demonstrates that a major determinant of the health and performance of animals is microbial colonisation of the GIT in early life. Additionally, the mother, pen environment and general husbandry practices such as cross-fostering and antibiotic administration to sows and piglets also influence the intestinal microbiota, therefore also impacting long-term piglet health, performance and survival. It is evident that studies developing understanding associated with initial microbiota colonisation are beneficial in order to determine how to target optimal microbial colonisation for industry benefits. However, the majority of literature in this area tends to focus either on piglets preweaning short-term or on the immediate post-weaning period. Further research is needed in order to elucidate the longer-term effects of normal husbandry practices on piglet intestinal microbiota, health and survival. Ultimately, this understanding will allow for the development of industry applicable practices that are targeted at optimal microbial colonisation for long-term benefit. This area of research presents significant potential for application within the pork industry, especially if more focus is placed on early-life events and setting piglets up early for long-term improvements.

Ethics approval

Not Applicable.

Data and model availability statement

Not Applicable. No original data or experimentation is presented in this article.

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Declaration of interest

None.

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