

MORPHOLOGICAL AND MOLECULAR-GENETIC ANALYSIS OF THE SPECIES *CORBICULA FLUMINALIS* DISTRIBUTED IN WATER ECOSYSTEMS OF SOUTH UZBEKISTAN

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Abstract. Specimens of the species *Corbicula fluminalis* belonging to the genus *Corbicula* distributed in the water bodies of South Uzbekistan were studied morphologically and molecularly genetically. According to the morphological structure, the species *Corbicula fluminalis* was found to be morphologically different from the species *Corbicula cor* and *Corbicula purpurea*. According to the results of molecular analysis, nucleotides with 660 base pairs belonging to the COI region of mtDNA were isolated from samples of *Corbicula fluminalis* species, and they were compared with *Corbicula fluminea* (KX192335) species in the International Genbank (NCBI) database. As a result, almost no differences were detected between their nucleotides.

Keywords: southern Uzbekistan, mollusk, *Corbicula fluminalis*, area, hydrobionts, molecular, water ecosystem.

INTRODUCTION. The inventory of biological resources and their use in the water ecosystems of South Uzbekistan is an urgent problem of great importance to humanity. At a time when the terrestrial part of the Earth is being widely used, it is important to improve the prospects of using biological resources and protect them, to further improve the lifestyle of the population and to use the existing resources wisely. The sudden change in the ecological situation observed on the globe today is mainly the result of the influence of anthropogenic forces, which affects the bioecological characteristics of the animal world, including the distribution of molluscs, resulting in the loss of their habitats, and this, in turn, changes the population of common species and rare species. and causing the extinction of rare species.

Previous studies have shown that there is a wide range of *Corbicula* species due to the study of genetic diversity, so the purpose of this research work is to make the morphology and molecular identification of *Corbicula fluminalis* distributed in the water ecosystems of South Uzbekistan.

Research methodology. The samples of molluscs belonging to the genus *Corbicula* collected from the Uchkizil reservoir coordinates: N 37°20'27", E 67°12'41" were collected for molecular genetic research. Samples were preserved in 96% ethanol solution and genomic DNA was extracted from them. The GeneJET Genomic DNA (Termofisher.com) reagent kit was used for DNA extraction.

Nucleotide analysis of COI fragments of mitochondrial DNA (mtDNA) from molluscs using primers LCO-1460: GGYCAACAAATCATAAAGATATTGG and HCO-219

TAAACTTCAGGGTGACCAAAAAAATCA (Folmer et al., 1994). Polymerase chain reaction (PTsR) was carried out according to the following scheme: 1 – step – DNA denaturation at 94°C for 5 minutes, 2 – step – DNA denaturation at 95°C for 45 seconds, 3 – step – DNA at 55°C Annealing of primers for 45 seconds, step 4 - elongation at 72°C for 1 minute 40 seconds, step 5 - chain elongation at 72°C for 5 minutes. From the second to the fourth step, the process was repeated up to 35 times in a loop form.

The presence of DNA in PTsR products was determined by electrophoresis on a 1.0% agarose gel with a voltage of 120 V. DNA amplification and DNA extraction from the gel were performed using a set of reagents manufactured by Sileks M (Moscow, Russia) following the manufacturer's instructions [1,2].

In DNA sequencing, ABI PRISM® BigDye™ Terminator v. Reaction products were sequenced at the Genome Center using reagent kit 3.1.

Research results and their analysis. Morphological studies *Corbicula fluminalis* is distributed in the water ecosystems of Tajikistan and Uzbekistan in Central Asia. In the period of research before us, it was collected and analyzed in the Amudarya, Syrdarya, Akhdarya and Karadaryas, in the ditches around the river, in the lakes and ponds around the Mirzachol, Dargom canal, in the Kattakorgan, Mirzachol and Southern Mirzachol canals.

