



**MICROBIAL HOMEOSTASIS IN THE ALIMENTARY CANAL OF CHICKENS
AND ITS RELATION TO SOME FACTORS INVOLVED: REVIEW ARTICLE**

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ABSTRACT:It should be noted that both eggs and meat of chickens are essential to human nutrition all over the world. In recent years, the modern poultry industry has undergone remarkable changes in its production methods over the past 50 years. Interestingly, intestinal microorganisms have evolved alongside the host, as gut health plays an essential and very important role for optimal production. When the health of the gut is negatively affected, the digestion and absorption of nutrients are also negatively affected, which has a bad effect on the feed conversion ratio, that leads to an economic loss and increased exposure to different diseases. Thus, the microbial communities that live in the gut of chickens are essential for intestinal homeostasis and metabolism of the host, which will subsequently affect the physiological and health status. Clearly, the dynamic equilibrium, composition and good diversity of microorganisms are influenced by many environmental and management factors. However, microorganisms increase dramatically during the first weeks of a bird's life, and the corresponding colonization patterns appear to differ between laying and meat-type chickens. On the other hand, the gut microbiota and their relationship to health and productivity in both broilers and laying chickens are difficult to determine with precision due to the great variation between flocks, which arises due to many environmental and management factors that affect the microbial load of both beneficial and harmful bacteria alike surrounding birds. In this article, we will focus on the importance of microbial homeostasis in the alimentary canal of chickens and the various factors that affect this balance, and the results of these reactions on general health and productivity.

Key words: chicken, microbiota, health status, environmental factors, alimentary canal.

INTRODUCTION

In recent years, there is a great demand for poultry products, where production reaching 130 million tons of chicken meat in 2020(OECD/FAO, 2017). Among traditional livestock species, poultry are the most efficient feed converters, with a feed conversion ratio in the range of 1.6–2.0. The maintenance of a high feed efficiency plays an essential role in the capacity of the poultry sector to meet the growing demand for poultry products. However, poultry are characterized by its great ability to convert feed, whether into meat or eggs, depending upon the gut environment. Thus, Akinyemi *et al.* (2020) indicated that gut microbiota plays essential roles in health, growth and development of all poultry species. They added that gut microbiota, health and productivity are interwoven and influenced by many factors including host derived, environmental and nutritional factors. In other reports, Carrasco *et al.* (2019) showed that gut microbiota plays a major role in maintaining gut health through their ability to modify the host's physiological functions required to maintain intestinal balance, mainly through competitive exclusion of harmful microorganisms and pathogens, preventing colonization and thus reducing the energy expenditure that birds usually possess in keeping the immune system active against these pathogens. They also added that "healthy" gut microbiota meant providing the host with energy, which translates into improved production performance of the birds. The results obtained by Yadav and Jha (2019) indicated that digestion, absorption, metabolism, and overall health and growth performance of poultry are significantly improved by gut microbiota and their metabolic products. Also, the health of poultry is affected by structure and function of the intestinal microbiota, as the development of the intestinal epithelium and the modification of the physiological functions are necessary to

maintain intestinal homeostasis (Kers *et al.*, 2018). Furthermore, Iqbal *et al.* (2020) showed that gut microbiota play an essential role in maintaining the optimum health of birds, where it helps in the process of digestion and absorption of feed as required and necessary to reach the desired body weight. There are many factors such as the environment, heat stress, and housing conditions that can cause changes in the gut resulting in poor health and production performance. Therefore, this article provides a brief and comprehensive description concerning the importance of microbiota homeostasis and their interactions with intestinal health and productivity and factors involved.

Definition the microbiota and importance of gut microbial homeostasis.

The microbiota can be briefly defined as an ecological communities of commensal, symbiotic and pathogenic microorganisms, which usually colonizes a specific area of human and animal organisms, and is more than twice the abundance of the host's physical and germ cells (Sender *et al.*, 2016). However, Shanget *al.* (2018) indicated the alimentary canal of chickens contains a complex groups of microbiota, which plays an important role in digestion and absorption of nutrients, immune system development and pathogen exclusion. Also, the microbial communities that live inside the digestive system of chickens are necessary for intestinal homeostasis, to reach the best metabolism and to maintain the physiological and health status (Borda-Molina *et al.*, 2018). Moreover, Clavijo and Fl'orez (2018) reported that the intestinal microbiota plays an important role in maintaining the overall health of the host as it has a positive effect on the immune system, digestive system, and productivity. On the other hand, dysbiosis can be defined as qualitative and/or quantitative imbalance of normal microbiota in the small intestine. While, Walker (2017) found that dysbiosis appears in the host in the event of a change in bacterial colonies or bacterial diversity that is accompanied by the emergence of the disease and the loss of certain bacteria, leading to an increase in the harmful bacteria.

