

Determination of microbiocenosis in the intestine of the Hisex Brown hens in ontogenesis using T-RFLP method

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Microbiocenosis in the gastrointestinal tract, especially in the ceca, play an important part in life processes of poultry. Identification of the structure and taxonomic composition of microorganisms in the cecum using molecular genetic methods serves as a crucial approach in understanding how a cecal microbiota interplays with the chicken organism during ontogenesis. For this purpose, we studied an intestinal bacterial community composition in the ceca of the Hisex Brown laying hens at age of 40, 155 and 315 days using T-RFLP and RT-PCR. In the chickens studied, development of the cecal microbial communities, changes in their content, and appearance of new microorganisms occurred in the ontogeny. A broader spectrum of bacteria was found in 40- and 155-day-old birds (221±11 and 258±9 phylotypes, respectively) as compared with 315-day-old laying hens (178±8 phylotypes). Also, 315-day-old birds showed the least content of unidentified phylotypes. In the ceca of adult hens, there was a change in the dominant microbial

taxonomic groups including a higher proportion of acid-utilising bacteria of the class Negativicutes and cellulolytic bacteria of the class Clostridia, with a lower content of the classes Bifidobacteriales and Bacillales. Lactobacteria (order Lactobacillales) showed a greater content in 315-day-old laying hens (33.15±1.05%) as compared with 40- and 155-day-old birds (5.13±0.23% and 24.58 ± 0.86%, respectively). The variety and number of bacteria in the ceca conventionally attributed to various pathogens of poultry diseases, including the genera *Enterobacter*, *Pantoea*, *Listeria*, *Acinetobacter* and *Mycoplasma*, families *Campylobacteraceae* and *Pasteurellaceae*, and phylum *Fusobacteria*, increased with the age of birds. Thus, during molecular genetic studies, the species composition and dynamics of the microbiocenosis in the cecum of the Hisex Brown laying hens was determined as related to their ontogeny.

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Biography

Michael N Romanov has his expertise in avian genetics and genomics including participation in many national and international research projects in the areas of avian genetic diversity, gene/genome mapping, candidate genes evaluation, and comparative genomics. After years of experience in studies and teaching in both research and education institutions, he recently began leading on a project sponsored by the Government of Russian Federation. The project is aimed at developing state-of-the-art biotechnologies to assess gene expression in relation to performance and disease resistance in poultry industry, and will be done in collaboration with the Moscow State Academy of Veterinary Medicine and Biotechnology in 2017–2019.

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