



INTERACTIONS BETWEEN EUKARYOTIC AND PROKARYOTIC MICROORGANISMS IN ACTIVATED SLUDGE: A MOLECULAR APPROACH TO IMPROVE WASTEWATER TREATMENT

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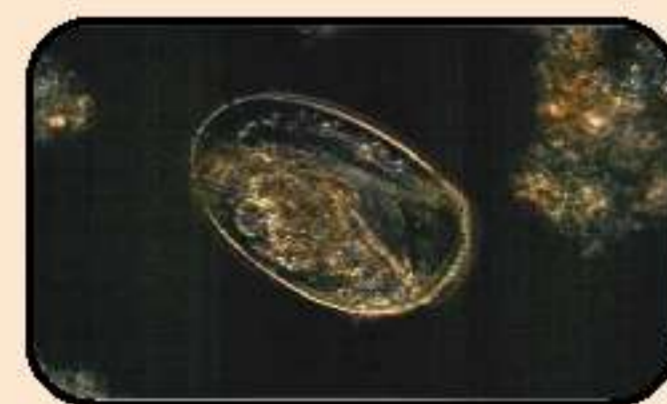
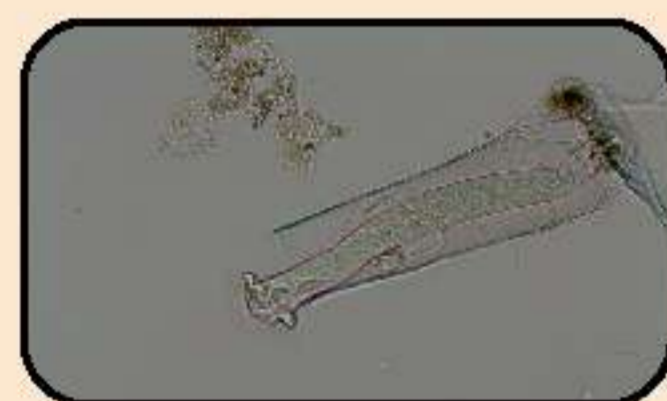
Wastewater and Microorganisms: a World to Discover



- Numbers**
- 3/4 2.4 billion people lack access to any type of sanitation equipment (World Health Organization).
 - 3/4 More than 492 million people in EU generated wastewater, domestic or industrial, a major source of pollution of natural waters.
 - 3/4 In Portugal, 392.8 millions of m³ wastewater were treated; 8.35 million people are covered with wastewater treatment facilities.

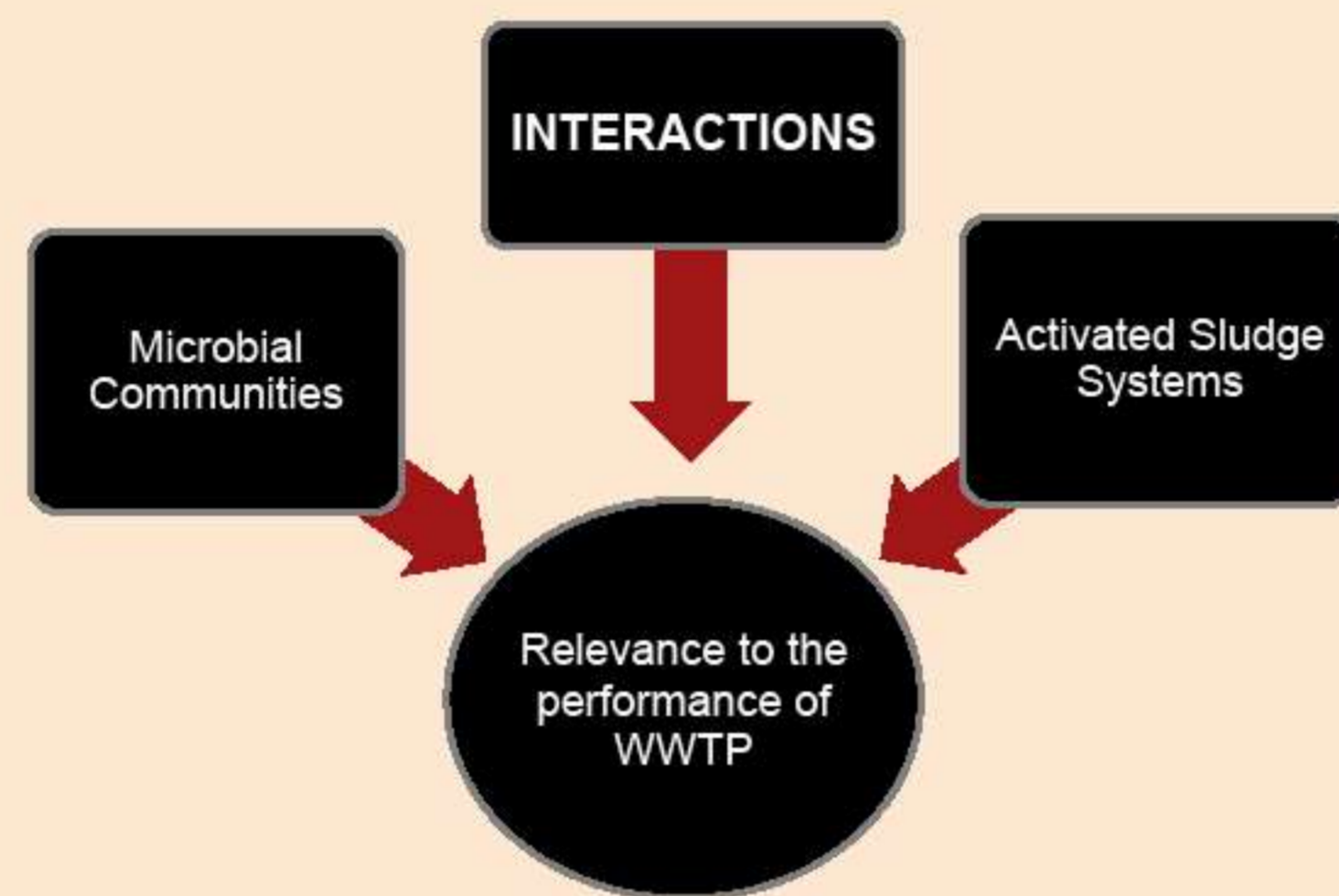
Bacteria clearly play a vital role in the conversion of the wide diversity of organic compounds and in the removal of nitrogen and phosphorus in aquatic ecosystems, particularly in activated sludge.