Chicken, microbiota, health status, environmental factors, alimentary canal.

Distribution of microbiota in the alimentary canal.

It is well known that at hatch the alimentary canal of chick is anatomically complete (Overton and Shoup, 1964), but the functional efficiency is not yet complete. The alimentary canal of chickens includes the crop, gizzard, duodenum, ileum, and cecum, where each section has different metabolic functions that suit the livelihood of the microbial community, which are microbiologically abundant with over 900 documented bacterial species (Wei *et al.*, 2013a). However, Apajalahti *et al.* (2004) reported that primary bacteria grow very quickly, and soon the sterile environment becomes populated with 10⁸ and 10¹⁰ bacteria per gram of feces in the ileum and cecum, respectively on the first and third days. Furthermore, the alimentary canal is composed of a large proportion of gram-positive, mainly facultative anaerobes from crop to lower ileum, while the ceca are composed of *Lactobacillus*, *Enterococcus*, *coliforms*, and *yeasts* (Gaskins, 2001). The results of Sergeant *et al.* (2014) indicated that the microbiota in chicken small intestine may be composed of between 200 and 350 different bacterial species. In other reports, Shang *et al.* (2018) showed that the alimentary canal of chickens contains a diverse and complex group of microorganisms that play an important role in digestion and absorption of nutrients as well as enhancing immunity and eliminating pathogenic bacteria. Clearly, Roto *et al.* (2016) observed that anaerobic bacteria dominate the small intestine and contain *Lactobacillus* and *Bifidobacterium* species in high concentrations as well as *Enterococcus faecium* and *Pediococcus spp.* Thus, although the presence of these bacteria in the small intestine, it was discovered that the concentrations of bacteria in the ceca area were the highest, at ~10¹¹ bacteria/g (Rehman *et al.*, 2007). They added that the microbial density and diversity is greater in the cecum as longer digestion times

allow for greater microbial fermentation. However, the majority of bacteria present in the gizzard are lactobacilli, enterococci, lactose-negative *enterobacteria*, and *coliform* bacteria. The duodenal bacterial community consists mainly of *Clostridium*, *Streptococci*, *enterobacteria*, and *Lactobacilli* (Waite and Taylor, 2015). Also, they added that the duodenal bacterial community mainly consists of *clostridia*, *streptococci*, *enterobacteria*, and *lactobacilli*. Ileum microbiota have been studied the most among the small intestine segments. In addition, the small intestine contains the highest concentration of bacterial cells, mainly *Lactobacillus*, *Enterococcus* and *Clostridiaceae*, where the *Lactobacillus* was the dominant genus making up nearly 70% of the total (Han *et al.*, 2016). In this connection, Lu *et al.* (2003) found that *Lactobacillus* bacteria make up the largest percentage of bacteria in the digestive system, as it constitutes about 70%, followed by *Clostridiaceae* family with a rate of 11%, then *Streptococcus* and *Enterococcus* with percentages 6.5% for both. On the other hand, anaerobic bacteria dominate the caecum of broiler chickens, where more than half of these bacteria belong to the order Clostridiales (families *Lachnospiraceae* and *Ruminococcaceae*, also referred to as Clostridial groups XIVa and IV, respectively) (Bjerrum *et al.*, 2006).

The relationship between gut health and microbiota homeostasis.

