

Title: DNA metabarcoding of tissue-associated microbiota in the Baltic blue mussel (*Mytilus trossulus*)

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The host-associated microbial communities (microbiota) in mussels play various important roles and are essential for the overall health of molluscs. They can be responsible for the metabolism of certain chemical compounds, such as nutrients, and protection from diseases; however, they may also cause numerous diseases. The composition of microbiota varies depending on the host species, environmental conditions, or exposure to pollutants. In this study, our aim was to characterise the microbiota of the Baltic blue mussel (*Mytilus trossulus*) through next-generation sequencing. The mussel may host an enzymatic complex able to perform aromatisation (estrogen synthesis from androgens); however, on a genetic level its existence is still not confirmed. It is also possible that microorganisms associated with the mussel tissue play a role in the aromatisation process. Therefore, we collected the gills and gonads from 10 male and female specimens in four different seasons of 2023/2024, from two sites: one impacted by the wastewater treatment plant (a source of exogenous hormones) and a reference site. Each time, together with the mussels, near-bottom water samples were collected. The microbiota was metabarcoded using the 16S V3-V4 marker and taxonomically assigned based on the Silva reference database. Comparative analyses of the taxonomic composition of microbial communities were performed taking into consideration variables such as sex, site, season and microbial community from water. The study presents the first microbiota characterisation in the blue mussel from the Baltic Sea.