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CHARACTERIZATION OF MICROBIAL COMMUNITIES OF THE RS ICS HABITAT USING  
MULTI-SUBSTRATE TESTING METHOD

**Abstract**

The MST method is applied for the first time to microbial communities isolated from the ISS RS habitat. The study of various structural and functional features of microbial communities formed in the internal volumes of the ISS RS allows us to study the species that easily adapt to the habitat conditions under the influence of various cosmophysical factors, to detect previously undetected species of biodegraders and to determine the species of microorganisms existing in favorable interaction with each other.

For the MST method, microbial communities obtained from the internal volumes of the ISS RS during different periods of ISS crew operations were taken. In parallel with MST, a direct seeding method was performed with subsequent identification of the isolated microorganisms using MALDI-TOF mass spectrometry. As a result, microorganisms frequently occurring in the habitat of ISS, such as *Staphylococcus epidermidis*, *Bacillus licheniformis*, *Staphylococcus hominis*, *Staphylococcus saprophyticus* and *Micrococcus luteus*, etc., were identified using the data obtained by the classical sowing method.

During microbiological sowing on various depleted nutrient media of the samples most actively consuming different types of substrates (from the wells of MST plates), such species as *Acinetobacter johnsonii* and *Sphingomonas paucimobilis*, which were not detected earlier by the classical method of sowing on nutrient media of the same samples, were identified for the first time. Representatives of the genus *Acinetobacter* are among the most relevant pathogens of opportunistic infections. As a result of the ongoing work with the isolation of microorganisms using the MST method, it was possible to isolate cultures that are also in the habitat in a non-culturable form or in a quiescent state. From the results of the MST, after photometric measurement of values for all substrates, a data set representing the SPS (substrate consumption spectrum) was obtained. As a result, data were obtained for 8 microbial communities. Based on the SPS, the coefficients of functional diversity of the studied microbial communities were calculated.

As a result, differences were found in functional biodiversity, as well as in the specific metabolic work of the microbial community and the coefficient of substrate rank distribution as a measure of microbial community stability. Four communities out of 8 were found to be the most stable.

This becomes relevant not only for orbital space stations, but also for bases on other objects of the Solar System.