JOURNAL OF MULTIDISCIPLINARY SCIENCES AND INNOVATIONS
VOLUME 04, ISSUE 10
MOPNTHLY JOURNALS
ISSN NUMBER: 2751-4390
IMPACT FACTOR: 9,08

MOLECULAR-GENETIC CLASSIFICATION OF THE SPECIES *LEUCOZONELLA HYPOPHAEA*

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Annotation: This article presents the results of a comparative analysis of the nucleotide sequences of the 18S ribosomal DNA genes of *Leucozonella hypophaea* (Gissarika, Alayiski and Zarafshan).
Key words: *Leucozonella hypophaea*, molecular genetic analysis, 18S ribosomal DNA, nucleotide, genetic polymorphism.
Relevance of the research. The malacofauna of Uzbekistan and adjacent regions has been studied by a number of malacologists, including Z.I.Izzatullayev (1970), A.Pazilov (2003, 2015), A.Karimkulov (2011), F.Gaibnazarova, J.Qudratov, Sh.Abdulazizova, Z.Mahmudjonov, whose works contain information on the taxonomic and zoogeographic composition of land mollusks, ecological characteristics and distribution, processes of conchological variability in widespread species, and economic significance [4,5,7,8].
In some studies [7], molecular genetic analysis of conchologically similar species was performed, and based on differences in nucleotide sequences, it was proven that these species are genetically separate and independent species. However, a literature review has shown that there is no information on the genetic polymorphism of terrestrial mollusks belonging to the same species with a geographically distant and wide range. Therefore, the aim of our study was to determine the genetic polymorphism and analyze the phylogeny of *Leucozonella hypophaea* (Gissarika, Alayiski and Zarafshan) by molecular genetic identification.
The purpose of the study: molecular genetic identification and scientific substantiation of the species *Leucozonella hypophaea* (Gissarika, Alayiski and Zarafshan).
Research materials and methods. The tissue of the species *Leucozonella hypophaea* Gissarika collected from the Hissar mountain range in the southern region of Uzbekistan during 2021-2024, as well as biological materials obtained from the species *Leucozonella hypophaea* Alayiski and *Leucozonella hypophaea* Zarafshan, and molecular genetic data of the land mollusk species *L. rufispirat* PP725472 for comparative analysis were used as research materials. The research work was carried out based on the results of the conducted molecular genetic study (sequence chromatography).
Results and their analysis. The 18S ribosomal DNA of *L. hypophaea* (Gissarika, Alayiski and Zarafshan) species with a length of 608 base pairs was isolated and subjected to molecular genetic analysis. For comparative purposes, the nucleotide sequence of the *L. rufispirata* species belonging to this genus (PP725472) obtained from the NCBI database was used. According to the results of the molecular-genetic comparative analysis, 4 (0.7%) differences were noted between the 18S ribosomal DNA nucleotide sequences of *L. hypophaea* Gissarika and *L. hypophaea* Alayiski, 4 (0.7%) differences between *L. hypophaea* Gissarika and L. hypophaea Zarafshan, and 3 (0.5%) differences between *L. hypophaea* Gissarika and *L. rufispirata* PP725472 obtained from the NCBI database. It was also found that there were 6 (1%) nucleotide differences between the *L. hypophaea* Alayiski and *L. hypophaea* Zarafshan samples, 6 (1%) nucleotide differences between the *L. hypophaea* Alayiski type and the *L. rufispirat* PP725472 sample obtained from the NCBI database, and 4 (0.7%) nucleotide differences between the *L. hypophaea* Zarafshan type and the *L. rufispirat* PP725472 sample obtained from the NCBI database (Figure 1). Studies have shown

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that the genetic polymorphism in 18S ribosomal DNA of *L. hypophaea* species Hissarika, Alayiski, and Zarafshan is 0.7-1%.

