Egypt. J. Vet. Sci. **Vol. 54,** No. 3, pp. 403-420 (2023)

Egyptian Journal of Veterinary Sciences
https://ejvs.journals.ekb.eg/

Chicken Gastrointestinal Microbiota, Composition, Function, and Importance

Mohamed M. Amer[1*], Aziza M. Amer[2] and Khaled M. El-Bayoumi[3]

[1] *Department of Poultry Diseases, Faculty of Veterinary Medicine, Cairo University, P.O. 12211, Giza, Egypt.*

[2] *Department of Pharmacology, Faculty of Veterinary Medicine, Cairo University, P.O. 12211, Giza, Egypt.*

[3] *Department of Poultry Diseases, Veterinary Research Institute, National Research Centre, P.O. Code 12622, Dokki, Giza, Egypt.*

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].

*Corresponding author: Mohamed M. Amer, E-mail: profdramer@y|ahoo.com, Tel.: +201011828228
ORCID: 0000-0001-8965-7698
(Received 24/01/2023, accepted 13/02/2023)
DOI: 10.21608/EJVS.2023.188397.1431

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 inhabitance 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 adopted 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. brevicauli)* 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 reached10^8 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 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 microbs 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 10^6-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 promotors 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 hostto 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 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 coccidioisis 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 ilum 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 poults 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 resulted in an immune imbalance and badly affects birds' health. We can also concluded that the understanding of nature and function of intestinal mycobiota will lead to develop novel strategies to improve both animal health and productivity. Therefore, GIT mycopiota 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*

Acknowledgments

Not applicable.

Authors' contributions

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.

Funding statements

Not applicable. This work was done by author's activity without any fund.

Availability of data and materials:

Not applicable.

Declarations

All data included in this review are collected from published article

Ethics approval and consent to participate

Not applicable.

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

References

1. Apajalahti, J. and Vienola, K. Interaction between chicken intestinal microbiota and protein digestion. *Animal Feed Science and Technology*, **221** (B), 323-330 (2016). https://doi.org/10.1016/j.anifeedsci.2016.05.004

2. Sender, R., Fuchs, S. and Milo, R. Revised estimates for the number of human and bacteria cells in the body. *PLoS Biology*, **14**(8), e1002533(2016). https://doi.org/10.1371/journal.pbio.1002533

3. Turnbaugh, P.J., Ley, R. E., Hamady, M., Fraser-Liggett, C.M., Knight, R. and Gordon, J.I. The human micro biome project. *Nature*, **449**, 804–810(2007). https://doi.org/ 10.1038nature 06244.

4. Williams, J., Kellett, J., Roach, P.D., McKune, A., Mellor, D., Thomas, J. and Naumovski, N. L-Theanine as a Functional Food Additive: Its Role in Disease Prevention and Health Promotion. *Beverages*, **2**(2),13 (2016). https://doi.org/10.3390/beverages2020013

5. Cani, P.D. Human gut microbiome: hopes, threats and promises. *Gut,* **67**(9),1716-1725 (2018). https://gut.bmj.com/content/67/9/1716

6. Durack, J. and Lynch, S.V. The gut microbiome: Relationships with disease and opportunities for therapy. *Journal of Experimental Medicine,* **216** (1),20-40(2019). https://doi.org/10.1084/jem.20180448

7. Amer, M.M. Short Communication: Chicken Intestinal Microbiota. *Acta Scientific Veterinary Sciences*, **3** (5), 21-23 (2021). https://actascientific.com/ASVS/pdf/ASVS-03-0138.pdf

8. Salanitro, J.P., Fairchilds, I.G. and Zgornicki ,Y. D. Isolation, culture characteristics, and identification of anaerobic bacteria from the chicken cecum. *Applied Microbiology*, **27**(4), 678- 687(1974). https://doi.org/10.1128/am.27.4.678-687.1974

9. Zhu, X.Y., Zhong, T., Pandya, Y. and Joerger, R.D. 16S rRNA-based analysis of microbiota from the ce-cum of broiler chickens. *Applied and Environmental Microbiology*, **68**(1), 124–137 (2002). https://doi.org/10.1128/AEM.68.1.124-137

10. Lu, J. and Domingo, J.S. Turkey fecal microbial community structure and functional gene diversity revealed by 16S rRNA gene and metagenomic sequences. *Journal of Microbiology,* **46**(5),469-477(2008). https://link.springer.com/article/10.1007/s12275-008-0117-z

11. Scupham, A.J., Patton, T.G., Bent, E. and Bayles, D.O. Comparison of the cecal microbiota of domestic and wild turkeys. *Microbial Ecology*, **56**(2),322-331 (2008). https://link.springer.com/article/10.1007/s00248-007-9349-4

12. Robinson, K., Xiao, Y., Johnson, T.J., Chen, B., Yang, Q., Lyu, W., Wang, J., Fansler, N., Becker, S., Liu, J., Yang, H. and Zhang, G. Chicken Intestinal Mycobiome: Initial Characterization and Its Response to Bacitracin Methylene Disalicylate. *Appled Environmental Microbiology*, **86**(13), e00304-320(2020) https://doi.org/10.1128 /AEM .00304-20

13. Pauwels, J., Taminiau, B., Janssens, G.P.J., De Beenhouwer, M., Delhalle, L., Daube, G., Coopman, F. Cecal drop reflects the chickens' cecal microbiome, fecal drop does not. *Journal of Microbiological Methods*, **117**, 164-170(2015). https://doi.org/10.1016 /j.mimet.2015.08.006 .

14. Huseyin, C.E., O'Toole, P.W., Cotter, P.D. and Scanlan, P.D. Forgotten fungi-the gut mycobiome in human health and disease. *FEMS Microbiology Review*, **41**(4),479-511 (2017). https://doi.org/10.1093/femsre/fuw047.

