

Microbial Monitoring in the EDEN ISS Greenhouse, a Mobile Test Facility in Antarctica

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The EDEN ISS greenhouse, integrated in two joined containers, is a confined mobile test facility in Antarctica for the development and optimization of new plant cultivation techniques for future space programs. The EDEN ISS greenhouse was used successfully from February to November 2018 for fresh food production for the overwintering crew at the Antarctic Neumayer III station. During the 9 months of operation, samples from the different plants, from the nutrition solution of the aeroponic planting system, and from diverse surfaces within the three different compartments of the container were taken [future exploration greenhouse (FEG), service section (SS), and cold porch (CP)]. Quantity as well as diversity of microorganisms was examined by cultivation. In case of the plant samples, microbial quantities were in a range from 10^2 to 10^4 colony forming units (CFU) per gram plant material. Compared to plants purchased from a German grocery, the produce hosted orders of magnitude more microorganisms than the EDEN ISS plants. The EDEN ISS plant samples contained mainly fungi and a few bacteria. No classical food associated pathogenic microorganism, like *Escherichia* and *Salmonella*, could be found. Probably due to the used cultivation approach, Archaea were not found in the samples. The bioburden in the nutrition solutions increased constantly over time but never reached critical values like 10^2 – 10^3 CFU per 100 mL in irrigation water as it is stated, e.g., for commercial European plant productions. The surface samples revealed high differences in the microbial burden between the greenhouse part of the container and the SS and CP part. However, the numbers of organisms (bacteria and fungi) found in the planted greenhouse were still not critical. The microbial loaded surfaces showed strong temporal as well as spatial fluctuations. In samples of the nutrition solution and the surface, the number of bacteria exceeded the amount of fungi by many times. For identification, 16S rRNA gene sequencing was performed for the isolated prokaryotic organisms. Phylogenetic analyses revealed that the most abundant bacterial phyla were Firmicutes and Actinobacteria. These phyla include plant- and human-associated bacterial species. In general, it could be shown that it is possible to produce edible fresh food in a remote environment and this food is safe for consumption from a microbiological point of view.

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