## Identification of the most probable causes for filamentous bacteria over-proliferation in Riqqa wastewater treatment plant, Kuwait

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## ABSTRACT

Excessive growth of filamentous bacteria in an activated sludge system is caused by a large number of factors that are related to the influent quality, the system's operating variables and/or the environmental conditions. Identification of the most probable cause(s) is very difficult from a large dataset that contains all of the information about these factors. Riqqa wastewater treatment plant (WWTP), which treats mainly domestic wastewater, is experiencing excessive growth of filamentous bacteria. Mixed liquor samples were collected from the aeration tank of Riqqa WWTP. The dominant filaments were identified using a molecular method called Vermicon Identification Technology (VIT). The significant associations between the filament growth, influent qualities, and operating conditions were then identified using multivariate statistical analysis, namely correlation analysis (ČA) and principal component analysis (PCA). Interestingly, CA has indicated that the abundance of the filaments was directly related to the temperature of wastewater. PCA has identified six factors that account for about 75% of the total variance in the dataset. In addition to confirming CA results, PCA has also indicated that abundance of Nocardioforms actinomycetes and Microthrix parvicella was inversely related to the concentrations of TSS and VSS in the influent. These results are of great importance for controlling the proliferation of filamentous bacteria not only in Riqqa WWTP, but also in other WWTPs situated in hot climates since very little is published about the dynamics of filamentous bacteria in such conditions.

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