15. Limon, J.J., Skalski, J.H. and Underhill, D.M. Commensal Fungi in Health and Disease. *Cell Host and Microbe,* **22** (2), 156-165 (2017). https://doi.org/10.1016/j.chom.2017.07.002

16. Iliev, I.D. and Leonardi, I. Fungal dysbiosis: immunity and interactions at mucosal barriers. *Nature Reviews Immunology,* **17**, 635-646 (2017). https://doi.org/10.1038/nri.2017.55

17. Gantois, I., Ducatelle, R., Pasmans, F., Haesebrouck, F., Gast, R., Humphrey, T.J., Van Immerseel, F. Mechanisms of egg contamination by Salmonella Enteritidis. *FEMS Microbiology Reviews*, **33**(4),718-738 (2009). https://doi.org/10.1111/j.1574-6976.2008. 00161.x

18. Roto, S.M., Kwon, K.M. and Ricke, S.C. Applications of in ovo technique for the optimal development of the gastrointestinal tract and the potential influence on the establishment of its microbiome in poultry. *Front Veterinary Science*, **3**, 63 (2016). https://doi.org/10.3389 / fvets.2016.00063

19. Pedroso, A., Menten, J.F.M., and Lambais, M.R. The structure of bacterial community in the intestines of newly hatched chicks. *Journal of Applied Poultry Research*, **14** (2), 232- 237 (2005). https://doi.org/10.1093/japr/14.2.232

20. Lumpkin, B.S., Batal, A.B. and Lee, M.D. Evaluation of the bacterial community and intestinal development of different genetic lines of chickens. *Poultry Science,* **89**(8), 1614-1621 (2010). https://doi.org/10.3382/ps.2010-00747

21. Apajalahti, J., Kettunen, A. and Graham, H. Characteristics of the gastrointestinal microbial communities, with special reference to the chicken. *World's Poultry Science Journal*, **60**(2), 223-232 (2004). https://doi.org/10.1079/WPS200415

22. Lan, Y., Verstegen, M.W.A., Stamminga, S. and Williams, B.A. The role of the commensal gut microbial community in broiler chickens. *World's Poultry Science Journal*, **61**(1), 95-104 (2005). https://doi.org/10.1079/WPS200445

23. Magdalena, C., Hradecka, H., Faldynova, M., Matulova, M., Havlickova, H., Sisak, F. and Rychlik, I. Immune response of chicken gut to natural colonization by gut microflora and to *Salmonella enterica* serovar enteritidis infection. *Infection and Immunity*, **79**(7), 2755-2763 (2011). https://doi.org/10.1128/IAI.01375-10

24. Borda-Molina, D., Seifert, J. and Camarinha-Silva, A. Current Perspectives of the Chicken Gastrointestinal Tract and Its Microbiome. *Computational and Structural Biotechnology Journal*, **16**, 131–139 (2018). https://doi.org/10.1016/j.csbj.2018.03.002.

25. Bjerrum, L., Engberg, R.M., Leser, T.D., Jensen, B.B., Finster, K. and Pedersen, K. Microbial community composition of the ileum and cecum of broiler chickens as revealed by molecular and culture-based techniques. *Poultry Science*, **85**(7),1151-1164 (2006). https://doi.org/10.1093/ps/85.7.1151.

26. Amit-Romach, E., Sklan, D. and Uni, Z. Microflora ecology of the chicken intestine using 16S ribosomal DNA primers. *Poultry Science,* **83**(7),1093-1098 (2004). https://doi.org/10. 1093/ ps/83.7.1093

27. Patterson J.A. and Burkholder K.M. Application of prebiotics and probiotics in poultry production. *Poultry Science*, **82**(4), 627-631(2003). https:// doi.org/10.1093/ps/82.4.627.

28. Liao, X., Shao, Y., Sun, G., Yang, Y., Zhang, L., Guo, Y., Luo, X. and Lu, L. The relationship among gut microbiota, short-chain fatty acids, and intestinal morphology of growing and healthy broilers. *Poultry Science*, **99** (11), 5883-5895 (2020). https://doi.org/10.1016/ j.psj.2020.08.033.

29. Gong, J., Forster, R.J., Yu, H., Chambers, J.R., Sabour, P.M., Wheatcroft, R. and Chen, S. Diversity and phylogenetic analysis of bacteria in the mucosa of chicken caeca and comparison with bacteria in the caecal lumen. *FEMS Microbiology Letter*, **208**(1),1-7 (2007). https:// doi.org/10.1111/j.1574-6968.2002.tb11051.x.

30. Wise, M.G, and Siragusa, G.R. Quantitative analysis of the intestinal bacterial community in one- to three-week-old commercially reared broiler chickens fed conventional or antibiotic-free vegetable-based diets. *Journal of Applied Microbiology,* **102**(4),1138-1149 (2007). https:// doi.org/10.1111/j.1365-2672.2006.03153.x

31. Bergman, E. N. Energy contributions of volatile fatty acids from the gastrointestinal tract in various species. *Physical Review,* **70**(2),567-590(1990). https://doi.org/10.1152/ physrev.1990. 70.2.567.

32. Rinttilä, T. and Apajalahti, J. Intestinal microbiota and metabolites—Implications for broiler chicken health and performance. *Journal of Applied Poultry Research*, **22** (3), 647-658 (2013). https:// doi.org/10.3382/japr.2013-00742.

33. Ungerfeld, E.M. Metabolic Hydrogen Flows in Rumen Fermentation: Principles and Possibilities of Interventions. *Frontiers in Microbiology*, 11, **589** (2010). https://doi.org/10.3389/ fmicb.2020.00589 .

34. 34. Cummings, J.H. and Macfarlane, G. The control and consequences of bacterial fermentation in the human colon. *Journal Applied. Bacteriology* , **70**(6), 443-459 (1991). https://ami-journals.onlinelibrary.wiley.com/doi/ pdf/10.1111/j.1365-2672.1991.tb02739.x

35. Boyen, F., Haesebrouck, F., Vanparys, A., Volf, J., Mahu, M., Van Immerseel, F., Rychlik, I., Dewulf, J., Ducatelle, R. and Pasmans, F. Coated fatty acids alter virulence properties of Salmonella Typhimuriumand decrease intestinal colonization of pigs. *Veterinary Microbiology*, **132**(3-4),319-327 (2008). https://doi.org/10.1016/j. vetmic.2008.05.008

36. Kubasova, T., Seidlerova, Z. and Rychlik, I. Ecological Adaptations of Gut Microbiota Members and Their Consequences for Use as a New Generation of Probiotics. *International Journal of Molecular Sciences*, **22**(11),5471 (2021). https://doi.org/10.3390/ijms22115471.