The role of the protozoa grazers on the prokaryotic populations clearly influence the performance of the treatment system and also lead to a change of the kinetic parameters from one wastewater treatment plant (WWTP) to another.



Several studies have demonstrated the potential of protozoa as bio-indicators of the process performance and effluent quality.

The Research



This research is focused on the interactions between the prokaryotic and the eukaryotic populations of activated sludge systems and on its relevance in the way of how microbial communities are established.

It will contribute to the knowledge of how these interactions can determine or influence the performance of WWTP, leading to a better predicting of the overall community evolution when measures are taken on to improve WWTP performance.



Then... Questions take place

- ? How do the biotic factors, along with the physical-chemical and the operational traits, determine the occurrence of particular groups of the prokaryotic component?
- ? Can the prevalence of the different groups of protozoa and little metazoa be associated with any or some of these prokaryotic groups?
- ? Can the occurrence or dominance of some groups of protozoa be the direct result of abiotic factors, or are they determined by the composition of the prokaryotic populations as well? And to what extend?

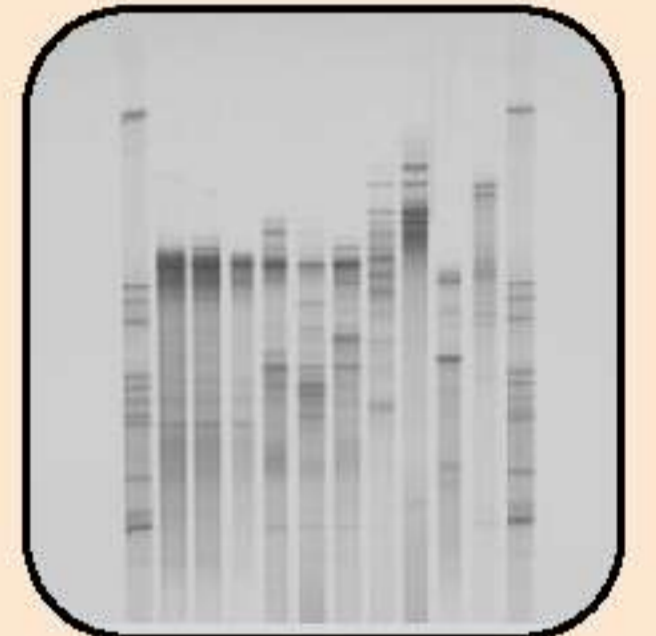
The highly complex microbial communities in WWTP are barely understood, remaining, most of the time, as a "black box". The application of molecular tools in wastewater microbiology has revolutionized our view on the microbial ecology of these systems.

A Molecular Approach

Molecular study of the diversity of the prokaryotic and eukaryotic communities

PCR-DGGE fingerprints

Evaluate the diversity of the prokaryotic component, including the general diversity and the diversity within certain interesting functional groups as the nitrifiers, the denitrifiers and the polyphosphate-accumulating organisms (PAO), the competitors glycogen-accumulating (GAO) organisms or other relevant groups



Gene expression in particular target groups

Real-time PCR

The expression on the functional genes previously used for DGGE will be evaluated in order to correlate the main activities of the target groups with the community composition and WWTP data. Also, it is intended to determine the genes of the eukaryotic community that can be involved with particular environmental conditions.

Predation assays

FISH - fluorescence in situ hybridization

Assays on the predation of eukaryotic populations on particular prokaryotic groups will be made to explore some of the suspected relations between the eukaryotic and the prokaryotic components.

