

Review Article

IMPORTANCE OF GUT MICROFLORA IN POULTRY

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Introduction

The development and composition of the gut microflora in poultry involves several complex mechanisms and are both dependant on many factors, ranging from the age of the birds to dietary ingredients as well as the environment in which the birds are reared. The physiological contribution of gut microflora in poultry nutrition include improvement in digestion through secretion of microbial enzymes, vitamin synthesis, detoxification of some anti-nutritional factors, competitive exclusion of pathogens, development of immune system and intestinal homeostasis. Recently it has been established that gut microflora also play role in the expression of gut gene.

Gut microflora can also directly interact with the lining of the gastrointestinal tract (Van Leeuwen *et al.*, 2004), which may alter the physiology of the tract and immunological status of the bird (Klasing *et al.*, 1999). Harmful members of the gut microflora may be involved in localized or systemic infections, intestinal putrefaction and toxin formation (Yegani and Korver, 2008).

Gut microflora on production

Gut microflora involved in competitive exclusion, which is resistance to colonization by pathogenic and other non-indigenous microbes (Snel *et al.*, 2002). Competitive exclusion relates to maintaining beneficial microflora in the host by suppressing the growth of pathogenic bacteria while encouraging the growth of beneficial bacteria. This protection occurs by resident flora suppressing colonization by secreting antimicrobial compounds such as organic acids, by direct stimulation of the immune system and by competing for nutrients and attachment to the mucosal surfaces (Dibner and Richards, 2005).

The gut microflora provides an extensive array of enzymes and substrates which together provides an extensive metabolome available for nutrient and energy derivation from

the diet (Stanley *et al.*, 2013). There is relationship between the apparent metabolizable energy of the diet and microbial composition in the hindgut of the host. This is due to direct conversion of some dietary components into high energy metabolites by specialized bacteria. The utilization of such fermentation end products as lactic acid and short chain fatty acid (SCFA) would provide more energy for the host (Lan *et al.*, 2005) and improved feed conversion efficiency (Rinttila and Apajalahti, 2013).

The commensal bacteria in broiler chickens generate SCFA such as acetate, propionate and butyrate (Van der Wielen *et al.*, 2000). The release of SCFA from fermentation of non-hydrolysable oligo and polysaccharides may provide an extra energy to the birds and improve the feed conversion ratio (Lan *et al.*, 2005). The undissociated form of SCFA play an important role in reducing the number of undesirable bacteria species in the caeca (Van der Wielen *et al.*, 2000; Snel *et al.*, 2002).

Gut microflora on energy utilization

An active microbial component in the gut may have an increased energy requirement for maintenance as well as a reduced efficiency of nutrient utilization and this is a nutritional burden in fast growing broiler chickens (Lan *et al.*, 2005). When dietary energy is supplied in the form of substrates which are easily digested by birds, the efficiency of energy utilization may be reduced due to the presence of gut microflora.

The microbes compete with the host for substrates (Muramastu *et al.*, 1994), which limits metabolizable energy (ME) values of the diets. Not all energy digested in chicks is necessarily utilized for growth, because the microflora will use part of it for their own metabolism, suggesting that although the gut microflora may have beneficial effects on the digestion of certain dietary components, they may also have a negative effect on ME utilization by the host. It is therefore expected that broiler chicks harbouring an active gut microflora apparently have an increased energy requirement for maintenance (Lan *et al.*, 2005).

Gut microflora on protein utilization

Diets contain high protein with unbalanced amino acid profile, have reduced digestibility in the upper gut and thus larger concentrations of these compounds, as well as their metabolites, are found in the lower gut (McDevitt *et al.*, 2006). These poorly digested proteins are known to act as substrates for the microflora in the lower gut. The proteins can be degraded to ammonia and amines, thus encouraging the proliferation of pathogenic bacteria such as *Clostridium* sp. Further the presence of these nitrogenous degradation

products tends to raise the pH of the lower gut because of their relatively high pKa values and counteract pH changes that would normally occur due to the bacterial production of acetic and lactic acids, thereby enhancing proliferation of *Clostridium* sp. (Lan *et al.*, 2005), which subsequently leads to necrotic enteritis (NE) in chickens.

Conclusion

The intestines of each animal are the complex and dynamic ecosystem with important effects to the host. The gut microflora or final products of this ecosystem influence nutrient digestion, absorption, mucosa metabolism, general physiology and local and systemic immunological responses of avian hosts. Better understanding of avian gut microbial communities are very important for the appropriate manipulation of diets to improve poultry performance, health, welfare and reduce food borne pathogens and the environmental impact of poultry production for a sustainable industry.

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