37. Pan, D. and Yu, Z. Intestinal microbiome of poultry and its interaction with host and diet, *Gut Microbes*, **5**(1), 108-119 (2014). https://doi. org/10.4161/gmic.26945

38. Rowland, I ., Gibson, G., Heinken, A., Scott, K., Swann, J., Thiele, I. and Tuohy, K. Gut microbiota functions: metabolism of nutrients and other food components. *European Journal of Nutrition,* **57**(1), 1–24 (2018). https://doi.org/10.1007/ s00394-017-1445-8

39. Qin, J., Li, R., Raes, J., Arumugam, M., Burgdorf, K.S., Manichanh, C., Nielsen, T., Pons, N., Levenez, F., Yamada, T., Mende, D.R., Li, J., Xu, J., Li, S., Li, D., Cao, J., Wang, B., Liang, H., Zheng, H., Xie, Y., Tap, J., Lepage, P., Bertalan, M., Batto, J.M., Hansen, T., Le Paslier, D., Linneberg, A., Nielsen, H.B., Pelletier, E., Renault, P., Sicheritz-Ponten, T., Turner, K., Zhu, H., Yu, C., Li, S. , Jian, M., Zhou, Y., Li, Y., Zhang, X., Li, S., Qin, N., Yang, H., Wang, J., Brunak, S., Doré, J., Guarner, F., Kristiansen, K., Pedersen, O., Parkhill, J., Weissenbach, J., Meta Consortium, H.I.T., Bork, P.,. Ehrlich, S.D and Wang, J. A human gut microbial gene catalogue established by metagenomic sequencing. *Nature*, **464** (7285),59-65 (2010). https://doi.org/10.1038/ nature08821

40. Dimitrov, D.V. The human gutome: nutrigenomics of the host-microbiome interactions. OMICS: *A Journal of Integrative Biology*, **15** (7-8), 419- 430 (2011). https://doi.org/10.1089/omi.2010.0109

41. Ley, R.E., Peterson, D.A. and Gordon, J.I. Ecological and evolutionary forces shaping microbial diversity in the human intestine. *Cell*, **124**(4), 837–848 (2006). https://doi.org/10.1016/j.cell.2006.02.017

42. Mead, G.C. Microbes of the avian cecum: Types presentand substrates utilized. *Journal of experimental zoology. Supplement,* **3**,48–54 (1989). https://doi.org/10.1002/jez.14 02520508

43. Engberg, R.M., Hedemann, M.S.,. Leser, T. D and Jensen, B.B. Effect of zinc bacitracin and salinomycin on intestinal microflora and performance of broilers. *Poultry Science*, **79** (9),1311–1319 (2000).. https://doi.org/10.1093/ps/79.9.1311

44. Torok, V.A., Hughes, R. J., Mikkelsen, L.L., Perez-Maldonado, R., Balding, K., MacAlpine, R., Percy, N.J. and Ophel-Keller, K. Identification and characterization of potential performance-related gut microbiotas in broiler chickens across various feeding trials. *Applied and Environmental Microbiology*, **77**(17), 5868–5878 (2011). https://doi.org/10.1128/AEM.00165-11

45. Kamada, N., Seo, S.U., Chen, G.Y. and Nunez, G., Role of the gut microbiota in immunity and inflammatory disease. *Nature Reviews Immunology*, **13**,321–335 (2013). https://doi.org/10.1038/nri3430.

46. Wei, S., Morrison, M. and Yu, Z. Bacterial census of poultry intestinal microbiome. *Poultry Science*, **92** , 671- 683 (2013). https://doi.org/10.3382/ps.2012-02822

47. Yudiarti, T., Yunianto, V.D.B.I. , Murwani, R. and Kusdiyantini, E. Isolation of fungi from the gastrointestinal tract of indigenous chicken, *Journal of the Indonesian Tropical Animal Agriculture*, **37**(2),115-120 (2012). https://doi.org/10.14710/jitaa.37.2.115-120

48. Shokri, H., Khosravi, A.and Nikaein, D. A comparative study of digestive tract mycoflora of broilers with layers. *Iranian Journal of Veterinary Medicine*, **5** (1),1-4 (2011). https://ijvm.ut.ac.ir/article_22662.html .

49. Sokol, I., Gawel, A. and Bobrek, k.. The Prevalence of Yeast and Characteristics of the Isolates from the Digestive Tract of Clinically Healthy Turkeys. *Avian Disease*, **62**(3),286-290 (2018). https://doi.org/10.1637/11780-121117-Reg.1

50. Byrd, J.A., Caldwell, D. Y. and Nisbet, D. J. The identification of fungi collected from the ceca of commercial poultry. *Poultry Science*, **96**, 2360 –2365 (2017). http://dx.doi.org/10.3382/ps/pew486 .

51. Hume, M.E., Hernandez, C.A., Barbosa, N.A., Sakomura, N.K.. Dowd, S.E and Oviedo-Rondón, E.O. Molecular identification and characterization of ileal and cecal fungus communities in broilers given probiotics, specific essential oil blends, and under mixed Eimeria infection. *Foodborne Pathogens and Disease*, **9** (9),853-860 (2012). https://doi.org/10.1089/fpd.2011.1093

52. Subramanya, S.H., Sharan, N.K., Baral, B.P., Hamal, D., Nayak, N., Prakash, P.Y., Sathian, B., Bairy, I. and Gokhale, S. Diversity, in-vitro virulence traits and antifungal susceptibility pattern of gastrointestinal yeast flora of healthy poultry, Gallus gallus domesticus. *BMC Microbiolology*, **492** (17), 113 (2017).https://doi:10.1186/s12866-017-1024-4

53. Suzuki, K. and Nakajima, A. New aspects of IgA synthesis in the gut. *International Immunopharmacology*, **26**,489–494 (2014). https://doi:10.1093/intimm/dxu059 .

54. Shang, Y., Kumar, S., Oakley, B. and Kim, W.K. Chicken Gut Microbiota: Importance and Detection Technology. *Frontiers in Veterinary Science*, **5**, 2297-1769 (2018). https://doi.org/10.3389/fvets.2018.00254

55. Perumbakkam, S., Hunt, H.D. and Cheng, H.H. Marek's disease virus influences the core gut microbiome of the chicken during the early and late phases of viral replication. *FEMS Microbiology Ecology,* **90**(1),300- 3012 (2014). https://doi.org/10.1111/1574-6941.12392

56. Robinson, C.M. and Pfeiffer, J.K. Viruses and the microbiota. *Annual Review of Virology*, **1**,55- 69 (2014). https://doi.org/10.1146/annurev-virology-031413-085550

57. Ghetas, A.M., Sedeek, D.M., Fedawy, H.S., Bosila, M.A., Mekky, H.M., Elbayoumi, Kh.M., and Amer, M.M. Detection of fungi in intestine of chicken associated with Infectious bursal disease virus infection. *Advances in Animal and Veterinary Sciences*, **10**(2), 514-520 (2022). http://dx.doi.org/10.17582/journal.aavs/2022/10.3.514.520

58. Hooper, L.V., Littman, D.R. and Macpherson, A.J. Interactions between the microbiota and the immune system. *Science,* **336** (6086):1268- 1273 (2012). https://doi.org/10.1126/ science.1223490

59. Stappenbeck, T.S., Hooper, L. V. and Gordon, J.I. Developmental regulation of intestinal angiogenesis by indigenous microbes via Paneth cells. *Proceedings of the National Academy of Sciences of the United States of America*, **99**(24),15451-1545 (2002) https://doi.org/10.1073/pnas.202604299

60. Spits, H. and Di Santo, J. P. The expanding family of innate lymphoid cells: regulators and effectors of immunity and tissue remodeling. *Nature Immunology*, **12**(1),21-27 (2011). https://doi:10.1038/ni.1962 .

