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THE TOTAL PROTEIN CONTENT IN THE HEMOLYPH OF *LYMNAEA STAGNALIS* AND *PLANORBARIUS CORNEUS* LIVING IN THE RIVERS OF MOZYR AND GOMEL REGIONS

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Currently, the level of technogenic load on the hydrosphere continues to be high, which causes an increase in the adverse impact on natural reservoirs and their flora and fauna. The status of freshwater ecosystems is estimated with the use of many components of the benthos, including shellfish. The high density of natural populations, lifestyle features (low mobility, feeding mainly on sedimentary detritus and periphyton), and ease of collection make it possible to use gastropods in both passive and active biomonitoring [1].

The study of protein metabolism under the influence of various environmental factors is relevant. These data will allow us to solve current and future ecological problems of the state of natural waters through the study of metabolism and its regulation in lung mollusks with different types of oxygen transport [2].

The aim of the study was to determine the total protein concentration in the hemolymph of two species of freshwater lung mollusks, *Lymnaea stagnalis* and *Planorbarius corneus*.

Material and methods. The Object of the study is pulmonary freshwater mollusks with different types of oxygen transport: copper-containing hemocyanin in pond fish and iron-containing hemoglobin in coils. Experiments were carried out on 36 pulmonary freshwater mollusks divided into two groups: 18 individuals of *Lymnaea stagnalis* (common pond fish) and 18 individuals of *Planorbarius corneus* (horn coil). Shellfish were collected in autumn

(september-october) from reservoirs in two districts of the Gomel region. Each research subgroup contained 9 mollusks.

Findings and their discussion.

Table 1 – shellfish collection location

Shellfish collection area	Collection site	The name of the body of water
Gomel district	Gomel	Lyubenskoye lake
Mozyr district	village Krasnaya Gorka	Pripyat river

Determination of the total protein in the hemolymph was performed by standard biochemical reactions using sets of reagents «Analysis X» (total protein) [3].

Mathematical processing of the obtained results was carried out by methods of parametric and nonparametric statistics using the package of statistical programs Microsoft Excel 2010, STATISTICA 12.5.

The results of determining the total protein content (mg / l) in the hemolymph are shown in table 2.

Table 2 – content of total protein (mg / l) in the hemolymph of lung mollusks depending on the habitat ($M \pm m$)

Shellfish collection area (n=9)	Total protein (mg / l)	
	Planorbarius corneus	*Lymnaea stagnalis*
Mozyr district	26,06±0,43[1]	11,66±0,29[1]
Gomel district	23,21±0,35	13,78±0,16

Note: [1]$p<0,05$ compared to shellfish from the Gomel district

There were no significant differences in the total protein content in the hemolymph of the coils living in the reservoirs of the Mozyr and Gomel regions. The protein content in the hemolymph of pond fish living in the reservoir of the Mozyr region is 1.2 times lower than that of shellfish from the Gomel region.

Conclusion. These values of the total protein content in the hemolymph of freshwater lung mollusks are associated with changes in the composition of the food supply, physical and physiological activity of organisms, and external environmental factors. Based on the obtained data, an algorithm for determining the ecological state of water can be created by analyzing simple and accessible methods for studying the total protein by two parameters — habitat and type of oxygen transport using two model organisms *Lymnaea stagnalis* and *Planorbarius corneus.*

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