The term 'gut health' refers to the health status of the gut and concerns with gut development and function. Therefore, Celi *et al.* (2017) illustrated that the effective functions of the alimentary canal and their health are determining factors in an animal's performance. Further, gut health is very important regarding animal nutrition, and there is still a lack of information in a clear scientific definition despite it being used frequently in animal health (Kogut and Ryan, 2016). Moreover, Borda-Molina *et al.* (2018) indicated in poultry that, the alimentary canal includes the microbial communities that play a fundamental role in gut homeostasis and host metabolism in addition to

animal physiology, production and health. It is important to note that the integrity of the microbial community in the alimentary canal of chickens is very important in good nutrient absorption and also has an important role in developing immunity and disease resistance. Also, changes in the microbial community may have adverse effects on feed efficiency, productivity and health status (Kohl, 2012). Interestingly, Kers *et al.* (2018) showed that the structure and function of the gut microbiota is extremely important to the health of poultry because the process of acquisition and maturation of the gut microbiota throughout the growth cycle of birds has a strong influence on the development of the intestinal epithelium and the modification of the physiological functions required to maintain intestinal balance (i.e. immunity, digestion of nutrients, and the integrity of the intestinal barrier). Thus, these functions are essential to improve the efficiency of extraction and energy utilization by the host. Also, Rinttilä and Apajalahti (2013) found that the intestinal flora has great metabolic capabilities that clearly affect both either nutrition or health of the host. However, **Clavijo and Florez (2018)** observed that the presence of microbiota in the alimentary canal of broiler chickens has an important role in obtaining good health and also plays a prominent and positive role on the immune system and in general the physiology of the alimentary canal. On the other hand, Polansky *et al.* (2016) found that gut health has a definite relationship with the existence of bacterial equilibrium, where these microbes have the ability to modify the physiological functions of the host in terms of their prominent role in the occurrence of intestinal balance and this occurs through the competitive exclusion of harmful microorganisms and pathogens and the prevention of colonization and thus reduce energy expenditures as birds usually

invest it in keeping the immune system active against these pathogens. While, Carrasco *et al.* (2019) showed that there is a clear difficulty in establishing the relationship between the presence of microbiota in the alimentary canal and its relationship to both health and productivity in broiler chickens, and this is due to the presence of a large discrepancy between flocks due to many environmental, nutritional and host factors that affect the microbial load of both commensal and pathogenic bacteria surrounding the birds during their growth cycle.

The role of microbiota in host nutrition and performance.

It is well known that digestive bacteria produce short chain fatty acids (SCFAs) during breaking down of dietary polysaccharides (Dunkley *et al.*, 2007). It has been found that there is a difference in the composition and proportions of these SCFAs, depending on the microbial composition, which is adaptable to some extent and is controlled by the composition and structure of the fiber component in the chicken diet (Topping and Clifton, 2001). However, Acetate is a precursor of SCFAs that is produced in most of the digestive system environments of chickens, following the production of both propionate and butyrate. Indeed, other SCFAs such as valerate, isobutyrate, and isovalerate are also produced in trace quantities as compared to acetate and propionate. It is noted that butyrate concentrations have a special physiological importance in the production of SCFAs, as they are the main energy source for the colon epithelium and have been shown to be required for homeostasis and the development of gastrointestinal morphology (Donohoe *et al.*, 2011). It is of utmost important, therefore, that SCFAs act and aid in fluid and electrolyte absorption and are absorbed via the epithelium and are an important source of energy, contributing between 10% (humans) and up to 70% (ruminants) of the host's daily energy requirement (Flint and Bayer, 2008). Therefore, Panda *et al.*, (2009) indicated that the SCFAs, butyrate have been shown to improve growth

Chicken, microbiota, health status, environmental factors, alimentary canal.

performance and carcass characteristics in chickens. The importance of intestinal microbiota for the performance of broiler chickens has been studied for decades. However, it is observed that the initial development of intestinal microbiota in poultry plays an important role in production performance (Kers *et al.*, 2018). In addition, an important thing to note is that the gut bacteria also contribute to the metabolism of the host nitrogenous compounds. For example, cecal bacteria can convert uric acid into ammonia which the bird later absorbs and is also used to produce some of the non-essential amino acids such as glutamine (Vispo and Karasov, 1997). Moreover, Metges (2000) indicated that some nitrogen from the diet is incorporated into the bacterial cellular protein, thus, the bacteria themselves can be a source of proteins / amino acids.

Factors affecting the microbial homeostasis.