61. Deplancke, B. and.Gaskins, H.R. Microbial modulation of innate defense: goblet cells and the intestinal mucus layer. *The American Journal of Clinical Nutrition* , **73**(6),1131S-1141S (2001). https://doi:10.1093/ajcn/73.6.1131S

62. Dillon, S.M., Lee, E.J., Kotter, C.V., Austin, G.L., Dong, Z., Hecht, D.K., Gianella, S., Siewe, B., Smith, D.M., Landay, A.L., Robertson, C.E., Frank, D.N. and Wilson, C.C. An altered intestinal mucosal microbiome in HIV-1 infection is associated with mucosal and systemic immune activation and endotoxemia. *Mucosal Immunology,* **7**(4), 983- 994 (2014). https://doi.org/10.1038/mi.2013.116

63. Perumbakkam, S., Hunt, H.D. and Cheng, H.H. Differences in CD8aa and cecal microbiome community during proliferation and late cytolytic phases of Marek's disease virus infection are associ-ated with genetic resistance to Marek's disease. *FEMS Microbiology Ecology*, **92**(12), fiw188 (2016). https://doi:10.1093/femsec/fiw188

64. Yitbarek, A., Weese, J.S., Alkie, T.N., Parkison, J. and Sharif, S. Influenza A virus subtype H9N2 infection disrupts the composition of intestinal microbiota of chickens. *FEMS Microbiology Ecology*, **94**(1),165-194 (2018). https://doi:10.1093/femsec/fix165 .

65. Oakley, B.B., Vasconcelos, E.J.R., Diniz, P.P.V.P., Calloway, K.N., Richardson, E., Meinersmann, R. J., Cox, N.A. and Berrang, M.E. The cecal microbiome of commercial broiler chickens varies significantly by season. *Poultry Science*, **97** (10), 3635-3644 (2018) . https://doi.org/10.3382/ps/pey214

66. Prakash, U.N. and Srinivasan, K. Beneficial influence of dietary spices on the ultrastructure and fluidity of the intestinal brush border in rats. *British Journal of Nutrition,* **104**,31–39 (2010). https://doi:10.1017/S0007114510000334 .

67. Marchesi, J.R, Adams, D.H., Fava, F., Hermes, G.D.A., Hirschfield, G.M., Hold, G., Quraishi, M.N ., Kinross, J., Smidt, H., Tuohy, K.M., Thomas, L.V., Zoetendal, E.G. and Hart, A. The gut microbiota and host health: a new clinical frontier. *Gut*, **65**,330–339 (2016). https://doi:10.1136/gutjnl-2015-309990

68. Knarreborg, A., Lauridsen, C., Engberg, R.M. and Jensen, S.K. Dietary antibiotic growth promoters enhance the bioavailability of α-tocopheryl acetate in broilers by altering lipid absorption. *Journal of Nutrition*, **134**,1487–1492 (2004).https://doi:10.1093 /jn/134.6. 1487

69. Han, G.G., Kim, E.B., Lee, J., Jin, G., Park, J., Huh, C-S., Kwon, I-K., Kil, D.Y., Choi, Y-J. and Kong, C. Relationship between the microbiota in different sections of the gastrointestinal tract, and the body weight of broiler chickens. *Springer Plus*, **5**, 911 (2016). https://doi.org/10.1186/s40064-016-2604-8

70. Gadde, U.D., Oh, S., Lillehoj, H.S. and Lillehoj, E.P. Antibiotic growth promoters virginiamycin and bacitracin methylene disalicylate alter the chicken intestinal metabolome. *Science Report*, **8**(1),3592 (2018). https://doi:10.1038/s41598-018-22004-6

71. Cross, D.E., McDevitt, R.M., Hillman, K. and Acamovic, T. The effect of herbs and their associated essential oils on performance, dietary digestibility and gut microflora in chickens from 7 to 28 days of age. *British Journal Poultry Science*, **48**(4),496-506 (2007). https://doi.org/10.1080/00071660701463221 .

72. Attia, Y., Al-Harthi, M. and El-Kelawy, M.. Utilisation of essential oils as a natural growth promoter for broiler chickens. *Italian Journal of Animal Science*, **18** (1), 1005-1012 (2019). https://doi.org/10.1080/1828051X.2019.1607574

73. Adewole, D. and Akinyemi, F. Gut Microbiota Dynamics, Growth Performance, and Gut Morphology in Broiler Chickens Fed Diets Varying in Energy Density with or without Bacitracin Methylene Disalicylate (BMD). *Microorganisms*, **9**(4), 787 (2021). https://doi.org/10.3390/microorganisms9040787

74. Pourabedin, M., Xu, Z., Baurhoo, B., Chevaux, E. and Zhao, X. Effects of mannan oligosaccharide and virginiamycin on the cecal microbial community and intestinal morphology of chickens raised under suboptimal conditions. *Canadian Journal of Microbiology,* **60**(5),255- 266 (2014). https://doi:10.1139/cjm-2013-0899

75. Neumann, A.P. and Suen, G. Differences in major bacterial populations in the intestines of mature broilers after feeding virginiamycin or bacitracin methylene disalicylate. *Journal of Applied Microbiology*, **119**(6),1515-1526 (2015). https://doi:10.1111/jam.12960 .

76. Park, S.H., Lee, S.I., Kim, S.A., Christensen, K. and Ricke, S.C. Comparison of antibiotic supplementation versus a yeast-based prebiotic on the cecal microbiome of commercial broilers. *PLoS One*, **12**, e0182805 (2017). https://doi.org/10.1371/journal. pone. 0182805

77. McCracken, V.J. and Lorenz, R.G. The gastrointestinal ecosystem: A precarious alliance among epithelium, immunity and microbiota. *Cell. Microbiology*, **3**(1),1-11 (2001). https://doi:10.1046/j.1462-5822.2001.00090.x

78. Belkaid, Y. and Hand, T.W. Role of the microbiota in immunity and inflammation. *Cell*, **157**(1), 121–141 (2014). https://doi.org/10.1016/j.cell.2014.03.011 .

79. Oakley, B.B. and Kogut, M.H. Spatial and Temporal Changes in the Broiler Chicken Cecal and Fecal Microbiomes and Correlations of Bacterial Taxa with Cytokine Gene Expression. *Front. Veterinary Science*, **19** (3), eCollection 11 (2016). https://doi:10.3389/fvets. 2016.00011 .

