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Mikrobiota of a rumen of sheep at feeding with oil-seed meal from genetically inoculated sunflower

Goal. To investigate the influence of genetically modified components in the composition of feed on the microbiota of the sheep's rumen content. Methods. The study was conducted on three analogue groups of 7-month-old lambs, a preparatory period of 8 days. During the month, the animals of the control group received a diet according to their physiological norm and animals of the experimental groups were replaced by a sunflower meal containing 12 and 100% DNA promoter 35S relative to the genomic DNA of soy (respectively, shroot / 12 and shrove / 100). After slaughter of lamb in the content of scar commonly used methods determined the total number of microorganisms, infusoria, mesophilic aerobic and optional anaerobic microorganisms, lactobacillus, microscopic fungi, activity of reductase and cellulosolytic activity, total acidity and concentration of hydrogen ions (pH). Results In animals fed with shrok / 100, compared to those in which the swine / 12 was fed, more general microorganisms were detected (40 times, P> 0.95), less infuzoria (1.75 times, P> 0.95), higher overall acidity (1.2 times, P> 0.95) and higher activity of reductases. Conclusions Reducing the number of infusoria in the lamb's scar tissue, to which the swab / 100 was fed, suggests the presence of factors unfavorable to the development of infusoria.

Key words: genetically modified sunflower, shrove, lamb, microbiota, scar contents, amount, activity.

The main source of energy and protein for livestock is corn, soybean and oilseeds, among which genetically modified organisms (GMOs) have recently dominated. Accordingly, animal consumption of feed containing GMOs increases. The feature of digestion of ruminants is that about 85% of all digestible dry matter is digested in the rumen during microbial fermentation. The microorganisms of the scar, on the one hand, provide primary digestion of the feed, on the other - is a source of microbial proteins and biologically active substances for the animal organism. The scar is comparable to a highly effective system of continuous cultivation of microorganisms, which are dominated by anaerobic bacteria and protozoa. Productivity of this system, first of all, determines the levels, ratio and source of nutrients coming from the feed. Consequently, the first reaction to changes in the quality of feed consumed by a bovine animal should be the change in the number of certain groups of microorganisms in the contents of the scar. Despite the fact that until now the microflora has not been shown to have a negative effect on the rumen's rumen's content for GM corn and soybean feed [11-14], many scientists believe that it is necessary to continue the in vivo study on high-performance farm animals to determine the safety and nutritional value GMO values.

The purpose is to investigate the effect of genetically modified components in feed on microbiota of the sheep's rumen content.

Materials and methods of research. There were formed 3 analogue groups of males aged 7 months. for 3 goals in each with a live weight of 32 - 40 kg. During the preparatory period of 8 days, the animals ate feed according to their physiological norm.

During the next 33 days, the animals in the control group received the same diet as in the preparatory period, and animals in experimental groups were replaced by a sunflower meal with different contents of the GMO. At the end of the experiment, blood was collected from animals for the determination of hematological parameters, weighed, scored, screened, and the samples of the internal organs and tissues for further study.

Before carrying out the experiment, by standardized or conventional methods, the presence of DNA promoter 35S (GMO marker) [5-7] was determined in sunflower meal and investigated the general toxicity

[9], the microbial contamination [1-4], and the chemical composition of the ration for animals. The amount and activity of the microflora of the rabbit's rumen content was determined by generally accepted methods [1 - 4, 8].

Research results. The diets of control and experimental animals in terms of chemical composition and nutrition were similar and consistent with the norm for sheep live weight 32-40 kg, except that experimental group animals received digestible protein by 23% more (Table 1, 2). During the experiment, there was no detectable difference in live weight between the control and experimental groups of sheep.

In the first batch of sunflower meal, the DNA content of the promoter 35S relative to the genomic DNA of soya was 100%, in the 2nd - 12%, although the latter did not have to contain GMOs (hereinafter - shrok / 100 and shrok / 12). Both parts of the sorghum were non-toxic. Regarding the insemination of microorganisms, the number of mesophilic aerobic and facultative anaerobic microorganisms (MAFANM) in the meadow / 100 was greater than in the meadow / 12 -6 times (correspondingly, 1.8 × 106 and 3.0 × 105 colony forming units (KUO) in 1 g), coagulase-positive staphylococci - 6.2 times (2.6 · 103 and 4.2 · 102 respectively), the bacteria of the Enterobacteriaceae family are the same (less than 2.0 · 101), and the mildew fungus is less than three times (2 · 104 and 6 · 104 CFU / g, respectively).

1. Chemical composition (%) and nutrition of used feed

2. The ration of feeding lambs during the trial period *

The total number of microorganisms in the scrap fat content, was found to be significantly higher (P> 0.95) than on the control, on average, 590 - 23 570 times (Table 3). At the same time, in animals that received scrotum / 100 (group I), this indicator was higher on average 40 times (P> 0.95) than those fed to shrok / 12 (group II). The number of infusions in the lamb's rumen's diet, which included the swine, was, on the contrary, less than that on the control, on average 46.7 - 81.8% (P> 0.95). At the same time, in animals that received scrotum / 100, the infusoria was 1.75 times less (P> 0.95) compared with those fed the scrotum / 12.

3. Composition and activity of the microflora, hydrogen index and total acidity of the rabbit's rumen content (M ± m)

The number of microscopic fungi in the scar tissue content of the animals was found to be higher in comparison with the control, and their diet consisted of scrotum (on average 2 519 - 14 815 times). However, the difference in this indicator among the animals of both experimental groups was only at the level of the trend (P> 0.90).

Differences in the number of MAPAN, in particular bacteria of the Enterobacteriaceae family, and galatolerant microorganisms between animals of different groups were unlikely. Regarding the presence of coagulase-positive staphylococci in the scar tissue content of animals fed with the scrotum, they were also detected in the samples of scrotum.

The activity of the microflora reductase in the content of the rabbit's scar, which received scrotum / 100, was higher: the discoloration of methylene blue was three times faster than that of animals, which fed the shroud / 12, and 4 times faster compared with the control.

The total acidity and the index of hydrogen ion concentration in the scar tissue of the animals to which the swab / 100 was fed were higher than that of those receiving the scrotum (12), and the control ones, on average, 1.2 and 1.4 times (P> 0,95), and on 0,22 (P> 0,95) and 0,11 units. pH, respectively.

According to the cellulosic activity of the microorganisms of the scar contents between the animals of the experimental and control groups, no probable differences were found.

The scar is an open system, therefore, from its contents, besides anaerobic, distinguish some aerobic and optional-anaerobic species of microorganisms present in the diet and the environment [10]. In our experiment, coagulase-positive staphylococci, bacteria of the Enterobacteriaceae family, and microscopic fungi present in the sow were detected in the framework of the rat's scar. However, the probable increase of 40 times the total number of microorganisms in the rabbit's rumen content, which was fed to shrok / 100, compared to those that received shrok / 12, can not be due only to the difference in the shoots of MAPANM corn.

Available in the literature, data on the influence of infusoria on the metabolism of ruminant rumines are controversial. However, it is believed that these protozoa break down 25-30% of fiber and stimulate its cleavage by bacteria [10]. There is evidence of an increase in the bacterial population in the scar tissue after

defacing. Infusions are also better than bacteria, consults of lactic acid, which helps to prevent lactic acidosis in the rumen. Consequently, the results of our studies do not contradict the above data: the total number of microorganisms in the composition of the scar lamb of different groups was inversely proportional to the number of infusions, as well as, to a degree, the total acidity.

Infusions are sensitive enough to the influence of external factors, so they are used as test organisms for the rapid determination of the overall toxicity of feed and feed additives. In view of this, the probable decrease in the number of infusoria in the rabbit's rumen's diet, which contained 100 scrotum / s, compared with those receiving scrotum / 12, suggests the influence of unfavorable factors for the development of infuzoria, but which it is impossible to determine at this stage of the research.

Conclusions

In the framework of the rabbit scar content, which fed 100% of the 35S DNA promoter to genomic DNA of soy, compared to those with a diet containing 12% DNA of the promoter 35S, a larger total microbial count was detected - nisms - on average 40 times (P> 0,95), 1,75 times smaller than infusoria (P> 0,95), 1,2 times higher than total acidity (P> 0,95) and higher activity of reductase. Reducing the number of infusors in the lamb's rumen's diet, which contained a scrotum containing 100% DNA promoter 35S in relation to genomic DNA of soy, indicates that there are unfavorable factors for infusoria development in it.

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