It is documented that the productive performance of the animal depends primarily on the effective functions of the digestive system and its health. Many complex mechanisms are involved in regulating the functions of the alimentary canal and its health. Therefore, it is necessary to study these interactions so that strategies can be developed to modify the functions of the alimentary canal and its health status. (Celi *et al.*, 2017). However, the health of the alimentary canal of chickens depends on many factors, including the environment, the feed, and the microbiota of the alimentary canal. Therefore, environmental factors such as level of biosecurity, housing, litter, access to forage, and climate also influence the formation of intestinal microbiota (Kers *et al.*, 2018). Also, the intestinal microorganisms share with the host's health and productive performance and are influenced by many other factors such as environmental and nutritional factors derived from the host, which consequently affect the

growth and performance of these birds (Akinyemi *et al.*, 2020).

1-Diet and feed supplements.

It is known that diet plays an important and essential role in the gut health of the host by modifying the alimentary canal bacteria, which can cause a positive or negative effect on the host, depending on the type of diet (Jha and Berrocoso, 2015). Thus, Rehman, *et al.* (2008) stated that the microbiota is important for the host's nutrition, proper metabolism, and the maintenance of the immune system. These microbiota can be affected by many factors such as age, stress, diet, and performance enhancers. Therefore, Gabriel *et al.* (2006) reported the main characteristics of feed that can affect the microorganism and one of these features is the grain shape (whole or ground grains, or pellets); type of grain; the amount of water-soluble non-starch polysaccharides; and sources of fats, starch and proteins. However, the use of feed additives in diet clearly modifies the gut microbiota by stimulating the growth of certain microorganisms as well as improving gut health. In the crop, phytase enhances the abundance of *Aeromonadaceae* and *Flavobacteriaceae* while decreasing the dominance of *Lactobacillus* (Witzig *et al.*, 2015). In this context, Ptak *et al.* (2015) found that the inclusion of phytase in diets increases the abundance of *Lactobacillus* sp., *Clostridium leptum* and *Enterococcus* sp., in the ileum of chickens. Also, Dittoe *et al.* (2018) argued that the use of acidic compounds including organic acids can be used as safe alternatives to antibiotics, where studies have shown that organic acids have a positive effect on improving the performance of the productive performance of poultry by changing the pH in the alimentary canal and thus changing the composition of the microbiota. However, DeMaesschalck *et al.* (2015) indicated that there is an increase in xylo-oligosaccharides in the colon, which increase the presence of *Lactobacillus* and the *Clostridium* cluster XIVa in the caeca which is known to possess genes related to butyrate

production such as the butyryl coenzyme A and acetate CoA transferase.

2- Heat and cold stress.

Many studies have indicated the relationship between changes in the gut microbiota and the occurrence of imbalance in the immune system in poultry, which is greatly affected by stress factors. It is noticeable that the climate in the poultry house is greatly influenced by the geographical location, which consequently affects the intestinal flora of the chickens (Zhou *et al.*, 2016). For more details, Song *et al.* (2014) observed that one of the most important negative effects of heat stress is that it leads to a decrease in the number of cecal *Lactobacillus* counts with an increase in the number of *Clostridium* populations in poultry. In addition to the above, there is also a loss or deficiency of beneficial bacteria, including *Lactobacilli* and *Bifidobacteria*, in poultry due to the occurrence of heat stress (Burkholder *et al.*, 2008), this indicates that its role against pathogen colonization may be weakened, thus enhancing the susceptibility of the gut to invade and colonize intestinal pathogens (Awad *et al.*, 2018). However, it has been observed that there are some morphological and physiological changes in the alimentary canal upon exposure to heat stress, and these changes include the function and integrity of the intestinal epithelium (Meddings and Swain, 2000). Also, Wang *et al.* (2018) indicated in general, that exposure to heat stress alters the composition and population of microorganisms in the intestine of chickens. Additionally, when the conditions causing the proliferation of pathogenic bacteria such as *Escherichia coli* and *Salmonella*, as well as the total aerobic bacteria in the cecum are present (Kammon *et al.*, 2019); where there is also a large and growing number of zoonotic pathogens such as the *Moraxellaceae* family and the *Pseudomonadales* order in the jejunum and the *Rickettsiales* order in the cecum (He *et al.*,

