Prokaryotic communities in drinking water biofilters using alternative filter medium
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INTRODUCTION

Biofilters are often the heart of drinking water treatment systems in Europe [1]. Research in biofilters has contributed to optimize water treatment. Often filter media consist of washed, dried and sieved quartz sand. The function of alternative filter media for drinking filters have been investigated [2–4]. These media include carbon products, ceramics, industrial waste products, and synthetic organics such as plastics, expanded clay, coated sands, and metal oxides. The duration of the start-up process has also been investigated [5–6]. However, the effect that alternative filter media may have on the microbial attachment and development of biofilm and therefore in the duration of the start-up period has received little attention. The overall objective is to investigate the microbial communities on the filter media coating during the start-up of biofilters.

METHODS

The investigations described in this poster were carried out at Fredensborg waterworks near Skanderborg, Denmark. The waterworks treats anaerobic groundwater using a simple process of aeration and filtration (2 filters in series).

Setup

After evaluation of several filter media properties, a filter column of calcium carbonate was selected to remove manganese as an inlet water between the waterworks filters. The water was spiked with manganese to achieve a constant concentration of 0.27 mg L⁻¹.

Water and Filter media samples

Filter medium properties of quartz sand, calcium carbonate, anthracite and manganese oxide were determined using gravimetric methods and a photometric particle analyzer (Camsizer®66, Retsch Technology GmbH). Water samples of the setup inlet (water between filters from the waterworks) were taken during the experiment and analyzed for standard parameters. Water samples (water between the filters and clean water from the waterworks) and filter media samples (second filter of the waterworks and filter column) were collected and analyzed DNA extraction, qPCR with broad range bacterial primers, and amplicon sequencing using 16S rRNA primers. The analysis identified the most abundant amplifiable Phyla and Genera in the samples.

RESULTS

Filter media properties

Water before filtration

Table 2 – Properties of the different filter media.

<table>
<thead>
<tr>
<th>Filter media</th>
<th>Shape</th>
<th>Grain Size (mm)</th>
<th>Porosity</th>
<th>Density</th>
</tr>
</thead>
<tbody>
<tr>
<td>Quarts</td>
<td>0.95</td>
<td>0.38</td>
<td>0.96</td>
<td>1.46</td>
</tr>
<tr>
<td>Calcium carbonate</td>
<td>0.95</td>
<td>1.35</td>
<td>0.80</td>
<td>1.15</td>
</tr>
<tr>
<td>Anthracite</td>
<td>0.94</td>
<td>1.39</td>
<td>0.80</td>
<td>0.44</td>
</tr>
<tr>
<td>Manganese oxide</td>
<td>0.62</td>
<td>1.01</td>
<td>0.80</td>
<td>1.15</td>
</tr>
</tbody>
</table>

DISCUSSION

DNA extraction, qPCR and pyrosequencing results

Table 3 – Sample overview and qPCR results.

<table>
<thead>
<tr>
<th>Sample</th>
<th>Exc DNA</th>
<th>Lon DNA</th>
<th>qPCR</th>
<th>qPCR</th>
<th>Results</th>
</tr>
</thead>
<tbody>
<tr>
<td>7M from Filter 2</td>
<td>1.1</td>
<td>7.6</td>
<td>1.28±0.6</td>
<td>1.4±0.4</td>
<td>WTW 7251</td>
</tr>
<tr>
<td>7M from setup</td>
<td>17.3</td>
<td>44.9</td>
<td>2.3±0.16</td>
<td>1.2±0.15</td>
<td>16122</td>
</tr>
</tbody>
</table>

Figure 3 shows that microbial analyses detected the presence of commonly reported prokaryotic groups: Alphaproteobacteria, Betaproteobacteria, Nitrosomonas, Acidobacteria and Gammaproteobacteria [7].

Pyrosequencing showed attachment of bacteria present in the inoculant, water between filters of the waterworks, on the filter medium surface (Figure 4).

Alphaproteobacteria and Bacteria were much more abundant (2-3 times) on the calcium carbonate column than in the water between filters (used as inlet).

CONCLUSIONS

• After 30 days of start-up, 20% of the manganese in the inlet was removed (contact time of 20 min). Even with low manganese removal, there was a selection for some taxonomic groups on the filter material relative to the inlet.

• 16S rRNA amplicon sequencing showed attachment of bacteria commonly reported as MnOB’s and AOB’s on the medium. These included bacteria present in the inoculant (water between filters). Further, bacteria undetected in the inoculant suggest that other MnOB’s were involved in the coating of the medium, such as: Hyphomicrobium and Hyphomicrobiae.

• Further investigations on microbial communities evolving on different filter media can have great importance for start up and management of biofilters for drinking water treatment.


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