80. Antonissen, G., Croubels, S., Pasmans, F., Ducatelle, R., Eeckhaut, V., Devreese, M., Verlinden, M., Haesebrouck, F., Eeckhout, M., De Saeger, S., Antlinger, B., Novak, B., Martel, A. and Van Immerseel, F. Fumonisins affect the intestinal microbial homeostasis in broiler chickens, predisposing to necrotic enteritis. *Veterinary Research*, **46**, 98, pages 1-15 (2015). https://doi:10.1186/s13567-015-0234-8

81. Kim, J.E , Lillehoj, H.S., Hong, Y.H., Kim, G.B., Lee, S.H., Lillehoj, E. P . and Bravo, D.M. . Dietary Capsicum and Curcuma longa oleoresins increase intestinal microbiome and necrotic enteritis in three commercial broiler breeds. *Research in Veterinary Science*, **102**, 150–158 (2015). https://doi:10.1016/j.rvsc.2015.07.022

82. Pickard, J. M., Zeng, M. Y., Caruso, R. and Núñez, G. Gut microbiota: Role in pathogen colonization, immune responses, and inflammatory disease. *Immunological Reviews*, **79**(1), 70–89 (2017). https://doi.org/10.1111/imr.12567

83. Fasina, Y.O., Newman, M.M., Stough, J.M. and Liles, M.R. Effect of *Clostridium perfringens* infection and antibiotic administration on microbiota in the small intestine of broiler chickens. *Poultry Science*, **95**(2),247-260 (2016). https://doi:10.3382/ps/pev329 .

84. Sokale, A.O., Menconi, A., Mathis, G. F., Lumpkins, B., Sims, M.D., Whelan, R.A. and Doranalli, K. Effect of Bacillus subtilis DSM 32315 on the intestinal structural integrity and growth performance of broiler chickens under necrotic enteritis challenge. *Poultry Science*, **98**(11),5392-5400 (2019). https:/// doi:10.3382/ps/pez368 .

85. Antonissen, G., Eeckhaut, V., Van Driessche, K., Onrust, L., Haesebrouck, F., Ducatelle, R., Moore, R.J. and Van Immerseel, F. Microbial shifts associated with necrotic enteritis. *Avian Pathology*, **45**(3),308-312 (2016). https://doi:10.1080/03079457.2016.1152625 .

86. Corr, S.C., Li, Y., Riedel, C.U., O'Toole, P.W., Hill, C. and Gahan, C.G. Bacteriocin production as a mechanism for the anti-infective activity of Lactobacillus salivari-us UCC118. *Proceedings of the National Academy of Sciences of the United States of America,* **104** (18), 7617-7621 (2007). https://doi.org/10.1073/pnas.0700440104 .

87. Gilani, S.M.H., Rashid, Z., Galani, S., Ilyas, S., Shagufta, S., Zahoor-ul-Hassan, Al-Ghanim, K., Zehra, S., Azhar, A., Al-Misned, F., Ahmed, Z., Al-Mulham, N. and Mahboob, S. Growth performance, intestinal histomorphology, gut microflora and ghrelin gene expression analysis of broiler by supplementing natural growth promoters: A nutrigenomics approach. *Saudi Journal of Biological Sciences,* **28** (6), 3169-3632 (2021). https://doi.org/10.1016/j.sjbs.2021.03.008

88. Hauck, R. Interactions between parasites and the bacterial microbiota of chickens. *Avian Disease,* **61**(4), 428-436 (2017) https://doi:10.1637/11675-051917-Review.1 .

89. Waldenstedt, L., Elwinger, K., Lunden, A., Thebo, P., Bedford, M.R. and Uggla, A. Comparison between effects of standard feed and whole wheat supplemented diet on experimental Eimeria tenella and Eimeria maxima infections in broiler chickens. *Acta Veterinaria Scandinavica*, **39**,461–471 (1998).. https://doi.org/10.1186/BF03547772 .

90. Waldenstedt, L., Elwinger, K., Lunden, A., Thebo, P., Bedford, M.R. and Uggla, A. Intestinal digesta viscosity decreases during coccidial infection in broilers. *British Poultry Science,* **41**(4),459-64(2000). https://doi:10.1080/713654959 .

91. Kimura, N., Mimura, F., Nishida, S. and Kobayashi, A. Studies on the relationship between intestinal flora and cecal coccidiosis in chicken. *Poultry Science*, **55**, 1375–1383 (1976). https://doi:10.3382/ps.0551375 .

92. Perez, V.G., Jacobs, C.M., Barnes, J., Jenkins, M.C., Kuhlenschmidt, M.S., Fahey, G.C., Parsons, C.M. and Pettigrew, J.E. Effect of corn distillers dried grains with solubles and Eimeria acervulina infection on growth performance and the intestinal microbiota of young chicks. *Poultry Science*, **90**(5), 958-964 (2011). https://doi:10.3382/ps.2010-01066 .

93. Stanley, D., Wu, S-B., Rodgers, N., Swick, R.A. and Moore, R.J. Differential responses of cecal microbiota to fishmeal, Eimeria and Clostridium perfringens in a Necrotic Enteritis challenge model in chickens. *PLoS ONE*, **9**(8), e104739 (2014). https://doi:10.1371/journal.pone.0104739 .

94. Stephens, J.F., Borst, W.J. and Barnett, B.D. Some physiological effects of *Eimeria acervulina, E. brunetti, and E. mivati* infections in young chickens. *Poultry Science*, **53**(5),1735- 1742 (1974). https://doi:10.3382/ps.0531735.

95. Tsiouris, V., Georgopoulou, I., Batzios, C., Pappaioannou, N., Diakou, A., Petridou, E., Ducatelle, R. and Fortomaris, P. The role of an attenuated anticoccidial vaccine on the intestinal ecosystem and on the pathogenesis of experimental necrotic enteritis in broiler chickens. *Avian Pathology*, **42**(2),163-170 (2013). https://doi:10.1080/03079457 .2013.776161.

96. Okulewicz, A. and Złotorzycka, J. Connections between *Ascaridia galli* and the bacterial flora in the intestine of hens. *Angew Parasitology*, **26** (3), 151–155 (1985). https://europepmc.org/article/med/4061960

97. Wen, C., Yan, W., Mai, C., Duan, Z., Zheng, J., Sun, C. and Yang, N. Joint contributions of the gut microbiota and host genetics to feed efficiency in chickens. *Microbiome*, **9**, 126 (2021). https://doi:10.1186/s40168-021-01040-x

98. Cui, L.,, Zhang, X., Cheng, R., Ansari, A.R., Elokil, A.A., Hu, Y., Chen, Y., Nafady, A.A. and Liu, H. Sex differences in growth performance are related to cecal microbiota in chicken. *Microbial Pathogenesis*, **150**, 104710 (2021). https://doi:10.1016/j.micpath.2020.104710

99. Mahmood, T. and Guo, Y. Dietary fiber and chicken microbiome interaction: Where will it lead to? *Animal Nutrition*, **6**(1),1-8 (2020). https://doi.org/10.1016/j.aninu.2019.11.004

100. 100. Markowiak, P. and Salizewska, K. Effects of probiotics, prebiotics, and synbiotics on human health. *Nutrients,* **9**, 1021 (2017). https://doi.org/10.3390/nu9091021 .