The distribution and density of the water ecosystems of the coastal reservoirs of the rivers of South Uzbekistan were studied for the first time. We found out that it is distributed in Tallimarjon, Tashloksoy, South Surkhan and Uchkizil reservoirs in South Uzbekistan. On average, they are spread from 1.1-1.9 pieces per 1 m² [3,5,6,7].

Shell shape and dimensions. The shell of this species is dark red to dark brown and larger than that of *Corbicila cor*, thick-walled, hard and evenly striated, but less swollen than that of *Corbicila purpurea*, light gray with apex, rounded triangular heart-shaped, shiny. Central teeth 2a, 2v, 3a are two-edged, teeth 3v and 4v are thin and sharp, and side teeth (AII, AIII, PII, PIII) are very long. The inner wall of the shell is purple. The length of the shell of *Corbicula fluminalis* from the Surkhandarya basin was 21.5 mm, the height of the shell was 18 mm, and the thickness of the shell was 12 mm (Fig. 1). The asymmetry of the crown position is not clear. The inner surface of the pallas was light inky, and the outer surface was light brown [4,8,9].

It lives in reservoirs and canals of South Uzbekistan, buried in mud at depths of 4-12 cm. Peloreophil. Co-occurs with *Corbicula cor*. It differs in that the number is relatively small. It is an egg-laying species that begins to breed in the spring as the water temperature rises.



Figure 1. Specimens of *Corbicula fluminalis* species collected from the reservoirs of South Uzbekistan (a. General view of *Corbicula fluminalis*, b. Inner side of shells)

According to the results of our morphological studies, the variability of conchological signs is manifested in the shape, color, thickness, and size of the shell, and the variability of all signs of the shell in the water environment is also dependent on the place of residence and the influence of external environmental factors.

After studying morphologically, the species *Corbicula fluminalis* belonging to the genus *Corbicula*, molecular-genetic studies were conducted on the samples.