2019). Finally, we can notice that heat stress leads to gut dysbacteriosis because the intestinal tract of poultry is highly susceptible to stress factors, which can lead to damage to the intestinal mucosa and the occurrence of changes and disruption of defense microbes (Dayou *et al.*, 2019). On the other hand, in relation to the effect of cold stress on microorganisms, Tsiouris *et al.* (2015) indicated that cold stress caused a marked increase in the number of pH and *C. perfringens* counts in the caeca, where cold stress increased susceptibility to necrotic enteritis in a subclinical experimental model, and therefore should be considered as physical environmental stresses that can significantly affect the well-being, health and intestinal ecosystem of broiler chicks. Also, the cold stress was associated with a significant increase in the pH of caecal contents in addition to an increase in *C. perfringens* in cecum in non-hostile birds. Increasing the pH of the caecal content leads to the proliferation of *C. perfringens* (Lan *et al.*, 2005). While, Williams (2005) reported that the exposure to cold stress in chickens caused the low pH of the jejunum, duodenum and ileum, where the reduction of pH in the small intestine also caused the increase of *Eimeria spp.* and *C. perfringens*.

3-Age

It is a known fact that with the advancement of the chicken's age, major changes occur in the microbial community in the alimentary canal, where there is an increase in the number of different microbial species during the first weeks of life, as one-day-old chicks already carry a different group of microorganisms in the Intestine (Ballou *et al.*, 2016). Therefore, the individual difference in the composition of the microorganism decreases with the age of the chickens (Crhanova *et al.*, 2011). Ultimately, pre-hatching microorganisms can be obtained directly from the mother into the hen's oviduct (Gantois *et al.*, 2009), or through the surrounding environment or from the egg shell openings (Roto *et al.*, 2016). Whereas, after hatching, young chicks may be colonized prior to their arrival on the farm by microbes from the

Chicken, microbiota, health status, environmental factors, alimentary canal.

environment in the hatchery or during transportation (Pedroso *et al.*, 2005). Nevertheless, several studies that have examined the effect of time on the microbiota alimentary canal of chickens have indicated that the caecum is the part that has a great diversity and abundance of microbes compared to the entire intestine (Sergeant *et al.*, 2014). Also, the numerous studies conducted in this field have described a major successive change in the taxonomic composition of bacteria, which becomes more abundant and taxonomic diversity as the life cycle progresses (Van Der Wielen *et al.*, 2002). Thus, it was observed that as the chick was one day old, the microbial concentration in its intestine was 10^8 to 10^{10} cells / g of digesta, but upon reaching age less than one week, the maximum concentration of bacteria reached 10^9 to 10^{11} cells / g (Rinttilä and Apajalahti, 2013). In a study reported by Kers *et al.* (2018) found the diversity of the intestinal microbiota of chickens had increased significantly during the first weeks of life, and that the patterns of bacterial colonies differed between layer and meat-type chickens.

4- The use of antibiotics

It is noted that the use of antibiotics in the treatment of diseases has a strong effect on the formation and composition of microbiota, which is attributed to the environment in which the chickens were raised, whether they were raised in cages or on the floor (Pedroso *et al.*, 2006). Studies have shown that the microbial change in the intestine when using antibiotics in one day old chick had a negative effect on the development of the immune system (Schokker *et al.*, 2017). However, Mancabelli *et al.* (2016) found among the recent confirmed evidence that the use of antibiotics in chickens resulted in a marked change in the bacteria and their stability later, which indicates a decrease in the stability of the microbiota and also leads to a decrease in the population of *Lactobacillus* in the intestine. Further, in the study reported by Danzeisen *et al.* (2011) indicated that the

microbial community including *Roseburia*, *Lactobacillus*, and *Enterococcus* showed a decrease, and *Coprococcus* and *Anaeroflum* were enriched as a result of using antibiotic such as monensin alone, or monensin in combination with virginiamycin or tylosin.

5- Probiotics and prebiotics supplementation.

