



Chicken Gastrointestinal Microbiota, Composition, Function, and Importance



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THIS review aims to summarize data on avian microbiota, its development, composition, effect, and factors that affect its diversity in the chicken gastrointestinal tract (GIT) to be available for students, practical poultry specialist, and researchers in the poultry industry. The GIT of chickens like other animals and human are harboring a diverse population or community of microorganisms, including bacteria (microbiota), fungi (mycobiota), protozoa, and viruses are in symbiotic to enhance vital activities and the health of birds. On the other hand, a bird's cecum microbiota has a high complex composition and fewer characteristic features than crop and all intestinal parts.

Microbiota starts to develop after hatching and gradually increased with age until the population reaches its balance. It can be affected by litter type, ration, as well as feed additives. The composition of poultry GIT microbiome was mainly investigated using microbiological culturing, while, molecular-based techniques provided more rapid and accurate characterization of the culture-able and un-culture-able members. The identification of intestinal microbiota helps in improving chickens' health and productivity programs.

Therefore, GIT microbiota and mycobiota should be carefully investigated for meat, litter, aerosol, and processing plant contamination to ensure both food and personnel safety.

Keywords: Chicken, Turkey, Microbiota, Distribution, Factors affect mycobiota.

Introduction

Each part of chicken's intestinal tract has a special population of microbiota which adapted to host physicochemical conditions, physiology, and feeds [1]. The microbial community or microbiota can include commensal, symbiotic, and pathogenic microorganisms in the form of human and/or animal's colonies which are double the hosts cells [2]. The Microbiota plays an important role in the development of performance [3].

Bacteria (microbiota) and fungi (mycobiota) are commonly found in the GIT of chicken and the smaller populations of archaea, protozoa, and viruses, and they positively affect the feed metabolism and immunization [4-7].

The microbial composition of the GIT in birds was investigated using microbial culture based methodology [8], recently with the application of both 16S rRNA gene-targeted analyses and ITS2 region of fungal rRNA genes a lot of information become available and updated [9-12].

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The intestinal health of the host is correlated with the microbial GIT [13]. In human, mycotic infection is associated with many diseases [14-16].

Development of avian intestinal microbiota:

The GIT of the newly hatched chick's is not sterile but contains microbiota which transmitted vertically from hens to chicks via the oviduct [17] or the eggshell pores [18]. Microbiota can be transmitted to chicks' gut in hatchery and transportation vehicle [19]. Microbe in chick's GIT can be found in the chick inside the shell [20]. The early stage of the post-hatch microbial contamination affects the immune system and intestinal microbiota [21]. The natural intestinal microflora (develops after hatching and rapidly increases [22] from the 1st to the 19th day of life [23]. The microbial colonization continuously grows until the GIT population reaches its balance [24]. The fungi are more inhabited in the upper GIT site than the lower parts, while the bacterial inhabitation is in an opposite pattern [12].

Distribution of microbiota in the gastrointestinal tract:

Different parts of the chicken GIT are inhabited by specified microbiota which adapted to host physicochemical properties, physiology and nutrients [1], with the highest number in the ceca from 10^{10} to 10^{11} cells/g [25,26], and lactobacilli concentrated in chicken's ileum [25]. Cecal dropping contains a bacterial profile in cecal drop similar to cecal content, which different from that in fecal drop [13].

The upper part of chicken GIT was reported to be richer in a diversity of microbiota than the other intestinal parts where *Scopulariopsis brevicaulis* (*S. brevicaulis*) and *Trichosporon asahii* (*T. asahii*) dominated at the 14th and 28th days of chicken's life [12].

Role of intestinal microbiota:

The commensal intestinal bacteria are essential to optimize the birds protection against pathogenic bacteria. The short chain fatty acids (SCFAs) are essential and produced through the fermentation process which proceeded by cecal microbiota [27,28].

The facultative aerobic bacteria including *Lactobacillus*, *Enterobacteriaceae*, and *Streptococcus* colonized initially the GIT of chicks. At hatching, the chick's intestinal environment ready for potential positive oxidation

or reduction leads to high oxygen consumption. The lowered oxygen provide suitable environment for obligatory anaerobic bacteria growth at lower gut [29,30]. The lost energy can recovered by absorption and metabolism of VFA and lactic acid produced by bacterial fermentation [31-33]. The distal ileum contains high bacterial count reached 10^8 cells/mL of digesta [21]. Proteins, as dilatory form and from GIT enzymes and secretions can supply intestinal bacterial nutrition [34]. Organic acids released in intestinal environment decreases pH and suppress bacterial pathogens virulence factor [35,36].

