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Abundance, Distribution and Diversity of Selected Microbial Groups in Rapid Sand Filters

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Introduction

Biological rapid sand filters are commonly used for drinking water production at thousands of waterworks across Denmark, Europe and worldwide. In general, rapid sand filtration consists of three steps: (a) intense aeration, (b) prefiltration and (c) afterfiltration, and several primary pollutants (e.g. ammonium, iron, methane) from groundwater can be removed by a combination of physico-chemical and biological processes. Although the contribution of microorganisms in the removal of the primary pollutants during post-filtration has been recognised step, the actual microbial composition of these sand filters is poorly documented. Neither is it known whether this microbial removal capacity is due to bacterial and/or archaeal activity and how this capacity is distributed in these rapid sand filters. A better understanding of the microbial community, its abundance, distribution, and its ecophysiological properties might ultimately improve filter management and ensure compliance with increasingly stringent drinking water regulations.

The aim of our work has been, therefore, to increase our knowledge on the abundance, diversity, and spatial distribution of microbial groups responsible for a range of core biological reactions at a set of rapid sand filters across Denmark. Here we report on the results from one reference waterworks. Microorganisms responsible for ammonium-, nitrite-, iron and methane oxidation were quantified at different depths, in different filters, and at different waterworks using a quantitative PCR approach targeting specific phylogenetic or functional genes.

MATERIALS AND METHODS

Sampling Rapid Sand Filters

The filter material was collected at a Danish waterworks, Islevbro, which is supplying drinking water to Copenhagen area. The ground water at the waterworks is subjected to aeration, prefiltration