

## MOLECULAR ANALYSIS OF MICROORGANISMS RESPONSIBLE FOR THE FIRST PHASE OF NITRIFICATION IN AN ANOXIC ENVIRONMENT

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**Abstract:** Ammonia-oxidizing bacteria communities were evaluated in a completely mixed, laboratory scale membrane reactor (MBR) working under anoxic conditions for 5 months. The microorganisms in activated sludge were fed a synthetic medium containing 66-150 mg NH<sub>4</sub><sup>+</sup>-N/l. The age of the activated sludge in MBR was 50 days and the hydraulic retention time (HRT) was 3.3 days. The estimation of the diversity and complexity of the AOB community together with the identification of the dominant bacteria in the activated sludge under anoxic conditions were performed using denaturing gradient gel electrophoresis (DGGE) and DNA sequencing. Molecular analysis of the microbial community carried out with two microbial molecular markers, 16S rRNA gene and *amoA* gene, suggested that nitrification was led by a *Nitrosomonas*-like species. In the biocenosis of the investigated bioreactor, oxygen was the crucial selective parameter. The results obtained in this work showed that *amoA* gene research is more suitable to study the stability and effectiveness of ammonia oxidation. This information emphasizes the necessity of the usage of molecular markers based on functional genes instead of ribosomal ones in order to present the actual state of the process performed in bioreactors. It was also stated that *Nitrosomonas* - like bacteria are able to perform nitrification even in anoxic environment, that is probably the reason why these bacteria are the most common AOB in different bioreactors.