Types of microbiota of chicken intestine:

In cultivation-based study on the intestinal microbiome of turkeys, most of the microbes (77%) were Gram-positive rods, followed by Gram-negative rods (14%), and Gram-positive cocci (9%) [37]. The gut microbiota provides the individual and the foods ingested, and the gut provides a specific genetically dependent bacterial growth [38]. The human's GIT has high numbers of microorganisms of up to one thousand species of microbes [39,40], and more than seven thousands of microbial strains [41].

Bacteria

Enterobacteria, lactobacilli, and enterococci genera are the most common bacteria in chicken's small intestine. While, Lachnospiraceae, Clostridiales Lactobacillales, Bacteroidales, Veillonellaceae and Ruminococcaceae families were mainly found cecum [9, 42-44]. The presence of amino acids and mono- and disaccharides in chicken's small intestine supports the growth of Proteobacteria and Lactobacillales [45].

The phyla *Proteobacteria*, *Firmicutes*, and *Bacteroidetes* were the highest identified from 13 bacterial phyla in chicken and turkey representing 117 bacterial genera in chicken and 69 genera in turkey [46]. The bacterial diversity in chicken and turkey covers up to 89 and 68% at species-level and 93 and 73% at genus levels, respectively. Intestinal microbiomes in chickens and turkeys are sharing only 16% similarity [46].

Fungi

Yudiarti et al. [47] used a specific medium to isolate fungi from GIT of chickens and the obtained fifty isolate were seven species (*Aspergillus niger*, *Aspergillus fumigatus*, *Chrysonilia crassa*, *Mucor* spp., and *Rhizopus* spp.). The upper part of chicken GIT has more mycobiota than the lower part (jejunum, ileum, and cecum), where

duodenum includes the highest diversity and the least diversity in cecum especially in layers [12, 48]. In turkeys, 50% of all fungal isolates were from the crop, 31% from the beak and 19% isolated from the cloaca [49]. The impact of fungi on the health of GIT is considered as an important point of evaluation under commercial conditions [50]. From broiler and layer chickens' 3,000 cecal content samples, 88 fungal species were identified where, the highest four genera were *Aspergillus*, *Penicillium*, *Sporidiobolus*, and *Verticillium* [49]. Many fungal phyla, classes, orders, families, and species were identified in ileum and cecum of broilers treated with probiotics, and essential oil after mixed infection with *Eimeria*, the fungal growth was concentrated pre- and post-infection conditions [50].

Using molecular identification out of 125 samples 468 unique were belong to four phyla and genera found in Chicken GIT, 90-99% of them Ascomycota [12], and 5 *Aspergillus* isolates as well as Genera *Trichosporon* and *Aspergillus* [12,48,49,52]. Different fungi and yeast species (88) including 18 unknown genera, *Aspergillus* spp., *Penicillium* spp., *Sporidiobolus* spp, were identified and separated using rep-PCR. These results provide a background on normal fungi genera present in commercial conditions and will be a stone for investigation of the fungal impact on the GIT health of poultry [50]. Furthermore, 3 phyla, 7 classes, 8 orders, 13 families, 17 genera, and 23 fungal species were identified in cecum and ileum of broilers chickens using the Pyro-sequencing [51].

Factors influencing the GIT microbiota populations

Chickens GIT microbiota affected by several factors specially feed ingredients, antibiotics treatments, temperature, genetics, and immunity. Also, sex, breed, age, GIT location, and prebiotics administration, can influence the intestinal microbiota populations [53]. In addition, the environmental and housing factors are influencing the composition of microbiota [54].

Immunosuppressive viral infections

The viral infection and microbes relations in GIT are affecting inflammation and immunosuppression of T and B cells in chicken [55, 56]. Nineteen fungal strains were detected in samples collected from immunosuppressed chickens. *Aspergillus* (42%), *Trichosporon* (10.5%), *Penicillium* (10.5%), *Fusarium* (5%), *Candida* (1%), and non-identified isolates (26%)

were detected in IBD infected chickens [57]. Bird immune system plays an important role in the host to control the microbiota composition [58]. Cellular and humoral immunity are cooperate lower pathogens minimize bacterial intestinal wall contact [59, 60].

