

Development of Phosphate-accumulating microbial community in a sequencing batch reactor (SBR)

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After 150 days of cultivation, a microbial community enriched in phosphate-accumulating organisms (PAO) was obtained in a laboratory bioreactor of sequential-batch action. An analysis of the dynamics of phosphates in the medium and the results of Raman spectroscopy of microbial cells indicated a typical PAO cycle of consumption and release of phosphates during the aerobic and anaerobic periods of cultivation respectively. Analysis of microbial aggregates by FISH revealed a high content of *Ca. Accumulibacter* in it (Fig. 1). *Ca. Accumulibacter* is a typical representative of phosphate-accumulating bacteria.

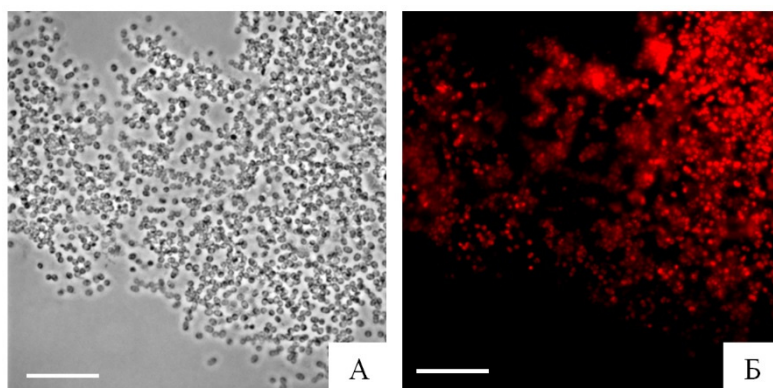


Fig. 1. *Ca. Accumulibacter* as part of the microbial community of aggregates: A – phase contrast, B – cells hybridized with the RAO651 probe (Zeiss 43 light filter). The scale ruler is 20 μ m

Taxonomic analysis of the studied samples revealed a change in bacterial forms in the microbial community during its development. At the initial stage, the Bacteria domain was represented by four main phyla: *Proteobacteria*, *Bacteroidota*, *Chloroflexota*, and *Patescibacteria*, as well as representatives of archaea, with the dominant phylum *Nanoarchaeota*, which accounted for 5.9 % of the total number of representatives of the microorganism community. During the operation of the bioreactor, the proportion of archaea decreased to zero, and representatives of the phylum *Proteobacteria* began to predominate. Their share by 150 days increased by more than 5 times, reaching 68 %. *Proteobacteria* were mainly represented by the genera *Ca. Accumulibacter*, *Ca.*

Competibacter, *Thiothrix*, *Propionivibrio*, *Dechloromonas*, *Thauera*, *Zoogloea*, which are typical for phosphate removal bioreactors [1–4]. Despite the fact that some representatives of these genera are considered phosphate-accumulating microorganisms (*Ca. Accumulibacter*, *Thiothrix*, *Dechloromonas*, *Thauera*), the dominant representative of this physiological group of bacteria was *Ca. Accumulibacter*, the number of which significantly increased compared to the initial activated sludge microbial community from 0.9 to 13 % of all 16S rRNA gene sequences.

Conclusion: Thus, during the operation of the bioreactor, there was a change in the taxonomic composition of activated sludge. By 150 days of cultivation in SBR, a stable functioning phosphate-accumulating microbial community was obtained with a high accumulation of phosphorus in the biomass (16.5 % of the dry weight of the biomass ash-free matter) and accumulation and release of phosphates typical of the PAO phenotype in the aerobic and anaerobic phases of the SBR cycle. The main representative of the PAO in the community was *Ca. accumulibacter*.

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