Abstract

Microorganisms involved in the transformation of nitrogen compounds in wastewater treatment systems form diverse communities influenced by both environmental factors and ecological relationships. Therefore, it is essential to develop new research methods and tools that enable the holistic study of these microecosystems, considering the composition of the population, potential interactions among community members, and the impact of environmental conditions. Thanks to advancements in next-generation sequencing methods and meta-omics techniques, it has become feasible to study microbiomes precisely. Meta-omics methods generate vast amounts of data, and selecting the appropriate information and interpreting it correctly requires a suitable approach. A promising method for analyzing such data may involve examining the correlations of the co-occurrence of different taxa. Correlated taxa can be represented in a network that illustrates the bacterial community structure. Network analysis is particularly beneficial for studying microbial communities in wastewater treatment systems, as it allows for the inclusion of operational factors within the network. This approach enables researchers to observe how changes in various technological parameters affect individual groups of bacteria and to identify which groups contribute most to pollutant removal. The aim of this study was to explore the use of microbial co-occurrence network analysis to investigate the ecological relationships and connections among bacteria involved in nitrogen compound transformation in water and wastewater treatment bioreactors. The research was conducted in reactors differing in usage, biomass type, and operating parameters, which influenced the types of nitrogen transformation processes occurring. Utilizing modern meta-omics analyses provided insights into potential relationships among the members of bacterial communities. This approach allowed for a comprehensive understanding of the taxonomic composition of the environments studied and identified which groups of microorganisms perform key functions. It was observed that, under conditions of limited substrate availability, competitive interactions among bacteria intensify. The ecological significance of nitrifying bacteria was evident in the network structure, with nodes representing these bacteria characterized by high centrality measures. Co-occurrence network analysis presents a promising tool for identifying potential ecological relationships within bacterial populations. A complete understanding of the relationships among functional groups of microorganisms could enhance the control of biological water and wastewater treatment processes in both laboratory and industrial settings in the future.