The very virulent infectious bursal disease virus (vvIBDV) was hypothesizing to modify Gut-associated lymphoid tissue (GALT) and composition of gut microbiota, leading to enhancement of pathogen invasion through the gut [61,62]. The microbial colonization of core gut flora was altered by Marek's disease virus (MDV) with changes in metabolic feature between MDV-susceptible and resistant chickens [55,63]. Also, avian influenza virus increases counts of *Proteobacterium*, *Clostridium*, *Pseudofalvonifactor*, and *Vampriovibrio* [64].

Season

During processing of poultry products, the microbial contamination of the carcass is highly affected by season. Bacterial contamination is significantly less affected in winter than spring or summer. Gram-positive and Gram-negative bacteria significantly impact the gut health at least in the fall [65].

Essential oils supplementation

Plant essential oils (PEOs) can promote birds' growth through enhancing microflora,improving nutrients and micronutrients absorption in the small intestine [66,67], and reducing harmful effect of the microbial metabolites [68-70] Essential oils may enhance protein, lipid, and fibre digestibility and increase the amount of edible parts and dressing percentage of carcasses [71,72].

Antibiotics treatments.

Antibiotics were used in feed as growth promoters to enhance production performance [73]. The traditional usage of growth promoters antibiotics in poultry feed to control enteric bacterial disease leads to emerging of resistant bacterial strains and alteration in the gut microbiota [12, 70, 74-76]. (

Enteric bacterial infections

The chicken's GIT mucosal surface composed of GIT epithelium, microbiota, and immune cells [77]. Intestinal epithelial physical barrier can protect bird's intestine by colonization of commensal microbiota, which protects epithillum against invading pathogenic microorganisms [78]. The beneficial inhabitant microbiota potentiate

natural microbial barriers against invasion by pathogens [79].

Symbiotic bacteria can inhibit pathogens' colonization by several methods, such as a direct bactericidal effect, nutrients limitations, and enhanced immunity. Pathogens often promote their replication ways to combat gut microbiota [80-82].

Beneficial bacteria can play an important role in suppression or elimination of *Clostridium perfringens* (CP) infection in chicken's intestine [83]. *Bacillus subtilis* (*B. subtilis*) DSM 32315 can ameliorate necrotic enteritis (NE) [83], reduce necrosis inducing activity of CP, butyrate-producing bacteria counter acting inflammation and preserving intestinal integrity [85].

A variety of SCFAs have a direct bacteriostatic effect on bacterial species or indirect effect via reducing pH, or increasing microbiota colonization that combati the pathogenic microbes. Some microbiota produce bacteriocins, which are small peptide molecules with microbicidal or microbiostatic properties [86], and can, replace antibiotics [87].

Parasitic infestations:

Eimeria spp. infection in poultry enhanced the growth of CP and inhibited the other bacteria, induced lesions in intestinal mucosa, and increased the pathogenesis of CP [88]. The cecal Clostridial counts in *E. tenella* experimentally infected chickens were increased from 4 to 100 times at 5 and 18 days post infection [92,93], increase of almost 10⁶-fold at 7 days after infection [91]. *Eimeria acervulina* infection reduced the bacterial counts, types and homogeneity in chicks ceca [92,93]. *Eimeria* infection decreased the intestine pH in the duodenum, jejunum, and ileum that affect microbiota activity and numbers [94,95]. *Histomonas meleagridis* induced lesions in the presence of beneficial bacteria with severe inflammation in turkeys and chickens ceca and a dramatic effect on microbiota [88]. *Ascaridia galli* (*A. galli*) infestation induced lower intestinal bacteria than in uninfected hens [96].

Host genetics on feed efficiency in chickens:

Wen *et al.* [97] found a week correlations between host genetic features and gut microbial similarities in different sampling sites. While, application of microbial genome-wide analysis indicates genetic markers near or inside the genes MTHFD1L and LARGE1 have abundances

of cecal Megasphaera and Parabacteroides, respectively. Host genetics effect on residual feed intake was 39%.

Gut microbiota may related bird gender, as Bacteroides and Megamonas genera were found to mainly colonized in male chickens' cecum, closely related to glycan metabolism, while it is reported to be more related to lipid metabolism in female chickens. Glycan and lipid metabolism gene expression levels differ in male than in female chickens [98].

Ration composition:

Different diets types and dietary supplementations that used as poultry growth promoters can affect the microbiota and reduce the risk of enteric infection [37]. Chicken's intestinal microbial ecosystem can be enhanced by non-dietary and dietary interventions, which considered as the highest effective to regulate/modulate microbiota [99].

