

Determination of microbial changes in freshwater mussel *Unio stevenianus* (Krynicky, 1837) living in a river contaminated with sewage and livestock waste by NGS

Ertuğrul Kankaya¹

¹Van Yuzuncu Yil Universitesi Su Urunleri Fakultesi

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Abstract

1. The rise in human population has led to the expansion of settlements and an increase in the types and amounts of wastes released into the aquatic environment. Bivalves have an important place among the invertebrate communities of freshwater environments. Mussels remove suspended substances from the water and contribute significantly to the regulation of the physical properties of water. 2. This study was conducted to determine the microbiome load in the intestinal tissue of the freshwater mussel *Unio stevenianus* (Bivalvia: Unionidae) living in Karasu river. 3. Amplification of the V3-V4 region of the bacterial 16s rRNA gene fragment was performed in tissue samples. Bacterial species were divided into operational taxonomic units using the Kraken metagenomics program. 4. The percentage bacterial distribution with the highest reading sequence at the phylum level was determined as Bacillota > Bacteroidota > Pseudomonadota > Actinomycetota > Cyanobacteriota > Campylobacterota > Fusobacteriota in Arisu samples; while in Zeve samples, it was determined as Pseudomonadota > Actinomycetota > Bacteroidota > Bacillota > Cyanobacteriota > Campylobacterota. 5. The detection of various bacterial phylum indicates that the water environment in which the mussel samples were collected is exposed to a large number of bacterial sources, especially domestic waste. The continued existence of freshwater mussels is necessary for them to fulfill their important duties in the ecosystem. To achieve this, uncontrolled and untreated waste discharges should be abandoned. Pollutants in the water and mussel populations should also be monitored through a monitoring program.

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