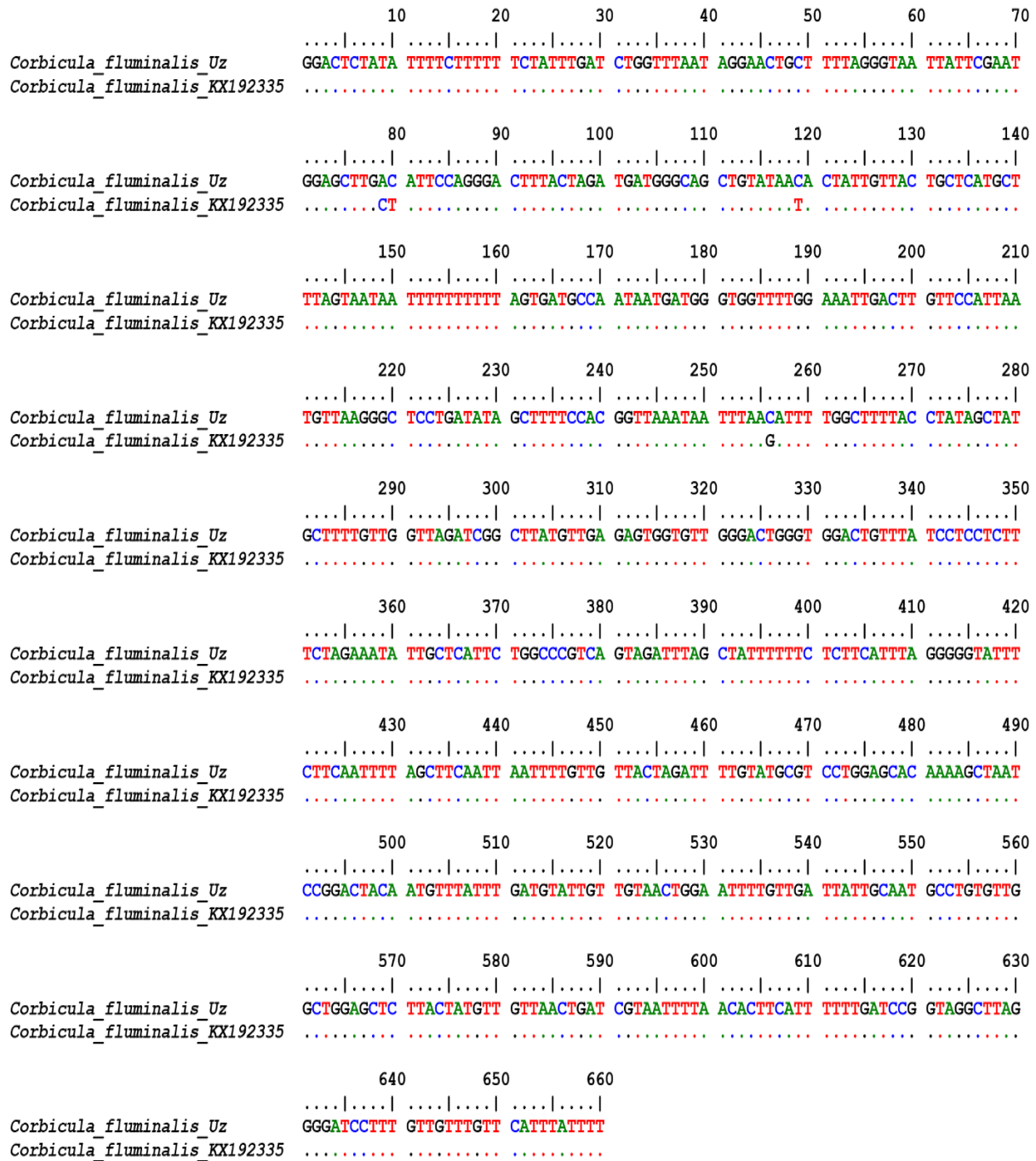


Figure 2. Comparison of the nucleotide sequence of the COI region of the mtDNA of *Corbicula fluminalis* and *C. fluminea* (KX192335) species (in the 5' to 3' direction, identical nucleotide bases are marked with dots).

According to the results of the conducted research, 4 nucleotide differences were detected between the *Corbicula fluminalis* species in the Genbank database and the *C. fluminea* (accession

number: KX192335) species in the Genbank database (Genebank, NCBI) and made up 0.6% of the total nucleotides (2- picture). The differences between these nucleotides are A-denine at the 79th nucleotide in the *C_fluminalis_Uz* sample, and S-cetosine in the *C. fluminea* (accession number: KX192335) sample, and S-cetosine at the 80th and 119th nucleotides in the *C_fluminalis_Uz* sample, and in the *C. fluminea* (accession number: KX192335) sample. T-temin was explained by S-cetosine in *C_fluminalis_Uz* sample, and G-guanine nucleotides in *C. fluminea* (accession number: KX192335) sample at 256 nucleotides.

These obtained data were deposited in the Genbank database of the National Center for Biotechnology Information (Genebank, NCBI) and received the accession number OR233337.

CONCLUSION. According to the results of our conducted morphological studies, the variability of conchological signs is manifested in the shape, color, thickness, and dimensions of the shell, and the variability of all signs of the shell in the water environment is also dependent on the place of residence and the influence of external environmental factors.

According to the results of the conducted molecular genetic research, 660 base pairs of nucleotides belonging to the COI domain of mtDNA were isolated from 3 samples of the species *Corbicula fluminalis* belonging to the genus *Corbicula* collected from different populations, and no differences were found between the nucleotides of these samples.

When the nucleotide sequence of *C. fluminalis* species was compared with the data in the Genbank database, it was found that it was 99.4% similar to the *C. fluminea* species (accession number: KX192335) and was deposited in the National Center for Biotechnology Information Genbank database (Genebank, NCBI) and accession number (OR233337) received.

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