

Highlight

Bacteria, archae, fungi and viruses: it takes a community to eliminate waste

José Angel Siles¹ and Carmen Michán^{2*} 

¹Departamento de Química Inorgánica e Ingeniería Química, Universidad de Córdoba, Campus Universitario de Rabanales, edificio Marie Curie C-3, planta baja, 14071 Córdoba, Spain.

²Departamento de Bioquímica y Biología Molecular, Universidad de Córdoba, Campus de Excelencia Internacional Agroalimentario CeIA3, Edificio Severo Ochoa C-6, 2ª Planta, 14071 Córdoba, Spain.

World population growth and the intensification of humans in localized areas have led to the generation of large volumes of highly polluted urban and industrial wastewaters. These residual streams are highly variable in composition and, as such, their disposal represents a serious environmental issue that needs to be solved. The multitude of sources and origins of wastewater (e.g. homes, agriculture, food industry, metalworking) create substantial engineering and scientific challenges for the management and treatment of polluted waters, or for assessing water quality status when trying to meet increasingly stringent legal regulations (Paruch *et al.*, 2019).

Wastewater treatments are usually based on the need to reduce the concentration of organic matter, nitrogen, phosphorus or suspended solids, among other minor pollutants. Among the different techniques available to treat urban wastewater, the first step usually involves the removal by mechanical processes of solid residues of variable dimensions and composition, fat and sand. After this primary settlement, a secondary biological treatment is usually carried out. The most common secondary treatment is the use of activated sludge which allows the removal of biodegradable and soluble organic matter at

low concentration. However, as highlighted in recent publications in Microbial Biotechnology, it has become increasingly popular to treat high chemical oxygen demand (COD) wastes anaerobically in bioreactors because they are usually very efficient, produce a low amount of the final residues and can generate methane as an added value side product (Plugge, 2017; Vyrides *et al.*, 2019). As a result of this additional secondary settlement, a clarified liquid effluent and a concentrated stream in depurative microorganisms (sewage sludge) are generated. A subsequent tertiary treatment (i.e. sorption on activated carbon) can be also applied to the clarified fraction depending on its final composition (Henze *et al.*, 1997).

The development of the chemical and pharmaceutical industries has led to the presence of emerging synthetic pollutants in wastewaters (i.e. analgesics, pesticides), which represents additional disposal problems (Deblonde *et al.*, 2011). Consequently, other kinds of technologies such as advanced oxidation processes (i.e. UV radiation, ozonation, Fenton technology or ultrasonic-based processes) or even filtration through membranes have emerged as promising alternatives for the treatment of industrial wastewaters containing recalcitrant compounds (Melero *et al.*, 2009; Chelme-Ayala *et al.*, 2010; Jianxiong *et al.*, 2011). However, biological processes are the most attractive treatments in terms of economic costs and environmental concerns. Unfortunately, they do not always provide satisfactory results, especially for the treatment of industrial wastewaters, because many of the containing organic substances are toxic or resistant to biological degradation (Lapertot *et al.*, 2006; Oller *et al.*, 2011). One of the best ways to tackle these problems is by improving and applying our knowledge of microbial communities to increase the efficiency in Waste Water Treatment Plants (WWTPs). Consequently, further research on the characterization of the complex microbial populations involved in wastewater processing is essential to improve the global efficiency of the treatment.

One of the key reviews about how microbiology can help to generate more efficient processes, and its application in Anaerobic Digesters (AD) was published in

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*For correspondence. E-mail cmichan@uco.es; Tel. +34 957 218082; Fax +34 957 218688.

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2016 (De Vrieze and Verstraete, 2016). This article shows that: (i) not only the composition of microbial communities is important, but their spatial organization is crucial for the communications between populations; (ii) microbial communication through quorum-sensing and nanowires is also very important for the efficiency of the system; and (iii) organism networks can be analysed at different levels (genes, genomes, interactions between organisms and the whole microbiome). The authors highlighted that one of the main problems when investigating these communities is to assume that their genome relative abundance corresponds to their metabolic activity. Most of the related published studies analyse the metagenomes by 16S rDNA sequencing. This approach has clear limitations because although it indicates the potential of protein synthesis, the real metabolic status of the microbiome and their response to short-term environmental changes may not be revealed, that is despite the low abundance (< 5%) of archaeas in AD, they are estimated to contribute to 30 % of the activity (De Vrieze and Verstraete, 2016). Metatranscriptomic and metaproteomic analysis can improve this approach but while mRNA isolation protocols are available, protein isolation from complex matrixes is still a difficult task. An intermediate solution may be to analyse rRNA which not only identifies the loci taxonomy, but also their protein synthesis potential. In a recent study published in *Microbial Biotechnology* (Langer *et al.*, 2019), the microbiome of nine AD operating under different temperatures or organic rates was analysed. Furthermore, this article not only focused on the bacterial and archaeal populations in the AD, but also on the not so commonly included fungal communities, which have potentially very important roles in anaerobic reactions with high load of fibrous (cellulose) plant material income. The authors showed a correlation between bacterial taxons and high biogas yields, low-temperature processes, organic loading rates or ammonium levels. Moreover, they also showed how archaea can contribute to methane generation by the hydrogen-dependent methylotrophy pathway, and how an astonishing variety of fungal taxa was related to the presence of feedstocks in the AD.

Bacteria, archaea, fungi, but, what about viruses? Are we eliminating pathogenic viruses from our waters? Can they modulate the microbiota of wastewater treatment plants? These and other questions are addressed in an interesting study recently published in *Microbial Biotechnology* about the viral and bacterial communities in WWTPs that used two different processes: biofilm and suspended growth (Petrovich *et al.*, 2019). The authors showed that wastewaters are the habitat for a huge variety of viruses and bacteria. One of the novelties of this study was the identification of both lysogenic and lytic virus in the water samples analysed. Although the same

dominant viral families were present, the viral communities proportion varied depending both on the process and throughout the treatments. The bacteria showed even higher variability, making it difficult to elaborate general protocols to control the efficiency of the treatments (Petrovich *et al.*, 2019). Viruses infecting microbes likely modulate host activities via mortality, horizontal gene transfer and metabolic control. Thus, could we use them to increase WWTP efficiency? They would certainly be a clean and agile way to do so.

Clearly, the real role of all these microorganisms, their interactions and precise influence in the digestion of waste need to be further investigated and validated by other methodologies (e.g. proteomic alterations, metabolic pathways). The more we know, the more we will be able to use bioreactors to diminish the negative consequences of the waste we create.

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Conflict of interest

None declared.

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