101. Ding, S., Wang, Y., Yan, W., Li, A., Jiang, H. and Fang, J. Effects of Lactobacillus plantarum 15–1 and fructooligosaccharides on the response of broilers to pathogenic *Escherichia coli* O78 challenge. *Plos One*, PLOS ONE **14**(9), e0222877 (2019). https://doi.org/10.1371/ journal.pone.0222877 .

102. Cao, B.H., Karasawa, Y. and Guo, Y.M. Effects of Green Tea Polyphenols and Fructo-oligosaccharides in Semi-purified Diets on BroilersPerformance and Caecal Microflora and Their Metabolites. *Asian-Austr. Journal of Animal Science,* **18** (1), 85– 89 (2005). https://doi.org/10.5713/ajas.2005.85.

103. Gadang, V., Hettiarachchy, N., Johnson, M. and Owens, C. Evaluation of antibacterial activity of whey protein isolate coating incorporated with nisin, grape seed extract, malic acid, and EDTA on a turkey frankfurter system. *Journal of Food Scince.,* **73**, M389–M394 (2008). https://doi.org/10.1111/j.1750-3841.2008.00899.x.

104. Engberg, R.M., Hedemann, M. S., Steenfeldt, S. and Jensen, B.B. Influence of whole wheat and xylanase on broilerperformance and microbial composition and activity in the digestive tract. *Poultry Science,* **83**(6), 925– 938 (2004). https://doi.org/10.1093/ps/83.6.925

105. Stanley, D., Geier, M.S., Denman, S.E., Haring, V.R., Crowley, T.M., Hughes, R.J. and Moore, R.J. Identification of chicken intestinal microbiota correlated with the eciency of energy extraction from feed. *Veterinary Microbiology*, **164** (1-2), 85- 92 (2013). https://doi:10.1016/j.vetmic.2013.01.030.

106. Stanley, D., Hughes, R. J. and Moore, R.J. Microbiota of the chicken gastrointestinal tract: influence on health, productivity and disease. *Applied Microbiology and Biotechnology,* **98**(10), 4301- 4310 (2014). https://doi:10.1007/s00253-014-5646-2

107. Yan, W., Sun, C., Yuan, J. and Yang, N. Gut metagenomic analysis reveals prominent roles of Lactobacillus and cecal microbiota in chicken feed efficiency. *Scientific Reports*, **7**, 45308 (2017). https://doi.org/10.1038/srep45308.

108. Clavijo, V. and Flórez, M.J.V. The gastrointestinal microbiome and its association with the control of pathogens in broiler chicken production: A review. *Poultry Science*, **97**(3), 1006-1021 (2018). https://doi:10.3382/ps/pex359.

109. Broom, L.J. and Kogut, M.H. Inflammation: friend or foe for animal production. *Poultry Science,* **97** (2), 510–514 (2018). https://doi.org/10.3382/ps/pex314 .

110. Sommer, F. and Backhed, F. The gut microbiota: masters of host development and physiology. *Nature Reviews Microbiology*, **11**, 227–238 (2013). https://doi.org/10.1038/nrmicro2974.

111. Den Hartog, G., De Vries-Reilingh, G., Wehmaker, A.M., Savelkoul, H.F.J., Parmentier, H. K. and Lammers, A. Intestinal immune maturation is accompanied by temporal changes in the composition of the microbiota. *Benef. Microbiology*, **7**, 677- 685 (2016). https://doi.org/10.3920/BM2016.0047.

112. Liu, S., da Cunha, A.P., Rezende, R.M. , Cialic, R., Wei, Z., Bry, L., Comstock, L.E., Gandhi, R. and Weiner, H.L. The host shapes the gut microbiota via fecal microRNA. *Cell Host and Microbe,* **19**, 32–43 (2016). https://doi:10.1016/j.chom.2015.12.005.

113. Luo, J., Zheng, A., Meng, K., Chang, W., Bai, Y., Li, K., Cai, H., Liu, G. and Yao, B. Proteome changes in the intestinal mucosa of broiler (Gallus gallus) activated by probiotic Enterococcus faecium. *Journal of Proteomics*, **91**, 226-241 (2013). https://doi:10.1016/j.jprot. 2013.07.017.

114. Quinteiro-Filho, W.M., Rodrigues, M.V., Ribeiro, A., Ferraz-de-Paula, V., Pinheiro, M.I., Sa, L.R.M., Ferreira, A.J.P. and Palermo-Neto, J. Acute heat stress impairs performance parameters and induces mild intestinal enteritis in broiler chickens: role of acute hypothalamic-pituitary adrenal axis activation. *Journal of Animal Science*, **90**(6), 1986-1994 (2012). https://doi:10.2527/jas.2011-3949.

115. Kogut, M.H., Lee, A. and Lizabeth Santin, E. Microbiome and pathogen interaction with the immune system. *Poultry Science*, **99**, 1906–1913(2020). https://doi.org/10.1016/j.psj.2019.12.011.

116. Medzhitov, R. Recognition of microorganisms and activation of the immune response. *Nature* , **449**, 819–826 (2007). https://doi.org/10.1038/nature06246

117. Kumar, H., Kawai, T. and Akira, S. Pathogen recognition by the innate immune system. *International Reviews of Immunology*, **30** (1), 16-34 (2011). https://doi:10.3109/08830185.2010.529976.

118. 118. Medzhitov, R. and Janeway, C.A. Innate immunity: impact on the adaptive immune response. *Current Opinion in Immunology*, **9** (1), 4- 9 (1997). https://doi.org/10.1016 /S0952-7915(97)80152-5.

119. Lee, M.S. and Kim, Y.J. Signaling pathways downstream of pattern-recognition receptors and their cross talk. *Annual Review of Biochemistry*, **76**, 447-480 (2007). https://doi:10.1146/annurev.biochem.76.060605.122847 .

120. Underhill, D.M. Collaboration between the innate immune re-ceptors dectin-1, TLRs, and NODs. *Immunological Reviews*, **219**, 75-87 (2007). https://doi:10.1111/j.1600-065X.2007.00548.x.

