

# **METAGENOMIC ANALYSIS OF THE MICROBIOME COMPOSITION OF APHIDS ADELGES (APHRASTASIA) PECTINATAE (HEMIPTERA: ADELGIDAE)**

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Aphids of the genus *Adelges* Vallot, 1836 are insects that feed by phloem sap sucking on host plant species of the conifer family Pinaceae, posing significant threats as pests. Bacteriocyte endosymbionts play a crucial role in the biology and ecology of these insects, residing within the host organism and participating in mutualistic relationships. Two classes of symbiotic bacteria are known in *Adelges* species: Betaproteobacteria and Gammaproteobacteria. In order to profile these symbiotic bacteria, total DNA was extracted from *Adelges (Aphrastasia) pectinatae* (Cholodkovsky, 1888) specimens, and subjected to next generation sequencing of 16S rRNA gene amplicon. Amplicon-based metagenomics targeted V3-V4 variable regions of bacterial 16S rRNA gene. It was determined that the representatives of the phylum Pseudomonadota were the most abundant (93.1

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