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1 Pollutants degradation performance and microbial community structure of aerobic 2 granular sludge systems using inoculums adapted at mild and low temperature

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11

12 Abstract

13 Three aerobic granular sequencing batch reactors were inoculated using different inocula from Finland,
14 Spain and a mix of both in order to investigate the effect over the degradation performance and the
15 microbial community structure. The Finnish inoculum achieved a faster granulation and a higher
16 depollution performance within the first two month of operation. However, after 90 days of operation,
17 similar physico-chemical values were observed. On the other hand, the Real-time PCR showed that *Archaea*
18 diminished from inoculum to granular biomass, while *Bacteria* and *Fungi* numbers remained stable. All
19 granular biomass massive parallel sequencing studies were similar regardless of the inocula from which
20 they formed, as confirmed by singular value decomposition principal coordinates analysis, expected effect
21 size of OTUs, and β -diversity analyses. *Thermoproteaceae*, *Meganema* and a *Trischosporonaceae* members
22 were the dominant phylotypes for the three domains studied. The analysis of oligotype distribution
23 demonstrated that a fungal oligotype was ubiquitous. The dominant OTUs of *Bacteria* were correlated with
24 bioreactors performance. The results obtained determined that the microbial community structure of
25 aerobic granular sludge was similar regardless of their inocula, showing that the granulation of biomass is
26 related to several phylotypes. This will be of future importance for the implementation of aerobic granular
27 sludge to full-scale systems.

28 Keywords: aerobic granular sludge; microbial community dynamics; granulation; inoculum; temperature
29 adaptation

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