



Chicken Intestinal Microbiota

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The gastrointestinal (GI) tract considered as one of the largest exposed surface in the body. The GI tract acts as a selective barrier between bird's tissues and its luminal environment. The GI barrier is composed of many factors including physical, chemical, immunological, and microbiological components [1].

Dysbiosis is microbial imbalance and mostly common in gastrointestinal tract (GIT) accompanying intestinal inflammation [2,3]. Knowledge of microbial dysbiosis with molecular studies of the digestive system in dogs, mice, and humans [4,5]. Microbiota in the GIT had significant effect in stimulating the immune system of animal through change in biochemical characters of gut, increase defense mechanism against pathogens and increase supplemental digestion for animal (e.g. release DEFS) [6].

Complex interactions their excretion of ingest between species and intestinal microbes was still unknown although recent studies in advances of sequencing technology used for detecting microbial communities. Pathophysiology of gastrointestinal diseases will give insights into clarifying of chickens and bacterial metabolites increase explanation on acute diarrhea [7]. A lot of literature explained broad range of genetic functional related to genetic variation [8]. The genetic variation for Avian pathogenesis of *E. coli* from commensal carriage and systemic infections had been reported [9,10]. It may be related to phylogenetic variation with same gene code to produce infection and pathogenicity of bacteria to show symptoms of infection [11,12].

In the chicken the microbiota is most developed in the ceca and fecal microbiotas are often used as a monitor for the intestinal microbiota even it has quantitative differences within the different bacterial groups [13]. Fungi and yeasts are consistent members of animal microflora and its presences in the GIT of cattle and pigs playing a role in the breakdown of fibrous plant material [14].

Role of beneficial bacteria can in improving pro-ductions parameters is known; however, fungi impact has ignored [15]. Although, the attention given to fungi in poultry have focused on feed-associated toxin-producers, yeast, and yeast products. Byrd., *et al.* [15] identified 88 different fungal and yeast species, including *Aspergillus* spp., *Penicillium* spp., and *Sporidiobolus* spp, and 18 unknown genera were separated using automated repetitive sequence-based PCR (rep-PCR) from the ceca of commercial poultry. Moreover, Yudiarti., *et al.* [16] isolated 50 of fungal isolate belonged to 7 species (*Aspergillus fumigatus*, *Aspergillus niger*, *Chrysonilia crassa*, *Mucor circinelloides*, *Mucor* spp, *Rhizopus oligosporus* and *Rhizopus oryzae*) from GIT of chicken and found that the largest number of isolate was found in ileum, then followed by caecum, jejunum and duodenum.

It is hypothesize that Very virulent Infectious bursal disease virus (vvIBDV) may lead to a modification of the gut associated lymphoid tissues (GALT) and subsequently the gut microbiota composition, which enhances the risk of pathogen invasion of the host through the gut [17,18]. Infectious bursal disease virus (IBDV) infection had a significant impact on the GALT and led to a modu-

lation of gut microbiota composition, which may lead to a higher susceptibility of affected birds for pathogens invading through the gut [19].

Regarding the available data, There is a need for specific, sensitive and reliable biomarkers to follow and judge the poultry GI health status to facilitate studies the pathogenesis, monitor the situation in the field, and thereby and build prevention strategies [7].

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