121. Takeuchi, O. and Akira, S. Pattern recognition receptors and inflammation. *Cell* , **140** (6), 805-820 (2010). https://doi:10.1016/j.cell.2010.01.022.

122. Yoo, J.Y., Groer, M., Dutra, S.V.O., Sarkar, A. and McSkimming, D.I. Gut Microbiota and Immune System Interactions. *Microorganisms,* **8**(10),1587 (2020). https://doi:10.3390/microorganisms8101587 .

123. Mesa, D. , Beirã, B.C.B., Balsanelli, E., Sesti, L., Caron, L.F., Cruz, I.M., Souza, E.M. and Beiko, R.G. Cyclophosphamide Increases Lactobacillus in the Intestinal Microbiota in Chickens. *mSystems*, **5** (4) e00080-20 (2020). https://doi.org/10.1128/mSystems.00080-20.

124. Forbes, J.D., Van Domselaar, G. and Bernstein, C.N.. The Gut Microbiota in Immune-Mediated Inflammatory Diseases. *Frontiers in Microbiology*, **7**, 1081 (2016). https://doi.org/10.3389/fmicb.2016.01081

125. Diaz Carrasco, J.M., Casanova, N.A. and Fernández Miyakawa, M.E. Microbiota, Gut Health and Chicken Productivity: What Is the Connection? Microorganisms, 7(10),374 (2019). https://doi:10.3390/microorganisms7100374 .

126. Morgan, N.K., Walk, C.L., Bedford, M.R. and Burton, E.J. The effect of dietary calcium inclusion on broiler gastrointestinal pH: Quantification and method optimization. *Poultry Science Association,* **93**(2), 354-363 (2014). https://doi:10.3382/ps.2013-03305.

127. Apajalahti, J, and Kettunen, A. Microbes of the chicken gastrointestinal tract. In: Perry, G.C. (Ed.), Avian Gut Function in Health and Disease. *Poultry Science Symposium Series,* 28. CABI Publishing, Wallingford, 121–113 (2006). https://www.cabdirect.org/ cabdirect/abstract/20073020052

128. Abbas Hilmi, H, Surakka, A., Apajalahti, J. and Saris, P.E.J. Identification of the most abundant lactobacillus species in the crop of 1- and 5-week-oldbroiler chickens. *Applied and Environmental Microbiology*, **73**, 7867–7873 (2007). https://journals.asm.org/ doi/10.1128/AEM.01128-07

129. Apajalahti, J. Comparative gut microflora, metabolic challenges, and potential opportunities. *Journal of Applied Poultry Research,* **14**, 444–453 (2005). . https://doi:10. 1093/japr/14.2.444.

130. Turnbaugh, P.J., Ley, R.E., Mahowald, M.A., Magrini, V., Mardis, E.R. and Gordon, J.I. An obesity-associated gut microbiome with increased capacity for energy harvest. *Nature*, **444** (7122), 1027-1031 (2006). https://doi:10.1038/nature05414

131. Li, M., Wang, B., Zhang, M., Rantalainen, M., Wang, S., Zhou, H., Zhang, Y., Shen, J., Pang, X., Zhang, M., Wei, H., Chen, Y., Lu, H., Zuo, J., Su, M. , Qiu, Y., Jia, W., Xiao, C., Smith, L.M., Yang, S., Holmes, E., Tang, H., Zhao, G., Nicholson, J.K., Li, L. and Zhao, L. Symbiotic gut microbes modulate human metabolic phenotypes. *Proceedings of the National Academy of Sciences, India Section A: Physical Sciences*, **105** (6), 2117-2122 (2008). https://doi.org/10.1073/pnas.0712038105.

132. Xu, J., Shao, X., Li, Y., Wei, Y., Xu, F. and Wang, H. Metabolomic Analysis and Mode of Action of Metabolites of Tea Tree Oil Involved in the Suppression of Botrytis cinerea. *Front Microbiology*, **8**, 1017 (2017). https://doi:10.3389/fmicb.2017.01017.

133. Brisbin, J.T., Gong, J. and Sharif, S. Interactions between commensal bacteria and the gut-associated immune system of the chicken. *Animal Health Research Reviews*, **9**, 101–110 (2008). https://doi:10.1017/S146625230800145X .

134. Alagawany, M., Abd El-Hack, M.E., Farag, M.R., Sachan, S., Karthik, K. and Dhama, K. The use of probiotics as eco-friendly alternatives for antibiotics in poultry nutrition. *Environmental Science and Pollution Research*, **25** (11), 10611-10618 (2018). https:// doi:10.1007/s11356-018-1687-x .

135. Ghareeb, K., Awad, W.A., Mohnl, M., Porta, R., Biarnés, M., Böhm, J. and Schatzmayr, G. Evaluating the efficacy of an avian-specific probiotic to reduce the colonization of Campylobacter jejuni in broiler chickens. *Poultry Science,* **9** 1(8), 1825-1832 (2012). https://doi:10.3382/ps.2012-02168.

136. 136. Park, J.H. and Kim, I.H. The effects of the supplementation of Bacillus subtilis RX7 and B2A strains on the performance, blood profiles, intestinal Salmonella concentration, noxious gas emission, organ weight and breast meat quality of broiler challenged with Salmonella typhimurium. *Journal of Animal Physiology and Animal Nutrition*, **99**, 326–334 (2015). https://doi:10.1111/jpn.12248.

137. Oh, J.K., Pajarillo, E.A.B., Chae, J.P., Kim, I.H., Yang, D.S. and Kang, D.K. Effects of Bacillus subtilis CSL2 on the composition and functional diversity of the faecal microbiota of broiler chickens challenged with Salmonella Gallinarum. *Journal of Animal Science and Biotechnology,* **8**, 1-5 (2017). https://doi.org/10.1186/s40104-016-0130-8.

138. Dibaji, S.M., Seidavi, A., Asadpour, L. and Da Silva, F.M. Effect of a synbiotic on the intestinal microflora of chickens. *Journal of Applied Poultry Research*, **23** (1),1–6 (2014). https://doi.org/10.3382/japr.2012-00709

139. Faseleh, J.M., Wesam, A.Y., Shokryazdan, P., Ebrahimi, R., Ebrahimi, M., Idrus, Z., Tufarelli, V. and Liang, J.B. Dietary supplementation of a mixture of Lactobacillus strains enhances performance of broiler chickens raised under heat stress conditions. *International Journal of Biometeorology*, **60** (7), 1099-1110 (2016). https://doi:10.1007/ s00484-015-1103-x

140. Ebrahimi, H., Rahimi, S., Khaki, P., Grimes, J. L. and Kathariou, S. The effects of probiotics, organic acid, and a medicinal plant on the immune system and gastrointestinal microflora in broilers challenged with Campylobacter jejuni. *Turkish Journal of Veterinary and Animal Sciences,* **40**, 329–336 (2016). https://doi:10.3906/vet-1502-68.

