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The Composition And Role Of The Microbiota Of Chickens' Gastrointestinal Tract.

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ABSTRACT

This article reflects current data on the study of the ecosystem of microorganisms inhabiting the poultry digestive tract. Information on the use of T-RFLP analysis (Terminal restriction fragment length polymorphism) - a molecular genetic method based on an analysis of the length polymorphism of amplified restriction DNA fragments of microorganisms in the study of the taxonomic diversity of microbial populations of the gastrointestinal tract and results obtained using this method is presented. The fact that about 800 species of microorganisms from nearly 300 genera have now been found in the poultry intestine, and less than 10% of this biodiversity. Moreover, many species and even genera of intestinal microorganisms detected by metagenomic methods are still not identified.

Keywords: microbiota of the gastrointestinal tract of birds, T-RFLP analysis.

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SHORT REVIEW

The problem of studying the ecosystem of microorganisms inhabiting the poultry digestive tract is highly relevant. The important role of the microorganisms of the gastrointestinal tract (GIT) in chickens is generally recognized: they provide the host organism with certain nutrients through the use of its own enzymes (amylases, cellulases and others), as well as antibiotic substances, proteins, hormones, vitamins and a number of other compounds [19, 20, 21]. Most information about the microflora inhabiting the gut of chickens, obtained using classical methods of microbiology, according to which the basis of the microbial community are bifidobacteria, streptococci, lactobacilli, lactate-fermenting bacteria, eubacteria, bacteroids and entero bacteria [12, 20, 21].

Unique molecular genetic methods open up to a researcher studying the composition of the intestinal microbiome of chickens, which demonstrated that it contains representatives of up to 140 genera of bacteria, of which only 10% are identified by the 16S rRNA gene, and the rest belong to new species or even new genera [1, 2, 4].

One of the most promising today is the T-RFLP analysis (Terminal restriction fragment length polymorphism) - a molecular genetic method based on an analysis of the length polymorphism of amplified restriction DNA fragments of microorganisms [22]. It is designed to determine the number, relative abundance and taxonomic affiliation of all bacteria in the microbial ecosystem. This allows wide and deep comparative study of microbiological communities in their development and change.

For the first time in Russia, based on an analysis of foreign studies, the T-RFLP methodology was modified to study the microflora of the gastrointestinal tract of agricultural birds [13, 14]. Recent studies of the intestine have allowed us to suggest that the gastrointestinal tract of a bird (for example, broilers) contains about 640 species of bacterial microorganisms. The number and variety of intestinal microflora vary in different parts of the intestine, and it is obvious that the departments with less favorable conditions (stomach) or faster passage of the contents of the intestine (duodenum) have fewer bacteria [12].

Modern molecular genetic analysis methods of the microbiome - real-time PCR, NGS, T-RFLP - have provided new insights into the real taxonomic diversity of the microbial populations of the gastrointestinal tract [1, 9, 12]. About 800 species of microorganisms from almost 300 genera have been found in the poultry intestine [9], and only less than 10% of this biodiversity can be isolated and cultured by laboratory [7]. Moreover, many species and even genera of intestinal microorganisms detected by metagenomic methods are still not identified [8].

It was previously believed that the digestive canal of a newly hatched chicken is microbiologically sterile and that it is inoculated with microorganisms in the first hours and days after hatching [21]. However, in recent studies, intestinal microflora was found even in 6-day-old chicken embryos, although the taxonomic diversity of embryonic flora is much less than in chickens a few days after hatching [2, 16, 17, 22].

Modern studies carried out using the modern molecular genetic method T-RFLP allowed us to establish quite clear standards for the maintenance of some major groups of microorganisms in the blind processes of the gastrointestinal tract of healthy broiler chickens and allowed us to conclude that the assumption that was based on the data of classical microbiological experiments that the main part of the microflora of the blind processes of the gastrointestinal tract of birds are bifidobacteria, lactobacilli and bacteroids[21] is incorrect.

Normal microflora is symbiotic with respect to the host organism, performing a number of important functions that are not limited to digestion. It participates in the function of the cardiovascular, endocrine, hematopoietic, nervous, immune and other systems of the host organism; produces a number of useful metabolites for it, such as endogenous antibiotics, proteins, enzymes, hormones, vitamins, low molecular weight fatty acids, etc .; serves as a barrier against invasion and uncontrolled reproduction of pathogenic microorganisms; participates in the neutralization of toxic xenobiotics; modulates gene expression in the intestines [5, 6, 10, 15, 18, 23, 24].

It has been established that bacteriocins produced by probiotic strains *L. salivarius* and *Paenibacilluspolymyxa* function as colonizing peptides, facilitating the introduction and / or domination of the producer in a niche already occupied by him [26]. These probiotic strains showed pronounced antagonistic activity against *C. jejuni* in vitro, but were inactive in vivo [26]. Based on the data obtained, it was hypothesized that the primary structure of the bacteriocin synthesized in vivo under the influence of various internal factors may differ from the primary structure of the peptide synthesized in vitro.

Along with mobility and adhesion, the invasion is an important step in the pathogenesis of campylobacteriosis. Probiotics are able to reduce invasion due to their competitive properties. Of considerable interest study in which the coaggregation of lactobacilli with *C. jejuni* is studied [27]. In evolution, bacterial co-aggregation emerged as an integral process in the development of multi vid biofilms [28]. An example of a multi-species biofilm is biofilm formed on human teeth [29]. However, some microorganisms, in particular, lactobacilli, use co-aggregation with *C. jejuni* to neutralize virulence factors and subsequent competing killing to ensure colonization resistance of the microecological niche of the host [27].

CONCLUSION

Thus, the analysis of current data on the study of the taxonomic diversity of the microbial populations of the bird's gastrointestinal tract suggests that the taxonomic diversity is much greater than that revealed by classical methods of microbiology, which opens up broad horizons for studying this issue.

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