From the general point of view, probiotics are "live microbial feed supplements, which beneficially affect the host by improving its intestinal microbial balance (Fuller and Gibson, 1998). In this context, Pereira *et al.* (2018) showed that the supplementation of probiotic *B. subtilis* resulted in lower richness and diversity indexes in the caecum contents, indicating a more stable microbiota which can be beneficial for the host, resulting in better performance of the chickens. However, prebiotics are indigestible oligosaccharides that have a positive effect on the host by stimulating the growth of some bacteria as well as they act as a source of nutrients for the commensal microbes and can suppress the pathogenic bacteria to stick to the oligosaccharide and secrete before sticking to the mucous membrane and causing inflammation (Gibson and Roberfroid, 1995). Therefore, Teng and Kim (2018) indicated that when using prebiotics, it leads to significant effects on the health of the poultry by modifying the microbial community in the intestine and the interaction between the host's immune system and the gut microbes. It was therefore indicated that prebiotics directly improved the microbial community, gut integrity, and host immunity. Also, some prebiotics affected protection against *Salmonella* by providing binding sites for bacteria to be expelled from the alimentary canal (Charalampopoulos and Rastall, 2009). Several studies have also indicated a decrease in *Salmonella* counts by increasing concentrations of short-chain fatty acids (Durant *et al.*, 2000) that can be reached through prebiotic administration (Ricke, 2015). Furthermore, Park *et al.* (2017) studied the effects of prebiotics on the alimentary canal microbiota by 16S microbiome sequencing. They have indicated changes in the

concentrations of the metabolite or metabolites, and this approach may be able to correlate changes in the microbiome with changes in the concentration of metabolites such as SCFAs and other metabolites, which may stunt the growth of *Salmonella*.

6-Maternal factors.

Chicks depend on maternal antibodies as the main source of passive natural humoral protection until they become immunocompetent. Immunoglobulin Y (IgY), the avian homologue of mammalian IgG is transferred from the circulation of the hen into the egg yolk and then absorbed by the embryo. In the post-hatching period, protein integrity within the yolk sac is critical for normal absorption of the yolk sac content and for IgY transfer to the circulation of the chick. Factors affecting transfer of IgY to the chick may threaten the chick's immune status and increase disease susceptibility during the early post-hatching period (Franco, 2012). It is seen that the microbiota composition is also affected by the maternal antibodies, which are transferred from the mother to the egg yolk. Therefore, the sufficient presence of antibodies provides the complete protection against some pathogens for up to two weeks after hatching (Hamalet *et al.*, 2006), and this may affect the intestinal microbiota of the chicks.

7- Chicken type and breed.

Studies conducted on broiler and layer chickens indicated that there is a paucity of research related to the formation of microorganisms in the alimentary canal. The host's genetic background has been identified as a factor that may affect enteric microbiota formation (Org *et al.*, 2015). Therefore, it is possible that differences in intestinal physiology between laying and broiler chickens influence the formation of microorganisms and vice versa. As far as we know, studies comparing bacterial formation between broiler and layer chickens are rare. Also, the difference in exposure to microbes in

the housing environment and the fundamental differences in the nutritional composition of both broilers and layer chickens also affect the formation of microorganisms (Videnska *et al.*, 2014). It has been found through other studies published by Persoons *et al.* (2011) that there are biological differences between laying and broiler chickens, and even further, there are also differences within the breeds of chickens of the same type. As a previous observational study showed that, the broiler breed was a factor associated with colonization by antibiotic-resistant strains of *Escherichia coli*. However, Schokker *et al.* (2015) showed that the mechanisms underlying the difference in intestinal microbiota between broiler breeds remain unclear, but it has been found that genetic background and immune system influence gut microbiota formation after hatching. Moreover, in faecal samples, the broiler strains with a better feed conversion ratio, indicating a more efficient use of feed for growth, showed higher numbers of *Lactobacillus* compared to the lines of broilers with an inferior feed conversion ratio (Mignon-Grasteau *et al.*, 2015).

8-Sex

It was observed through studies that factors not related to growth affect the differences in bacterial communities between males and females in chickens, and no differences in the growth rate were observed until day 21, while differences were actually observed on the third day in the formation of intestinal microbiota (Lumpkins *et al.*, 2008). A study, reported by Torok *et al.* (2013) showed differences in the abundance of *Lactobacillus salivarius*, *L. crispatus*, *L. aviarius* and *E. coli* in ceca of female and male broiler chickens. However, the composition of the intestinal microbiota in the 245-day-old chickens and the lines of the different broilers, i.e., the high and low body weight line, the relative abundance of 48 species of microbes was significantly different between the sexes (Zhao *et al.*, 2013).

9-Sampling the alimentary canal of chickens.

It is well known that the alimentary canal of the chicken includes the crop, proventriculus, gizzard,

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duodenum, jejunum, ileum, caeca, large intestine, and cloaca (Yeoman *et al.*, 2012). Each part of the alimentary canal has a specific function in the digestion of feed, indicating that there are differences in the requirements for the types of microorganisms that should be present in each of these parts. The differences in the composition and abundance of bacteria between different areas of the alimentary canal were reviewed in detail earlier. It is noteworthy that the duodenum and ileum are all dominated by the *Lactobacillus* species (Stanley *et al.*, 2014). While, Videnska *et al.* (2013) stated from the information that has been confirmed, the caecum is the part of the alimentary canal that has the highest microbial richness and is mainly colonized by anaerobic microorganisms. While, with regard to the bacteria present in gizzard it was found to contain *Lactobacillus*, *Enterococcus*, *lactose-negative Enterobacteria*, and *coliform* bacteria. (Rehman *et al.*, 2007). Also, as for the duodenum, it was found to contain mainly *Clostridium*, *Streptococci*, *Enterobacteria* and *Lactobacilli*. Also, Lu *et al.* (2003) evaluated the ileum bacterial community by examining the 16S rRNA gene sequence and found that *Lactobacillus* was the main group (70%) followed by members of the *Clostridiaceae* family (11%), *Streptococcus* (6.5%) and *Enterococcus* (6.5%).

10-Biosecurity level .

Relatively, high levels of hygiene in hatcheries are important in poultry production, as it has been found that cleanliness has an effect on the development of the alimentary canal and immune systems. This is due to the delay in exposure to "healthy" microbiota (Bailey, 2010), which can be compared to the assumed "hygiene hypothesis" for humans (Lashner and Loftus, 2006). On the other hand, high levels of hygiene inside hatcheries can lead to the presence of altered intestinal microbiota between batches of newly hatched chickens. It is observed that the intestinal bacterial

community is somewhat random and completely heterogeneous due to the bacteria being exposed to a variety of environmental sources after hatching, rather than colonizing the mother-derived bacteria (Stanley *et al.*, 2013). Also, Forder *et al.* (2007) found that there are different sources that affect the microbiota and among these sources are people who deal with chicks, transport boxes, feed and litter in poultry houses. It has been observed that in poultry raised in isolators, the intestinal morphology was found to change with shorter villi, more shallow crypts, and decreased acidic mucin production compared to conventional elevated broilers, which may lead to the formation of different microorganisms.

11-Housing

Numerous studies have indicated the effect of housing on microorganisms. The results obtained indicated that the type of production system can affect the formation of microorganisms. There are some other studies that compared organic farms with traditional farms, as they indicated that there is a large number of *C. perfringens* in ileum and caecum samples from broiler chickens kept in organic farms (Bjerrum *et al.*, 2006). Moreover, the previous author found lower numbers of *Enterobacteriaceae* and higher numbers of *Lactobacilli* in the ileum content of birds raised in organic farms. The possibility of reaching an external range of *Bifidobacterium* enrichment in caeca and ileum has been demonstrated in broiler chickens (Gong *et al.*, 2008), which resulted in a high proportion of *Bacteroidetes* in the cecum and a low proportion of *Firmicutes* / *Bacteroidetes* in Dagu chickens (Xu *et al.*, 2016). On the other hand, a decrease in the growth performance and bacterial formation was observed in the caecum samples when the flock was stocked at a density of 17 birds per square meter, compared to the breeding density of 12 birds per square meter (Guardia *et al.*, 2011).

12-Litter

It was observed that there is a great variation in the quality of litter within the same poultry house, where the bacterial composition varies depending on the type of litter, the quality of the litter and the

litter management. (Pan and Yu, 2014). A study reported by Oakley *et al.* (2013) indicated that there is greater microbiological diversity observed in wet litter compared to dry litter and this has an effect on the intestinal microorganisms as well. Moreover, the microorganisms that grow on poultry droppings have an effect on the gut microbiome and may constitute a source of infection. It has been demonstrated that the microorganism composition of litter samples collected from different production systems clustered with the corresponding microbial composition of the caecal samples (Mancabelli *et al.*, 2016). In addition, the type of litter has been shown to influence the formation of the intestinal microbiota. For example, birds reared on soft sawdust showed significant differences in microbial communities in the caecum at 28 days of age versus samples taken from birds raised on chopped straw (Torok *et al.*, 2009). When raising broilers on fresh 7-day-old litter, the dominance of the ileal microbiota was observed on *Lactobacillus* spp., whereas a group of unclassified *Clostridiales* was the dominant bacteria in ileal microbiota (Cressman *et al.*, 2010). As reported by another study reported by Wei *et al.* (2013b) showed that samples taken from young birds raised in reused litter had higher bacterial diversity as compared to mature ones that were kept under the same conditions.

