

Microbial evaluation of full-scale wastewater treatment plants by microscopy survey and chemometric analysis

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Activated sludge (AS) systems, are constituted by living organisms, mainly bacteria (floc-forming and filamentous), protozoa and metazoa. The later play an important role on grazing bacteria, and are known to be dependent on the working operational parameters (incoming effluent, dissolved oxygen, nitrification, hydraulic and sludge retention times, transient phenomena, etc.) and the system itself (conventional activated system – CAS, oxidation ditch – OD, trickling filter – TF, etc.). Floc-forming bacteria, such as aerobic heterotrophic, autotrophic (nitrifying and sulfur-oxidizing), denitrifying, sulfate-reducing and phosphate accumulating bacteria (PAO), are the main organisms responsible for pollution reduction in AS systems. On the other hand, the major role played by filamentous bacteria, rests on the establishment of the microbial aggregates structure, a key feature regarding sludge settling ability.

It is known that AS systems are prone to be affected by bulking, foaming, pin point flocs and dispersed growth occurrences, causing poor sludge settling abilities and affecting the wastewater treatment plant (WWTP) performance. In fact, an excess of filamentous bacteria, resulting in filamentous bulking or foaming events, or a shortage, resulting in dispersed growth or pinpoint flocs formation, leads to settling problems in the secondary clarifier. Furthermore, it is possible to establish a close correlation between the predominance of certain protozoa and metazoa taxa, several AS systems operational and settling problems occurrences.

In a previous study [1] the protozoa (crawling, free-swimming and sessile ciliates, testate amoeba and flagellates) and metazoa communities of three different WWTP types (one OD, four TF and three CAS reactors), were determined in terms of contents and relative abundance. The collected data was further processed by chemometric techniques, such as cross-correlation (CC), principal components (PCA) and decision trees (DT) analyses, allowing to successfully identify, and characterize, the different studied WWTP, and being able, thus, to help diagnosing and solving operational problems. In fact, the protozoa and metazoa based chemometric analyses allowed distinguishing the extended aeration systems (presenting high sessile and crawling ciliates contents), high sludge retention times systems (high metazoa contents), high nitrification abilities systems (highly predominant testate amoeba) and systems presenting transient phenomena (higher contents on flagellates and swimming ciliates).

On the other hand, another study [2] focused on the assessment of foaming events in full-scale WWTPs (one CAS and one OD) by surveying their biota and sludge characteristics. The biota community (protozoa, metazoa and filamentous bacteria) was monitored by microscopic observation and a new filamentous bacteria index was developed to quantify their occurrence. Furthermore, sludge structural characteristics (aggregated and filamentous biomass contents and aggregates size) were also determined (by quantitative image analysis) and further used. The obtained data was then processed by PCA, CC and DT to assess the foaming occurrences. It was found, in this study that such events were best assessed by the combined use of the relative abundance of testate amoeba and nocardioforms filamentous index, presenting an overall 92.9% success rate for foaming events.

References

- [1] Amaral, A.L., Leal, C.S., Vaz, A.I., Vieira, J.C., Quinteiro, A.C., Costa, M.L., Castro, L.M. Assessment of biological wastewater treatment systems by protozoa and metazoa monitoring and chemometrics analysis. *Atas da 16th Conference on Chemometrics in Analytical Chemistry*, (06-10/06/2016), CD-ROM, P-148. Barcelona, 2016.
- [2] Leal, C., Amaral, A.L., Costa, M.L. Microbial based evaluation of foaming events in full-scale wastewater treatment plants by microscopy survey and quantitative image analysis. *Environmental Science and Pollution Research*, 23, 15638–15650, 2016.