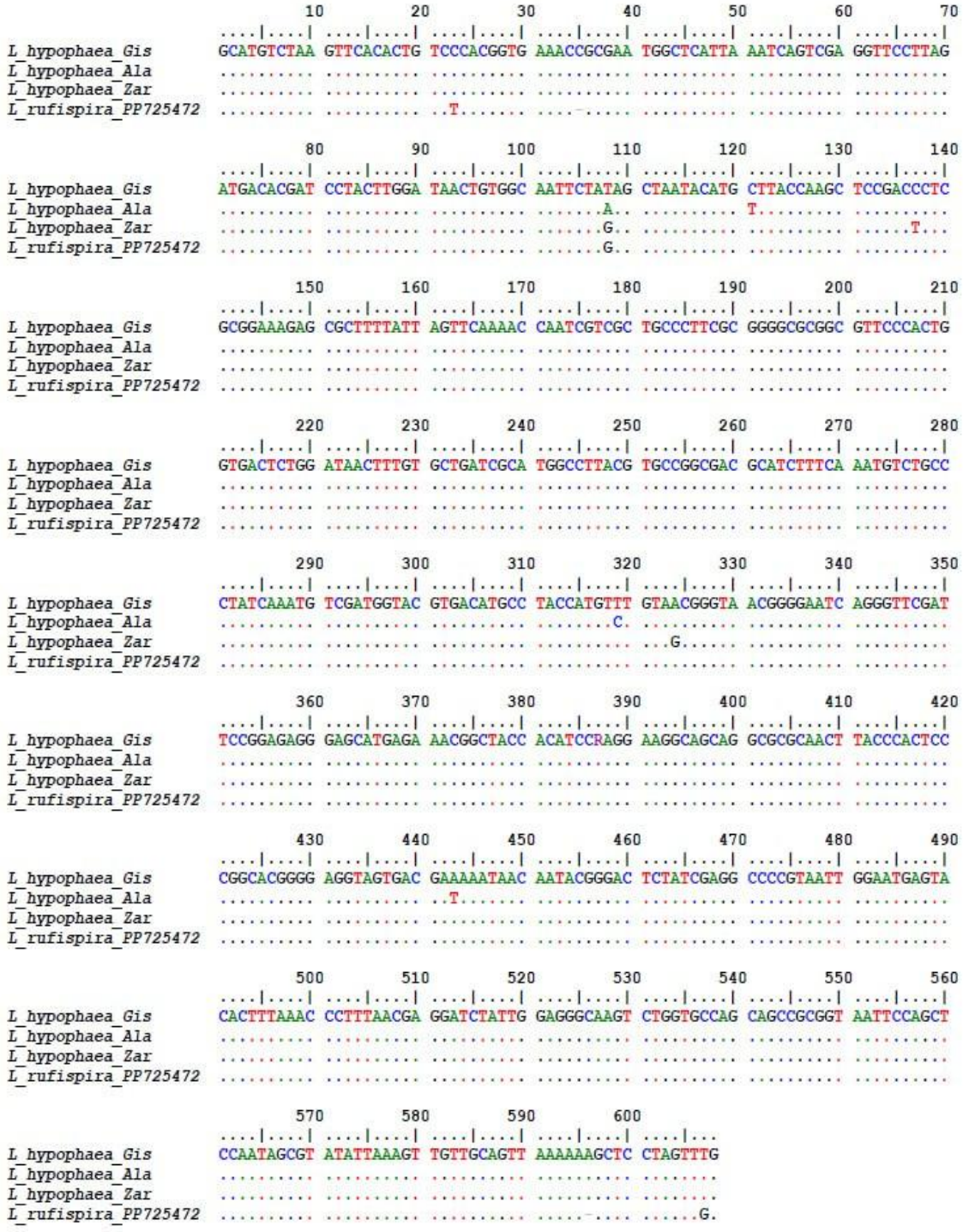

Figure -1. The nucleotide sequence of the 18S domain of ribosomal DNA of *L. hypophaea*, a species distributed in the Hissar, Zarafshan and Aloy mountain ranges

The lack of significant differences between nucleotides in the 18S ribosomal DNA of *L. hypophaea* suggests that this species is a single species with three distinct populations in the Hissar, Zarafshan, and Aloy mountain ranges, exhibiting variability as a result of adaptation to the ecological environment.

Based on the results of the study, the following conclusion was made: the genetic polymorphism in the Hissarika, Alayiski and Zarafshan representatives of the L. hypophaea species is 0.7-1% in 18S ribosomal DNA. These analyses indicate that the Hissarika, Alayiski and Zarafshan representatives of the Leucozonella hypophaea species consist of morphologically distinct, but genetically close populations.

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