Geophysical Research Abstracts
Vol. 20, EGU2018-1848, 2018
EGU General Assembly 2018

Microbial community in a high-elevation wastewater treatment plant

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The high-elevation waste water treatment plants usually cannot reach the required quality of contaminants removal. We hypothesize that extreme natural environment would take responsible for this situation via affecting the microbial community of the sludge. Particularly, we pay more attention to the N-relative microbial communities since N removal is another central demand in the WWTPs. Sludge samples were taken from the WWTP of Lhasa (around 3600 m). The total genomic DNA of sludge was extracted. The 16S rRNA gene of V4-V5 was amplified. Sequencing libraries were set up on an Illumina HiSeq 2500 platform (Illumina, USA). There was a total of 77589 qualified reads. The sequences were grouped into 829 OTUs and 169 genera. These results demonstrated the WWTP of Lhasa had a low microbial diversity. There were 9 abundant genera (>1%), among which Gemmata, Flavobacterium, Dechloromonas, Planctomyces, Zoogloea, Ferruginibacter were commonly found in WWTPs; meanwhile, Candidatus Accumulibacter, Pirellula, and Sulfuritalea indicated relatively high metabolisms of anaerobic processes, phosphate accumulation, and sulphur oxidizing. Besides, Ideonella and Halomonas accounted for 0.70% and 0.52%, respectively. These two genera were considered attitude-dependent and more abundance were found in the high attitude WWTPs. These results indicated that the abundant bacteria group showed they exerted more metabolisms that suitable for extreme environments, such as facultative/ anaerobic, salt-tolerant, altitude-tolerant. In terms of bacteria related to nitrogen cycle, nitrifiers only accounted for 1.98% of the total genera, compared to 17.0% of denitrifiers and/or nitrate reducers and 6.44% nitrogen fixers. These results indicated that natural high altitude can alter the microbial communities in an artificial WWTPs.