

## Comparison of gut microbiota in hens of the crosses Hisex Brown and Lohmann Brown

Michael N Romanov<sup>1,2</sup>, Darren K Griffin<sup>1,2</sup>, Aleksandr N Panin<sup>2</sup>, Ivan I Kochish<sup>2</sup>, Vladimir I Smolensky<sup>2</sup>, Georgy Yu Laptev<sup>3</sup>, Ilya N Nikonov<sup>3</sup> and Larisa A Ilyina<sup>3</sup>

<sup>1</sup>University of Kent, UK

<sup>2</sup>Moscow State Academy of Veterinary Medicine and Biotechnology, Russia

<sup>3</sup>Biotrof+ Limited, Russia

Changes in the composition of the intestinal microbiota in the cecum of poultry could have a direct impact on the quality and safety of poultry products. This study presents the results of comparative molecular genetic analysis of the cecal microbiocoenoses in laying hens of two commercial crosses, Hisex Brown and Lohmann Brown, during ontogeny. According to the analysis of overall taxonomic representation, more than 70% phylotypes determined can be attributed to three: phyla, Firmicutes, Bacteroidetes, and Proteobacteria. Less represented were Actinobacteria, Tenericutes and Fusobacteria, and the presence of significant amounts of unidentified bacteria was also revealed. During ontogenesis, birds exhibited marked changes in the ratio of the number of phylotypes and taxonomic groups of the intestinal microbiota. Chickens of both crosses went through several stages in the development of microbial communities, including a stabilization period at the age of 20 to 40 weeks, as evidenced by the biodiversity assessment using ecological indexes. The stabilization period was characterised with a significant increase in representatives of class Clostridia involved

in the metabolism of carbohydrates, and in bacteria with high antagonistic properties (genera *Lactobacillus* and *Bacillus*). There was also a significant reduction of number of opportunistic and pathogenic taxa, such as families *Campylobacteraceae* and *Enterobacteriaceae*, order *Pseudomonadales*, and phylum *Tenericutes*. Despite the similar conditions of housing and feeding, the Lohmann Brown hens had a maximum level of representatives of the normal flora observed by 40 weeks of age. This probably determines a smaller number of pathogens like *Staphylococcus*, family *Campylobacteraceae*, and phyla *Tenericutes* and *Fusobacteria* found by 40 to 60 weeks of age and greater stability of intestinal microbiocoenosis in the Lohmann Brown birds as compared with the Hisex Brown chickens.

*This research is supported by a grant of the Government of Russian Federation, Contract No. 14.W03.31.0013*

### Biography

Michael N Romanov has his expertise in avian genetics and genomics including participation in a number of 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.

m.romanov@kent.ac.uk

 Notes: