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Changes in Blood Parameters of Laboratory Animals Under the Influence of Mycotoxin T2

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At the moment, about 400 different types of mycotoxins have been studied, which are capable of exhibiting a toxic effect even in very small doses. Mycotoxins are products of microscopic fungi of the genera *Aspergillus*, *Penicillum*, *Fusarium*, *Claviceps* and *Alternaria*. Among these substances, trichothecene mycotoxins are singled out as one of the most numerous groups produced by fungi of the genus Fusarium. In turn, one of the representatives of this group is T2 toxin, which is characterized by provoking various kinds of disturbances in metabolic processes, it also has the ability o selectively act on the organs of the immune system and disrupts the corresponding immune processes. The above, in turn, contributes to increased sensitivity to diseases, both infectious and non-infectious [1].

Therefore, in our opinion, it is relevant and timely to determine the dynamics of changes in biochemical indicators in the tissues of a living organism under the influence of T2 toxin, in order to further develop appropriate and effective methods for diagnosing animals at risk of mycotoxin infection.

It is well known that blood is an extremely sensitive and very informative indicator of the state of the body, which is characterized by rapid dynamics in response to the action of both exogenous and endogenous factors. The corresponding indicators and the speed of their changes are a marker of the state of the animal organism, and can characterize the quality of the environment. To explain the general state of the animal organism, in particular fish, the study of biochemical indicators of blood serum is important, which makes it

possible to obtain adequate data on the physiological state of these hydrobionts [2].

The purpose of the work: to study the effect of T2 toxin on the biochemical parameters of the blood of scaly carp (*Cyprinus carpio* L.) and common crucian carp (*Carassius carassius*) when kept in laboratory conditions.

The study was conducted on sexually mature carp and crucian carp weighing 200–250 g. According to the results of ichthyopathological observations, the causative agents of known parasitic diseases were not detected in hydrobionts. Experiments on the impact of the toxicant were conducted in 200-liter aquariums with settled tap water, in which fish were placed at the rate of 1 specimen per 40 dm3 of water. The adaptation period was 3 days, exposure to the toxicant was 14 days. The temperature regime of the water corresponded to the natural one. The concentration of mycotoxin T2 in aquariums (2 maximum permissible concentrations) was created by introducing the calculated amount of the toxicant. Statistical processing of the results was carried out by generally accepted methods, and the probable difference between the average arithmetic values was determined using the Student's test. Differences between the compared groups were considered probable at $P < 0.05$.

As you know, ammonia, urea, creatinine, indican, etc. are formed as a result of protein catabolism. There is a close relationship between the metabolism of creatinine, which is formed from arginine, glycine, methionine and creatine. It was established that the content of creatinine in the blood serum of carp and crucian carp under the influence of T2 probably decreases by 26.7 and 63.8%, respectively. The maximum changes in the protein content were detected under the influence of T2 in the blood of the crucian carp. The decrease in the content of proteins in the blood serum of animals due to the action of mycotoxin should be explained by the features of their detoxification processes associated with additional energy expenditure, for the recovery of which, in addition to carbohydrates and lipids, certain fractions of proteins are necessary, which are consistent with the previously obtained data [3].

Under the influence of T2, the activity of ALT in fish is suppressed, which may be caused by a change in the direction of the reaction towards the formation of alanine [3; 4]. Under experimental conditions, the activity of AsAT also changes in the blood serum of animals. The value of the studied indicator decreases by 89% in carp and 9% in carp. The processes of redistribution of amino acid reserves and the level of amino acid metabolism under the action of toxicants can be explained by the participation of the studied enzymes in the redistribution of intermediate products of the tricarboxylic acid cycle [4]. First of all, this affects the functional state of the liver, as it reacts to external and internal adverse factors earlier than other organs. Comparing the biochemical changes in the blood of fish of the two species, it can be concluded that greater changes are characteristic of crucian carp compared to carp.

Conclusions. Blood is the most sensitive and dynamic indicator of the living conditions of animals, since changes in biochemical indicators quite clearly reflect the dynamics of the general physiological state of fish. Biochemical indicators of the blood of fish exposed to T2 toxicity indicate general exhaustion and a violation of the protein synthesis function of the fish's liver. The content of mycotoxin in water affects the rate of transamination of amino acids in AlAT and AsAT reactions. In turn, this affects the functional state of the liver, as it reacts to external and internal adverse factors earlier than other organs.

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Application of Modern Bioinformatics Methods to Solve the Problems of Searching For Pathogenic Genes and Proteins of the Dysentery Strain *E. coli O104:H4*

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The research approach of bioinformatics is that it creates a focus on the development and application of computationally intensive methods to achieve this goal. The main efforts of researchers in the field of bioinformatics are aimed at solving the problems of sequence alignment, gene discovery (search for the DNA region encoding genes), genome deciphering, drug design, drug development, protein structure alignment, protein structure prediction, gene expression prediction, and protein-to-protein, search for full gene associations and evolution modeling.

The BLAST system is one of the most widely used sequence search programs in bioinformatics. It addresses a fundamental problem of bioinformatics research. Using a heuristic algorithm is much faster than other approaches, such as calculating the optimal alignment.

The purpose of our research was to study two strains of the laboratory *E.coli strain clinical laboratory strain K12* and pathogenic strain *E. coli O104:H4*. Since both strains are quite well-studied in morphology and physiology, a unique method of comparing the homology (proteins) of the cell walls was provided.

The object of the study was a bioinformative study using modern Internet databases – membrane proteins (surface effectors of TTSS proteins).