The gut microflora populations naturally proved the intestinal bacterial dynamics by the organic acids. Also the supplementation in chickens feed with a significantly reduction of harmful bacterial growth e.g. *E. coli*, CP and Campylobacter [100]. (Propionic acid suppressed the growth of the caecal *E. coli* and Salmonella without negative effects on *Lactobacillus* spp. growth and counts in chickens [101]. Green tea has polyphenols which increase the Lactobacilli, decrease the pathogenic load, and improve the weight gain [4,102,103]. Feed form and composition, and housing environment are positively affecting intestinal microbial feature in chickens [68,104].

Beneficial effects of microbiota

Productivity

Productivity of chickens is potentiated by a high diversity and composed beneficial GIT microbiota [105-108]. The effects of intestinal microbiota on the performance of broiler chickens have been studied [32], and the results indicated a growing evidence of correlation between the apparent metabolized energy of the diet and the microbiota composition in the hindgut of the host [108].

Immunity

The pathobionts and their products are prevented by intestinal immune system [109]. The intestinal microbial community seems to interact directly with the immune system of the

host, contributing to maintaining the integrity of the epithelial barrier, and stimulating local and systemic immune interactions [67, 110]. Immunoglobulin A (IgA) [111], and miRNAs that regulate bacterial transcripts and bacterial growth [112]. Luo et al. [113] observed an increase in immune proteins and changes in the intestinal microbiota in chickens treated with a probiotic, while Oakley and Kogut [79] found a correlation between intestinal microbiota and cytokines in chickens.

Interaction between the microbial community and the host immunity

It was found that the interaction between the microbial community and the host has a crucial role in the both mucosal homeostasis and host health status [114]. In addition, the GIT provides a home to many microbial inhabitants and acts as an active immunological organ, where more resident immune cells are organized in Peyer's patches lymphoid aggregations = and the cecal tonsils lymphoid follicles. Macrophages, various subsets of T cells, B cells, and dendritic cells, and the secondary IgA are donate to the proper immune response generation against invading pathogens. Plasma cells producing IgA, the intraepithelial lymphocytes, and gdT cell receptor-expressing T cells are present in the mucosa. In addition, the gdT cells that inhibit lamina propria of intestine, it was reported that a significant numbers of regulatory T and IL-17-producing. The presence of intestinal microbiota regulates the mucosal leukocytes accumulations and function, as well as enhances the mucosal barrier function, that allowing the host to overcome the invasive pathogens with an immune homeostasis [115].

The communication between microbiota and immune system is mediated by the interaction of bacterial components with pattern recognition receptors expressed by intestinal epithelium and various antigen-presenting cells resulting in activation of both innate and adaptive immune responses [58,116,117]. At the cellular level, phagocytes migrated from the blood, including granulocytes, monocytes, and macrophages [118].

Cellular defense mechanisms produced pro-inflammatory cytokines, and increase immune cells in the site of infection, and stimulate reactive oxygen species and antimicrobial peptides [119-121].

Dynamic interactions between GIT microbiota and the innate and adaptive immunity of the host play important roles in maintaining both intestinal

homeostasis and inhibiting inflammation. The gut microbiota metabolizes complex carbohydrates and protein, synthesizes vitamins, and produces a lot number of metabolic products that can mediate cross-talk between the gut epithelial and immune cells [122]. For the host's defense mechanism, a mucosal barrier segregates the microbiota from host immune cells and reduces the intestinal permeability. Furthermore, the impaired interaction between gut microbiota and its mucosal immune system can result in a very large quantity of potentially pathogenic Gram negative bacteria and their accompanied metabolic changes drastically alter the epithelial barrier and subsequently increasing susceptibility to infections. Gut dysbiosis or negative alterations in the composition of gut microbiota can prevent regulation of the immune responses and resulting in both inflammation and oxidative stress [122]. A correlation between microbiota and immunity has been indicated by increased lactobacillus count in immunosuppressed birds with low intestinal IgA antibody levels as well as other alterations in the microbiota [123]. The correlated cytokine profile and gut microbiota potentiated the intestinal defense against many bacterial invasion and inflammation [79,124], and enhanced the pro-inflammatory cytokines [125].

