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Bioinformatic Analysis of NGS Sequencing Data of the Intestinal Microbiome in Broilers Fed Supplements of Glyphosate, Probiotic Bacterial Strains and Antibiotics

Елена А. Йылдырым

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Аннотация

Xenobiotics have a negative impact on the composition and function of the intestinal microbiome; this requires measures to correct these disorders. The aim of the study was thus to conduct bioinformatic processing and analysis of NGS sequencing data of the intestinal (caecum) microbiome in broiler chickens, including the analysis of the taxonomic composition and predicted metabolic pathways. Experimental groups of broilers included: Group I fed the basic diet (BD); experimental Group II received BD and glyphosate; experimental Group III fed BD, glyphosate and probiotic bacterial strains; and experimental Group IV received BD along with a combination of glyphosate, antibiotics and probiotic bacterial strains. As a result, a reduction in the live weight of broilers by 4.2% ($p < 0.05$) was observed in Group II (against the background of glyphosate present in feed). Introduction of a mixture of probiotic bacteria into feed (Group III) resulted in an increased body weight compared

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to Group II ($p < 0.05$). In Group II, dysbiotic changes in the composition of the caecum microbiome were observed: an 8.7-fold increase in the number of *Streptococcus* genus members compared to the control Group I ($p < 0.05$). In Group IV, an increase in Bacteroidota by 6.2% was observed compared to Group II ($p < 0.05$). In birds from Group II, compared to Group I, a decline ($p < 0.05$) in the intensity of various types of predicted metabolic pathways of the microbiome in the intestinal chyme was established. In particular, those associated with energy, carbohydrate, protein types of metabolism, methanogenesis, synthesis of cofactors, etc. were noted.

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Bioinformatic Analysis of NGS Sequencing Data of the Intestinal Microbiome in Broilers Fed Supplements of Glyphosate, Probiotic Bacterial Strains and Antibiotics

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Keywords: NGS sequencing, gut microbiome, broiler chickens, bioinformatics, glyphosate, antibiotics, probiotic bacterial strains

Abstract

Xenobiotics have a negative impact on the composition and function of the intestinal microbiome; this requires measures to correct these disorders. The aim of the study was thus to conduct bioinformatic processing and analysis of NGS sequencing data of the intestinal (caecum) microbiome in broiler chickens, including the analysis of the taxonomic composition and predicted metabolic pathways. Experimental groups of broilers included: Group I fed the basic diet (BD); experimental Group II received BD and glyphosate; experimental Group III fed BD, glyphosate and probiotic bacterial strains; and experimental Group IV received BD along with a combination of glyphosate, antibiotics and probiotic bacterial strains. As a result, a reduction in the live weight of broilers by 4.2% ($p < 0.05$) was observed in Group II

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(against the background of glyphosate present in feed). Introduction of a mixture of probiotic bacteria into feed (Group III) resulted in an increased body weight compared to Group II ($p < 0.05$). In Group II, dysbiotic changes in the composition of the caecum microbiome were observed: an 8.7-fold increase in the number of *Streptococcus* genus members compared to the control Group I ($p < 0.05$). In Group IV, an increase in Bacteroidota by 6.2% was observed compared to Group II ($p < 0.05$). In birds from Group II, compared to Group I, a decline ($p < 0.05$) in the intensity of various types of predicted metabolic pathways of the microbiome in the intestinal chyme was established. In particular, those associated with energy, carbohydrate, protein types of metabolism, methanogenesis, synthesis of cofactors, etc. were noted.

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