13-Feed access.

Some studies indicated that the growth of the intestinal surface area is affected by delay in obtaining feed for young chicks (Uni *et al.*, 1998; Lamot *et al.*, 2014), thus the formation of microorganisms is also possible (Flint *et al.*, 2012). Feed withdrawal later in life has also been associated with changes in microbiota composition. Temporary withdrawal of feeds can increase colonization of intestinal pathogens (Thompson *et al.*, 2008), for example with *Salmonella* (Burkholder *et al.*, 2008). After 6 hours of feed deprivation,

significant changes in the bacterial community were observed in the proximal part of the alimentary canal (Vossen *et al.*, 2009).

CONCLUSION AND PERSPECTIVES

In general, and through the previous review, we can see that the health status of chickens depends mainly on the so-called microbial balance within the alimentary canal. On the other hand, the microbial balance is very important in maintaining the integrity of the intestine and its normal functions, and this undoubtedly will affect productivity after that. Currently and in recent years, interest has increased in understanding the taxonomic composition of microbes in the alimentary canal and its contributions to gut health. Progress in this field will help us to better understand how to manage the gut microbiota based on the management and environmental factors, that affecting homeostasis of microbiota, thus providing new opportunities for improving overall health of the poultry. There is no doubt that progress in this field has helped to better understand how bacterial balance occurs and its relationship to many environmental and management factors that affect the balance of microorganisms in the alimentary canal. Therefore, the dynamic balance of bacteria in the alimentary canal has a close relationship with the general health of poultry and thus improving productive performance. However, there is still an urgent need for more studies to confirm the importance of bacterial balance and its relationship to general health and good production. Finally, a better understanding of the gut microbiota and their interaction or balance with other organisms is critical in understanding the composition of the gut environment.

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الملخص العربي

الاتزان الميكروبي في الجهاز الهضمي للدجاج وعلاقته ببعض العوامل: استعراض مرجعي

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يعتبر كل من البيض واللحوم الناتجة من الدجاج ضروريين لتغذية الإنسان في جميع أنحاء العالم. وتجدر الإشارة إلى أنه في السنوات الأخيرة شهدت صناعة الدواجن الحديثة تغيرات ملحوظة في طرق الإنتاج على مدار الخمسين عامًا الماضية. ومن المثير للاهتمام أن الكائنات الحية الدقيقة المعوية قد تطورت جنبًا إلى جنب مع المضيف حيث ان صحة الأمعاء تلعب دورا اساسيا ومهما جدًا للإنتاج المثالي. وعندما تتأثر صحة القناة الهضمية سلبا يتأثر سلبا هضم وامتصاص العناصر الغذائية أيضا مما يكون له تأثير سيئ على نسبة تحويل الغذاء مما يؤدي إلى خسارة اقتصادية وزيادة التعرض للأمراض. وبالتالي فإن المجتمعات الميكروبية والتي تعيش في القناة الهضمية للدجاج ضرورية لاستتباب الأمعاء والتمثيل الغذائي للمضيف مما سيؤثر لاحقًا على الحالة الفسيولوجية والصحية. من ناحية أخرى يصعب تحديد ميكروبيوتا الأمعاء وعلاقتها بالصحة والإنتاجية في كل من دجاج التسمين والبيض بدقة بسبب الاختلاف الكبير بين القطعان والتي تنشأ بسبب العديد من العوامل البيئية والرعايه والتي تؤثر على الحمل الميكروبي لكل من البكتيريا المفيدة والضارة على حد سواء والمحيطه بالطيور. وعموما سنركز في هذا المقال على أهمية التوازن الميكروبي في القناة الهضمية في الدجاج والعوامل المختلفة التي تؤثر على هذا التوازن ونتائج هذه التفاعلات على الصحة العامة والإنتاجية.