The metabolism of microbiota

The proximal parts of chicken GIT (crop, proventriculus, and gizzard) are characterized by low pH, which strongly select the growth of some bacteria species and limit the growth of many other species [126]. The crop and small intestine of broiler chickens are usually dominated by lactic acid-producing bacteria, mainly *Lactobacillus* spp., *Enterococcus* spp. and *Streptococcus* spp. [25,127,128]. However, the caecum of broiler chickens is dominated by anaerobic bacteria, where more than their half are belonging to the order Clostridiales (families Lachnospiraceae and Ruminococcaceae), which are referred to Clostridial clusters XIVa and IV, respectively [25,127].

Intestinal microbiota plays a great beneficial role in the intestinal morphology, nutrient digestion and absorption, immunity, and general host health [46,129,130]. Intestinal microbiota take a part in many metabolic pathways, such as amino acid synthesis and lipid metabolism [131,132]. The mechanism by which the PEOs promote the growth of host may be related to the alteration of the gut microflora, –improving

the absorption of nutrients [67], increasing the absorption of micronutrients in the small intestine [66], and reducing the deleterious effects of microbial metabolites [68,70].

Interactions between host gut–microbiota and co-metabolism of the host

Energy and nutrients produced food resulted from biochemical reactions and GIT microbiota, and play essential role in production, metabolism, immune modulation, and protection against pathogens [133]. The chicken small intestine is inhabited by lactic acid bacteria which need complex nutrient requirements similar to those of the chicken host itself. As, lactobacilli are not able to synthesize the amino acids required for their anabolism. Therefore, there is a competition for amino acids between the intestinal microbiota and the chicken host. Lactobacilli in chicken small intestine may assimilate 3–6% of total dietary amino acids. Exogenous enzymes which promote protein digestion are providing a competitive advantage to the chicken, offering less growth potential for amino acid-dependent bacteria [1].

Microbiota as an alternative to antibiotics:

Usage of probiotics as antibiotics alternatives has several benefits on poultry health and production. In fact, probiotics are now considered one of the best alternative options for antibiotics in poultry industry [83,134]. Adding of probiotic to poultry feeds reduced numbers of gut pathogenic bacteria e.g. *S. enteritidis*, *S.typhimurium*, *S. Gallinarum*, and *C. jejuni* [135-137].

Usage of the probiotics as feed supplement increased the numbers of lactobacilli and reduced both *E. coli* and total coliform counts of broiler chickens intestine [138]. Probiotic mixture (*L. pentosus* ITA23 and *L. acidophilus* ITA44) enhanced bacterial count of the cecal contents, by altering *E.coli* population and increasing the beneficial bacterial count [139], these beneficial actions were attributed to many modes of actions caused by direct-fed microbes and depended on strains/kinds presented in different products. The commercial product (PrimaLac®) protected chicken from *C. jejuni* challenge when it was given to broiler chickens in the drinking water (120/1 g/L until day 14), or mixed in feed (454/1000 g/kg) until day 28 of age, and also at 225/1000 g/kg for modification of growth period. These results were attributed to both the organic acid and proteinaceous molecules produced by

probiotic bacteria which lowered the intestinal pH which kills the pathogenic *Campylobacter* spp. [140]. In using *B. subtilis* C-3102 as poultry feed additive *Campylobacter* colonization was reduced [141]. *C. jejuni* adhesion, colonization and invasion were inhibited by *L. gasseri* SBT2055 [142]. Various *Bacillus* sp. protected chickens against *Campylobacter* sp. Because of *in-vivo* study on chickens [143]. Also, administration of *L. salivarius* 59 and *E. faecium* PXN33 mixture reduced *S. Enteritidis* S1400 colonization in poultry [144]. The genetically modified probiotic strain of *E. coli* Nissle 1917 was able to secrete Microcin J25, which is antimicrobial peptide. Using of this modified *E. coli* strain reduced *S. enterica* in the GIT of turkeys [145]. *Bacillus subtilis* (*B. subtilis*) isolates were studied in vivo for their ability to reduce *C. jejuni* colonization. Many researchers suggested that the good motility of bacterial isolate increased capability to reduce colonization due to its ability to reach the site of *C. jejuni* faster [146]. Probiotics had plenty of mechanisms of anti-*Campylobacter* activity under *in vitro* conditions; they can reduce *Campylobacter* spp. population count in poultry gastrointestinal tract and reduce carcass contamination [146,147]. Probiotic supplementation in water and feed improved production performance and resistance of chickens to coccidiosis caused by *Eimeria* spp. [148]. In an *ovo* study the administration of probiotic bacteria (PrimaLac®) in rate of 1×10^6 colony forming unit (cfu) at the day 18th of the embryonic life resulted in protection of the hatched chicks from challenge with mixed *Eimeria* spp. at the 3rd day post-hatching [149]. These results can be attributed to their modulating effect on immune response genes of ileum and caecal [150]. Feed supplementation of broilers with *Bifidobacterium animalis*, *B. subtilis animalis*, *Enterococcus faecium*, and *L. reuteri animalis*, as well as multi-bacterial spp. probiotic at 5×10^8 cfu/kg improved both intestinal health and growth performance criteria [151]. Probiotics supplementation could also be beneficial in controlling *Listeria monocytogenes* infection in chickens [152]. PrimaLac® probiotic administration in chicken's diets augmented antibody production and counter viral diseases, ND and IBD [153]. An study was carried out in turkey poult to detect the mucosal immunity against NDV that induced by feeding *Echinacea purpurea* and protexin® probiotic, the results e indicated that the used probiotic helped in induction of a high immunity [145,155].

