

Meta-analysis of microbial communities from wastewater-activated sludge

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Traditional mathematical models utilized in wastewater treatment plants (WWTPs) design encounter limitations in accurately characterizing the intricate metabolic functions transpiring within bacterial cells. Nevertheless, the progress in sequencing technologies and computational power has made it easier to study and identify the taxonomic and functional aspects of microorganisms present in wastewater treatment plants (WWTPs). Furthermore, adopting a systems biology approach enables a holistic comprehension of the ecological interactions between microbial communities and their subsequent effects on the efficiency of the treatment process. This study conducted a meta-analysis to identify the core microbial community members of municipal wastewater treatment plants, community diversities across the different regions, and correlations among key microbial families. A mathematical model was developed to represent the relationship between relative abundance and occurrence frequency of microbial families. Principal component analysis and network analysis were used to identify community diversities and microbial correlations. While important microbial species and their relationships were identified, no significant variations were observed among different geographical regions. Through the application of meta-analysis, it is possible to leverage the obtained results to provide a comprehensive understanding of the factors that influence the dynamics of the process.

Keywords: Wastewater, microbial, community, bioinformatics, bacteria