141. Fritts, C.A., Kersey, J. H., Motl, M.A., Kroger, E.C., Yan, F., Si, J., Jiang, Q., Campos M. M., Waldroup A. P. and Waldro P.W. Bacillus subtilis C-3102 (Calsporin) improves live performance and microbiological status of broiler chickens. *Journal of Applied Poultry Research,* **9** (2),149–155 (2000) https://doi.org/10.1093/japr/9.2.149.

142. Nishiyama, K., Seto, Y., Yoshioka, K., Kakuda, T., Takai, S., Yamamoto, Y. and Mukai, T. Lactobacillus gasseri SBT2055 reduces infection by and colonization of Campylobacter jejuni. *PLoS*, **9**(9), e108827 (2014). https://doi:10.1371/journal.pone.0108827.

143. Saint-Cyr, M.J., Guyard-Nicodème, M., Messaoudi, S., Chemaly, M., Cappelier, J.M and Dousset, X. and Haddad, N. Recent advances in screening of anti-campylobacter activity in probiotics for use in poultry. *Front Microbiology*, **7**, 553 (2016). https://doi:10.3389 / fmicb.2016.00553.

144. Carter, A., Adams, M., La Ragione, R.M. and Woodward, M. J. Colonisation of poultry by *Salmonella Enteritidis* S1400 is reduced by combined administration of Lactobacillus salivarius 59 and Enterococcus faecium PXN-33. *Veterinary Microbiology,* **199**,100-107 (2017). https://doi:10.1016/j.vetmic.2016.12.029.

145. Forkus, B., Ritter, S., Vlysidis, M., Geldart, K. and Kaznessis, Y.N.. Antimicrobial probiotics reduce *Salmonella enterica* in turkey gastrointestinal tracts. *Science Reports* **7**, 40695 (2017). https://doi.org/10.1038/srep40695

146. Mohan, V. The role of probiotics in the inhibition of *Campylobacter jejuni* colonization and virulence attenuation. *European Journal of Clinical Microbiology & Infectious Diseases*, **34**, 1503–1513 (2015). https://doi:10.1007/s10096-015-2392-z.

147. Smiałek, M., Kowalczyk, J. and Koncicki, A. The Use of Probiotics in the Reduction of Campylobacter spp. Prevalence in Poultry. *Animals,* **11**, 1355 (2021). https://doi.org/10.3390/ani11051355

148. Ritzi, M.M., Rahman, W., Amohnl, M. and Rami, A. Effects of probiotics and application methods on performance and response of broiler chickens to an Eimeria challenge. *Poultry Science*, **93** (11),2772–2778 (2014). https://doi.org/10.3382/ps.2014-04207

149. Pender, C.M., Kim, S., Potter, T.D., Ritzi, M.M., Young, M. and Dalloul, R.A. Effects of in ovo supplementation of probiotics on performance and immune-competence of broiler chicks to an Eimeria challenge. *Beneficial Microbes*, **7** (5), 699-705 (2016). https://doi: 10.3920/BM2016.0080.

150. Pender, C.M., Kim, S., Potter, T.D., Ritzi, M.M., Young, M. and Dalloul, R.A. In vivo supplementation of probiotics and its effects on performance and immune-related gene expression in broiler chicks. *Poultry Science*, **9**(5),1052-1062 (2016). https://doi.org/10 .3382/ps/pew381. . .

151. Giannenas, I., Papadopoulos, E., Tsalie, E., Triantafillou, E. L., Henikl, S., Teichmann, K. and Tontis, D. Assessment of dietary supplementation with probiotics on performance, intestinal morphology and microflora of chickens infected with Eimeria tenella. *Veterenary Parasitology,* **188**, 31-40 (2012). https://doi:10.1016/j.vetpar.2012.02.017.

152. Dhama, K., Karthik, K., Tiwari, R., Shabbir, M.Z., Barbuddhe, S., Malik, S.V. and Singh, R.K. Listeriosis in animals, its public health significance (food-borne zoonosis) and advances in diagnosis and control: a comprehensive review. *Veterinary Quarterly,* **35**(4), 211-235(2015). https://doi:10.1080/01652176.2015.1063023.

153. Murarolli, V.D.A., Burbarelli, M.F.C., Polycarpo, G.V., Ribeiro, P.A.P. and Moro, M.E.G. Albuquerque R. Prebiotic, probiotic and symbiotic as alternative to antibiotics on the performance and immune response of broiler chickens. *British Poultry Science*, **16** (3), 279–284 (2014). https://doi.org/10.1590/1516-635x1603279-284

154. Tolouei, T., Hassanzadeh, M., Gh, N., Alkaragoly, H., Rezaei Far, A. and Ghahri, H. Efficacy of Echinacea purpurea and protexin on systemic and mucosal immune response to Newcastle diseases virus vaccination (VG/GA strain) in commercial turkey poults. *Iranian Journal of Veterinary Medicine,* **11**(1), 85-95 (2017). https://doi:10.22059/IJVM.2017. 60684.

155. Williams, J., Kellett, J., Roach, P.D., McKune, A., Mellor, D., Thomas, J., Naumovski, N., Yadav, S. and Jha, R. Strategies to modulate the intestinal microbiota and their effects on nutrient utilization, performance, and health of poultry. *Journal of Animal Science and Biotechnology,* **10**, 2 (2019). https://doi.org/10.1186/s40104-018-0310-9.

الجراثيم المعدية المعوية النافعه للدجاج وتكوينها ووظيفتها وأهميتها.

محمد محروس عامر [١] * ، عزيزة محروس عامر [٢] و خالد محمد البيومي [٣]
[١] قسم أمراض الدواجن - كلية الطب البيطري - جامعة القاهرة - ص.ب. ١٢٢١١ - الجيزة - مصر.
[٢] قسم الصيدلة - كلية الطب البيطري - جامعة القاهرة - ص.ب. ١٢٢١١ - الجيزة - مصر.
[٣] قسم أمراض الدواجن - معهد البحوث البيطرية - المركز القومي للبحوث - ص. كود ١٢٦٢٢ - الدقي - الجيزة - مصر.

تهدف هذه المراجعة إلى تلخيص البيانات من الأوراق المنشورة حول الميكروبيوتا المعويه 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. تؤوي القناه الهضميه 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 والحصص 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 واماكن التخزين والمحيط الجوي وتلوث المجازر و المعالجة لضمان سلامة الغذاء والعاملين.

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

* **المؤلف المسؤل:** محمد محروس,عامر. profdramer@yahoo.com