

FEMS-2739 Microbial communities

## TRACKING RELATIONS AMONG BACTERIAL AND PROTOZOAN COMMUNITIES IN WASTEWATER TREATMENT PLANTS

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**Background:** Understanding the interactions between prokaryotic and eukaryotic populations in complex environments can be challenging. Particularly, there is a recognized difficulty in establishing how the interactions between the bacterial and the protozoan populations can affect the performance of wastewater treatment plants (WWTP).

**Objectives:** In order to determine the relationships between microbial communities (protozoa, metazoa and filamentous bacteria) and abiotic parameters (physical-chemical and operational), thirty seven WWTP with activated sludge process were studied in Portugal, during two years, in a trimestral sampling strategy.

**Methods:** Samples were collected to enable a molecular characterization of the microbiota. In order to ensure the diversity of microorganisms, 100 samples were selected based on their geographic localization and time-spaced to track relationships within bacteria and protozoa. A 16S rRNA gene PCR-DGGE approach was carried out for bacterial community fingerprinting. The resulting profiles were analysed together with the results obtained from the survey of the protozoa populations. Finally, the study of the correlations between the physical-chemical and operational parameters and the microbial communities was also investigated.

**Conclusions:** The study of these interactions constitutes a strategy for the understanding of how the different metabolic groups of prokaryotic and protozoa are affected by the relations between this populations, allowing a better prediction of the overall community dynamics. This will allow setting the conditions that better contribute to improve the wastewater treatment while increasing the knowledge of overall communities networking in complex environments.