Conclusion

A range of factors can affect the bacterial community of GIT microbiome, e.g host, litter management, and ration and feed additives. The composition of poultry GIT microbiome was initially investigated using bacterial cultivation methodologies but in our time and by using the DNA-based molecular biology techniques which was characterized by both the speed and accuracy in characterization for the culture-able and uncultivable members. Also, the microbiota is found to be involved in the immune homeostasis of the GIT of birds, therefore any imbalance it can result in an immune imbalance and badly affects birds' health. We can also conclude that the understanding of nature and function of intestinal microbiota will lead to develop novel strategies to improve both animal health and productivity. Therefore, GIT microbiota needs to be carefully monitored for possibility of contamination in poultry ration, aerosol, meat, litter, and processing plant for poultry industry, human food and personnel safety.

List of abbreviations:

B. subtilis: *Bacillus subtilis*

ND: Newcastle disease

NDV: Newcastle disease virus

IBD: Infectious Bursal Disease

IBDV: Infectious Bursal Disease virus

MD: Marek's disease

GIT: gastrointestinal tract

DNA: Deoxyribonucleic acid

CP: *Clostridium perfringens*

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Mohamed M. Amer, Aziza M. Amer and Khaled M. El-Bayoumi collected data, wrote and revised the original draft. Mohamed M. Amer supervised the manuscript. The authors read and approved the final manuscript.

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Competing interests

The authors declare that they have no competing interests.

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الجراثيم المعدية المعوية النافعة للدجاج وتكوينها ووظيفتها وأهميتها.

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تهدف هذه المراجعة إلى تلخيص البيانات من الأوراق المنشورة حول الميكروبيوتا المعوية في الطيور وتطورها وتكوينها وتأثيرها والعوامل التي تؤثر على تنوعها في الجهاز الهضمي للدجاج (GIT) لتكون متاحة للطلاب ورجال الدواجن العمليين والباحثين في الدواجن. صناعة. تؤدي القناة الهضمية للدجاج مثل الحيوانات الأخرى والإنسان مجموعة متنوعة من الكائنات الحية الدقيقة ، بما في ذلك البكتيريا (Microbiota) والفطرية (Mycobiota) والبروتوزوا والفيروسات) في تكافلي لتعزيز الأنشطة الحيوية وصحة الطيور. من ناحية أخرى ، تحتوي الكائنات الحية الدقيقة في الأعور على تركيبة معقدة للغاية وخصائص مميزة أقل من المحاصيل والأمعاء.

تبدأ الكائنات الحية الدقيقة في التطور بعد الفقس وتزداد تدريجياً مع تقدم العمر حتى يصل السكان إلى توازنهم. يمكن أن تتأثر بنوع القمامة والحصى الغذائية وكذلك إضافات الأعلاف. تم فحص تركيبة ميكروبيوم GIT للدواجن باستخدام الزراعة الميكروبيولوجية ، بينما قدمت التقنيات الجزيئية خصائص دقيقة سريعة للأعضاء القادرين على الاستزراع وغير القادرين على الاستزراع. يعتقد العديد من الباحثين أن تحديد الجراثيم المعوية يساعد في تحسين برامج صحة وإنتاجية الدجاج.

لذلك ، يجب التحقق بعناية من كل من الجراثيم والفطريات GIT في اللحوم وأماكن التخزين والمحيط الجوي وتلوث المجازر و المعالجة لضمان سلامة الغذاء والعاملين.

الكلمات الرئيسية: الدجاج ، الميكروبيوتا ، الميكوبيوتا ، التوزيع ، العوامل التي تؤثر على الفطريات الفطرية

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